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THE STRUCTURAL CHEMISTRY OF CHOLINERGIC NEURAL TRANSMISSION SYSTEMS

by

Richard J. Radna

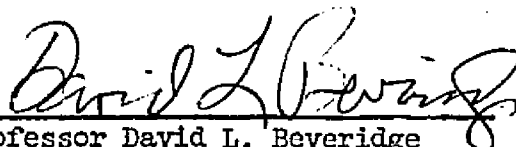
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Professor David L. Beveridge
Chairman of Examining Committee

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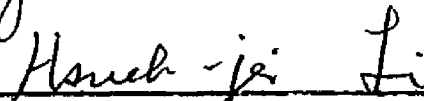
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Abstract

THE STRUCTURAL CHEMISTRY OF CHOLINERGIC NEURAL TRANSMISSION SYSTEMS

by

Richard J. Radna

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The results of INDO molecular orbital calculations on the molecular geometries and electronic structures of acetylcholine, choline, muscarine, nicotine, acetyl- α -methylcholine, acetyl- β -methylcholine^{1,2,3,4} and acetyl- α,β -dimethylcholine are presented. The conformations predicted to be preferred in the free space approximation are discussed in terms of intramolecular interactions, and the calculated potential energy surfaces and electronic charge distributions for each compound are considered in terms of crystallographic, spectroscopic and bio-assay data. Local minima in the potential energy surfaces can be identified with crystal geometries, the geometries implicated in muscarinic and nicotinic neural transmission systems, and the geometry favorable for hydrolysis by acetylcholinesterase. A total consideration of the above results in a biological perspective, and a critical evaluation of the current theories of cholinergic action are presented.

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A. Introduction:

A.1 Objectives. It is the aim of this study to characterize as fully as possible the structural chemistry of acetylcholine (Ach) and a series of its congeners through use of self consistent field (SCF) molecular orbital theory (MOT) at the intermediate neglect of differential overlap (INDO) level of approximation. This work involves the systematic calculation of expectation values for total energy and atomic charge densities as functions of atomic internal displacement coordinates. The potential energies calculated in the free space approximation are used to construct surfaces of conformational energy, and detailed considerations of charge density as a function of conformation are carried out in order that they might provide theoretical evidence for the nature of stabilizing intramolecular interactions. Consideration of theoretical evidence for such interactions is facilitated through the reduction of the expression for total energy into monoatomic and diatomic contributions, (energy breakup). Evaluation is made of the similarities and differences in the above results for selected cholinergic compounds, and the relationship between these results and results reported from x-ray crystallography, molecular spectroscopy and molecular pharmacology is fully developed. Current thought concerning the role of structure and conformation in cholinergic action is developed in the context of accumulated data.

A.2 Background. The transmission of information in neural systems involves the passage of impulses of electrical current throughout a network of nerve cells (neurons). When the membrane potential of a neuron is decreased below a critical level, an action potential mechanism is triggered. The action potential sweeps along the axonal fiber and invades the terminal region of the cell. For impulse propagation, the excitation must then be transferred across the synapse to the next cells in sequence, be they other neurons or operator cells such as those of smooth or striated muscle. In many nervous transmission systems, this transfer is mediated by the liberation of acetylcholine, which according to currently accepted theory interacts with specific receptor sites; the exact sequence of events is still an area of active research. This interaction effects a structural reorganization of the post-synaptic membrane, resulting in an increased ionic permeability. The influx, particularly of sodium ions, depresses the membrane potential below the critical level and initiates an action potential, thereby transmitting the nerve impulse. Acetylcholine is rapidly removed from the synaptic region by an enzyme-catalyzed hydrolysis, allowing the entire process to be repeated at a rate of several hundred times a second for brief periods.

The spatial conformation and electronic structural characteristics of acetylcholine in neurohumoral transmission are specifically complementary to some yet unelucidated structural entity incorporated in the post-synaptic membrane. A number of neurochemically active substances appear to function by adopting geometries and electronic charge distributions resembling those of acetylcholine, and interacting with acetylcholine receptors. Cholinergic receptors have traditionally been characterized

on the basis of the biological activities of these structural analogs of acetylcholine. Data accumulated in this regard make possible a rough differentiation of acetylcholine receptors into two types: muscarinic, where the action of acetylcholine is mimicked by muscarine and blocked by atropine, and nicotinic, where the action of acetylcholine is mimicked by nicotine and inhibited by curare and hexamethonium.^{7,8}

Further classification is no doubt possible since nicotinic receptors in motor endplates and ganglia are preferentially blocked by different methonium compounds,⁵ and some receptors considered nicotinic are not necessarily activated by nicotine.⁹ The evidence with regard to poly-functional active sites complicates matter still further.¹⁰ Nevertheless, the muscarinic/nicotinic terminology is in wide clinical use, and the molecular structural basis of this differentiation, and of the enzymatic hydrolysis of cholinergic substances by the cholinesterases is of considerable importance in molecular pharmacology.

An understanding of all types of cholinergic neural transmission systems clearly requires a detailed knowledge of the molecular electronic structural properties of acetylcholine. For future reference the molecular geometry of acetylcholine can be specified in terms of the four dihedral angles: $\tau(C5-C4-N-C3)$, $\tau(O1-C5-C4-N)$, $\tau(C6-O1-C5-C4)$ and $\tau(O2-C6-O1-C5)$, defined with respect to the numbering system given in Fig. 1. In the crystal structures of a large number of Ach analogs, the coordinates $\tau(C5-C4-N-C3)$ and $\tau(O2-C6-O1-C5)$ are observed to be antiplanar and synplanar respectively.⁸ Interesting variations are found in $\tau(O1-C5-C4-N)$, which positions the ester oxygen with respect to the trimethylammonium cationic head, and in $\tau(C6-O1-C5-C4)$, which positions the acetate moiety with respect to the choline group.

The crystal structure of acetylcholine bromide has been investigated by Canepa, Pauling and Sörum following up earlier work by Sörum; the geometry reported is shown in Fig. 1. The C5-C4-N-C3 sequence of atoms does form an antiplanar extended chain, $\angle(C5-C4-N-C3) = 180^\circ$, as expected on the basis of steric factors. The acetoxy group is planar with $\angle(O2-C6-O1-C5) = 0^\circ$, presumably stabilized by the partial double bond character of the C6-O1 bond. Since no large variation in $\angle(C5-C4-N-C3)$ or $\angle(O2-C6-O1-C5)$ is observed over the crystal geometries of a number of Ach's structural analogs, specification of the geometry of Ach in terms of $\angle(O1-C5-C4-N)$ and $\angle(C6-O1-C5-C4)$ is sufficient to characterize the three dimensional molecular structure. In the geometry reported for acetylcholine bromide, $\angle(O1-C5-C4-N) = 77^\circ$ and $\angle(C6-O1-C5-C4) = 79^\circ$, henceforth denoted as $\{77^\circ, 79^\circ\}$. The structure of acetylcholine chloride was reported by Herdtklotz and Sass as $\{85^\circ, -168^\circ\}$. The nature of the forces stabilizing $\angle(O1-C5-C4-N)$ in a synclinal conformation is of considerable interest, since an antiplanar form would be favored from purely steric considerations. The possibility of intramolecular N-C-H \cdots O hydrogen bonding in this structure was originally suggested by Sutor based on the proximity of the trimethylammonium hydrogens and ester oxygen. A number of laboratory investigations have been directed toward gaining infrared spectroscopic evidence with regard to intramolecular hydrogen bonding. No strong supportive data have been reported, but the collected results are not inconsistent with such interactions. Culvenor and Ham report nuclear magnetic resonance spin coupling evidence that a synclinal conformation of $\angle(O1-C5-C4-N)$ persists in aqueous solution as well as in the crystalline solids, but specific intramolecular hydrogen bonding was unresolvable. In a lively review, Donahue discounts collected evidence for intramolecular C-H \cdots O hydrogen bonding on the grounds

that unequivocally observed C-H...O distances are not appreciably less than the expected van der Waals contact distance of 2.5-2.6Å.

Theoretical calculations of the conformational stability of acetylcholine have been reported by Liquori, Damiani and de Coen using pairwise interaction potential functions and by Kier using extended Hückel molecular orbital theory (EHT). Four energy minima in a four dimensional potential energy hypersurface were found in the Liquori et al. analysis; two minima involve antiplanar conformations of $\angle(OL-C5-C4-N)$ and two favor synclinal conformations around this coordinate. EHT gives a positive synclinal $\angle(OL-C5-C4-N)$ of 80°.

The angle $\angle(C6-OL-C5-C4)$ specifies the orientation of the acetoxy group with respect to the rest of the molecule. This angle establishes another geometrical parameter important for biological activity: the distance between the trimethylammonium cationic head and the electronegative carbonyl oxygen atom. Early studies of Ach and related compounds established this distance as ca. 4.5Å; this played a key role in the design of a drug (pyridine-2-aldoxime methiodide, PAM) to interact with the acetylcholine receptor on acetylcholinesterase. PAM is now used clinically to treat alkyl fluorophosphate poisoning.

In crystalline acetylcholine bromide with $\angle(C6-OL-C5-C4)$ at 79°, the acetoxy group is folded around toward the cationic head. For acetylcholine in solution, infrared spectral studies of the carbonyl vibrational frequency of acetylcholine and related compounds have been reported, but the structural implications are inconclusive. The nmr spectral data for acetylcholine in D₂O support an antiplanar conformation, as normally expected for a primary ester. Two of the four minima on the Liquori energy surface correspond to antiplanar

$\tau(\text{C6-O1-C5-C4})$ as does the geometry reported for EHT calculations.

Most recently, the investigation of conformational aspects of acetylcholine has focused on the coordinate $\tau(\text{O1-C5-C4-N})$.¹⁶ Subsequent to the Culvenor and Ham study, methylene proton spin coupling analyses of nmr spectra of acetylcholine have been reported²¹ by Cushley and Mautner,²² Casy, Hassan and Wu,²³ Inch, Chittenden and Dean,²⁴ and Partington, Feeney and Burgen. There is unanimous agreement that $\tau(\text{O1-C5-C4-N})$ is synclinal in aqueous solution. The detailed analysis of Partington et al. shows the system exclusively with this orientation.²² Casy et al. report synclinal values of $\tau(\text{O1-C5-C4-N})$ for a range of solvents, with chloroform the least polar. They concluded that the energetically preferred conformation on this coordinate was established by intramolecular interactions.

Muscarine and nicotine each have recognizable analogs of $\tau(\text{O1-C5-C4-N})$ and $\tau(\text{C6-O1-C5-C4})$ with asymmetrically substituted atoms imparting a possible degree of stereospecificity. The active form of muscarine was determined by Waser²⁵ to be the C6(S),C9(R),C5(S) isomer shown in Fig. 3. The crystal geometry for this isomer as determined by Jellinek²⁶ corresponds to $\{74^\circ, 144^\circ\}$. For nicotine, the naturally occurring²⁷ 2(S) isomer has been demonstrated by Barlow and Hamilton to be more active than the 2(R) form, but the difference in activity depended somewhat on the preparation. The crystal structure of nicotine-1(R), 2(S)-dihydroiodide as determined by Koo and Kim,²⁸ and given in Fig. 4, corresponds to the $\{-60^\circ, 180^\circ\}$ geometry. Theoretical calculations on muscarine have been described by Liquori²⁹ using empirical classical energy calculations,¹⁹ and for muscarine and nicotine by Kier and Pullman³⁰ using molecular quantum mechanics.

Many other cholinergic substances bear obvious structural similarities to Ach and usually have clearly defined analogs of $\tau(01-C5-C4-N)$ and $\tau(06-01-C5-C4)$. Recent papers dealing with the structural basis of cholinergic action are due to Kier, Pauling, Chothia and coworkers, and Beers and Reich; the area has recently been reviewed by Shefter. The proposed theories differ mainly in relative emphasis on functional groups and molecular conformation. The trimethylammonium group is generally accepted as a primary effector in both muscarinic and nicotinic action. The ideas that the ester oxygen of Ach (or its equivalent in a structural analog) figures in muscarinic activity whereas the carbonyl oxygen of Ach or its equivalent is pertinent to nicotinic action are evident in early work in this area. Kier studied the role of conformation by comparing the molecular structure of Ach with muscarine, muscarone and nicotine. He proposed that the geometry of Ach at nicotinic receptors differs from that at muscarinic receptors, and appears to implicate the Ach carbonyl oxygen in muscarinic activity. From Fig. 4 of Ref. 31, his muscarinic conformer appears to be $\{-sc,ap\}$ with $\tau(02-C6-01-C5) = 0^\circ$; his nicotinic Ach conformer, Fig. 12 of Ref. 31, is $\{-sc,ap\}$ with $\tau(02-C6-01-C5) = -90^\circ$.

Chothia and Pauling correlated the crystal structure analyses of six nicotinic agonists and proposed the Ach geometry implicated in nicotinic action to be $\{75^\circ, 180^\circ\}$. Baker, Chothia, Pauling and Petcher considered ten muscarinic agonists of varying potency, and concluded that the Ach geometry complementary to muscarinic receptors was $\{85^\circ, 150^\circ\}$. The acetate methyl group but not the carbonyl oxygen was implicated in the muscarinic pharmacophore. The resonance energy stabilizing a synplanar orientation of $\tau(02-C6-01-C5)$ was presented as 24 kcal/mol, which would preclude the geometry proposed by Kier for

the nicotinic pharmacophore. Earlier Chothia, reasoning from the observation that the muscarinic and nicotinic Ach geometries were nearly the same, identified the side of Ach having the cationic head, acetate methyl group and ester oxygen on the periphery with muscarinic action, and the side with the cationic head and carbonyl oxygen on the periphery with nicotinic activity. The basis for these conclusions rested on the blocking actions of C4 and C5 substituents, which presumably interfere with the agonist-receptor interaction. Related studies by Chothia³⁷ and Pauling describe collected evidence that a $\{150^\circ, 180^\circ\}$ geometry is optimal for the hydrolysis of Ach by acetylcholinesterase,³⁸ consistent with the model proposed by Krupka and Laidler.

³⁴ Beers and Reich presented structural correlations of twelve muscarinics and eight nicotinic in support of the role of the cationic head and ester oxygen in muscarinic action, and the cationic head and carbonyl oxygen in nicotinic action. The presence of the acetate methyl group or its equivalent was not necessary for muscarinic action, but when present seemed to potentiate the effect. No role for a carbonyl oxygen in muscarinic action was indicated. The correlations were based on possible conformations deduced from molecular models, rather than from consideration of experimentally observed or calculated preferred structures.

⁸⁰ Studies by Smissman et al. on rigid ring analogs of acetylcholine and other cholinergic substances implicate an antipolar $\tau(01-C5-C4-N)$ in muscarinic activity.

Of all the cholinergic substances considered in the correlations described above, the compounds most closely related to Ach but with more specific activities are the α and β methyl and dimethyl Ach derivatives.

Considerable structural information is available on each compound. In addition, this set of compounds includes significant possible exceptions to each of the theories previously described. The methyl and dimethyl derivatives of Ach figure significantly in current structural theories of cholinergic action; but the actual roles of the α and β methyl groups are not clearly established. There are several mechanisms by which a change such as addition of a substituent methyl group to a neurotransmitter may influence its biological activity. The substituent may sterically prevent the compound from accessing a biologically active conformation which properly orients the functional groups, or electronically influence the position of preferred conformations. Alternatively, the substituent group may conceivably cause a charge redistribution on functional groups leading to either enhancement or decrease in biological activity. Finally, it is possible for substituent groups to have direct bonded or non-bonded interactions with biological receptors. Such interactions might be of a steric, hydrophobic or electrostatic nature, and might enhance or diminish biological activity.

The crystal structure analysis of acetyl- α (R)-methylcholine³⁹ by Chothia and Pauling revealed two polymorphic forms, $\{90^\circ, 170^\circ\}$ and $\{212^\circ, 176^\circ\}$ ³⁶. In Chothia's theory the α (R) substituent blocks the methyl(muscarinic) side, leaving the nicotinic side available. Acetyl- α (R)-methylcholine is indeed a nicotinic agonist, but according to Lesser⁹ so is acetyl- α (S)-methylcholine, wherein the carbonyl (nicotinic) side of Ach would be at least partially blocked. The active enantiomer of the β -methyl derivative as determined by Ellenbroek and van Rossum and Beckett,⁴⁰ Harper and Clitherow⁴¹ is

acetyl- β (S)-methylcholine, which Chothia and Pauling have found to be in the $\{85^\circ, 203^\circ\}$ conformation in the crystalline solid. Beckett et al. observed that the β (R) derivative is not hydrolyzed by acetylcholinesterase, and inferred that a positive orientation of $\hat{\gamma}(O1-C5-C4-N)$ is complementary to the cholinesterase receptor; this is not inconsistent with the (+)-antiperiplanar form proposed by Pauling and Chothia. Casy, Hassan and Wu presented nuclear magnetic resonance data showing that a $\{sc, ap\}$ conformation of acetyl- β -methylcholine in solution, while a lack of conformational preference was reported for $\hat{\gamma}(O1-C5-C4-N)$ in acetyl- α -methylcholine.

The pharmacological properties of erythro and threo dimethylacetylcholine have been studied by Smigman, Nelson, LaPridus, and Day. The erythro(\pm) derivative has 10% the muscarinic activity of Ach, and is negligibly hydrolyzed by cholinesterase, whereas the threo(\pm) derivative shows negligible muscarinic activity and 10% the hydrolysis rate of Ach. The crystallography of erythro- α (S), β (R)- and threo- α (R), α (R)-dimethylacetylcholine was determined to be $\{284^\circ, 155^\circ\}$ and $\{217^\circ, 95^\circ\}$ respectively. Shefter tested the Chothia theory with these compounds and pointed out that whereas the muscarinic side would be predicted to be blocked in erythro- α (R), β (S)-dimethylacetylcholine and open in threo- α (S), β (S)-dimethylacetylcholine, the erythro isomer is observed to be a more potent muscarinic agonist. All of the methyl and dimethyl derivatives possess the functional groups necessary for dual muscarinic and nicotinic action along the lines described by Beers and Reich; the observed specificity indicates that these conditions can be necessary but not sufficient for agonist action.

Conformational energy maps as functions of $\tau(01-C5-C4-N)$
and $\tau(C6-01-C5-C4)$ for acetyl- α -methylcholine, acetyl- β -methylcholine,
and acetyl- α, β -dimethylcholine as well as for Ach itself have
recently been contributed by Pullman et al.^{46,47} using the PCILO-CNDO
method. These studies⁴⁸ as well as the recent theoretical calculations⁴⁹
on Ach by Ajo et al. and Froimowitz and Gans⁵⁰ using pairwise potential⁵¹
functions, and by Genson and Cristofferson and Port and Pullman using
non-empirical theoretical methods will be discussed with the presentation
of the INDO results.

A.3 Rationale. As described in the preceding section, the relationship for cholinergic agonists between structure, conformation and biological activity has been studied through means of x-ray crystallography, molecular spectroscopy, molecular quantum mechanics and bio-assay techniques. At the outset of the thesis research described herein, however, the stabilization of $\gamma(OL-C5-C4-N)$ in cholinergic compounds was incompletely understood, and several geometries for Ach and cholinergic agonists were implicated in the crystalline solid, solution and in the theoretical free space approximation. Thus a total energy minimization of Ach as a function of conformation was in order. The aim here was to locate energy minima in the surface, to develop an understanding of the minima in terms of structural forces, and to consider the relationship between the calculated minima and molecular geometries considered in experimental studies.

Examination of Fig. 1 shows that if bond lengths and angles for heavy atoms are directly adopted from crystallographic data, and if hydrogen bond lengths and angles are assumed to be standard, conformational designation of Ach reduces to an 8 parameter problem: $\gamma(C5-C4-N-C3)$, $\gamma(OL-C5-C4-N)$, $\gamma(C6-O1-C5-C4)$, $\gamma(O2-C6-O1-C5)$ and the four dihedral angles which position the methyl hydrogens of the acetate and trimethylammonium groups. It has been noted in the preceding section that $\gamma(C5-C4-N-C3)$ and $\gamma(O2-C6-O1-C5)$ can be taken to be antiplanar and synplanar respectively, based upon the crystallographic results on a large number of cholinergic compounds. The validity of these assumptions are readily confirmed by INDO MOT. The methyl hydrogens are expected to be freely rotating in a biological solution but should be positioned at a minimum energy configuration for input

to the INDO wavefunction routine. This configuration of methyl hydrogens can be determined through study of Ach and model compounds such as tetramethylammonium (TMA) and choline.² Thus with six parameters fixed, a total energy minimization of Ach reduces to a consideration of $\psi(01-C5-C4-N)$ and $\psi(06-01-C5-C4)$. Accordingly the INDO potential energy surface of Ach as a function of $\psi(01-C5-C4-N)$ and $\psi(06-01-C5-C4)$ ^{1,3} was generated. Accumulated data were studied both in terms of basic stereochemical principles, and the conformations of Ach proposed to be active at cholinergic receptors. Further characterization of the nature of the intramolecular forces stabilizing a gauche conformation of the cholinergic O-C-C-N group is developed through study of the model compound choline with an energy breakup.²

With the molecular electronic structure of acetylcholine well characterized on a theoretical basis, the next logical step in an approach to a comprehensive theoretical treatment of cholinergic neural transmission systems involves a systematic study of the potential energy surfaces and electronic structures of nicotinic and muscarinic substances at a comparable level of approximation, and a detailed consideration of the similarities and differences between energetically preferred conformations of cholinergic substances and those found for acetylcholine. The α and β methyl derivatives of Ach are of particular interest in this regard, and thus are subjected to systematic study in terms of conformational energy and atomic charge densities.³ The structural similarities and differences of these muscarinic and nicotinic substances should manifest themselves naturally from this approach, and the energetically preferred conformations should match with the analogous local minima on the Ach potential surface. Theories currently offered on the

structural chemistry of cholinergic action may be constructively criticized on this basis, and reorganized to a more comprehensive form.

B. Specific Aims:

The specific aims of this study are as follows:

1. The quantum theoretical calculation of Ach's $\uparrow(01-C5-C4-N)$ vs. $\uparrow(C6-01-C5-C4)$ potential energy surface and molecular electronic structure using approximate SCF MOT including all valence electrons.
 - a. Methyl hydrogens are positioned through preliminary calculations on Ach, choline and TMA.
 - b. The symplanar orientation of $\uparrow(02-C6-01-C5)$ is confirmed through calculation of a preliminary INDO potential energy surface as a function of $\uparrow(02-C6-01-C5)$ and $\uparrow(C6-01-C5-C4)$, ($\uparrow(01-C5-C4-N)$ is held antiplanar).
2. Consideration of the above results in terms of basic stereochemical principles, and specific evaluation of intramolecular interactions which stabilize the gauche orientation of the O-C-C-N group in the model cholinergic compound choline. The latter is accomplished through use of an energy breakup.
3. The calculation of potential energy surfaces and profiles, and atomic charge densities analogous to those generated for Ach for the compounds:
 - muscarine
 - nicotine
 - acetyl- α -methylcholine
 - acetyl- β -methylcholine
 - erythro- α, β -dimethylacetylcholine
 - threo- α, β -dimethylacetylcholine.
4. The computerized plotting of the potential energy surfaces for accurate presentation and location of minima, and the computerized stereographic display of energetically preferred conformations of each substance under consideration..
5. A detailed development of the relationship between the results of the quantum theoretical calculations and results reported from x-ray crystallography and molecular spectroscopy for each molecule.
6. A detailed comparison and correlation of energetically preferred conformations of the muscarinic compounds, the nicotinic compounds, and of the preferred muscarinic and nicotinic conformations with Ach conformations corresponding to minima on the Ach potential energy surface.
7. Total consideration of the above results in a biological perspective and a critical evaluation and reconsideration of current theories of the structural chemistry of cholinergic action.

C. Methods and Theory:

The calculation of a potential energy surface for a molecule involves the calculation of the total energy of the system as a function of internal atomic displacement coordinates. In quantum mechanical systems, the energy is an expectation value of the Hamiltonian operator and molecular wavefunction, and thus a calculation of the wavefunction at a number of points in configuration space is required. For the Hamiltonian operator H and molecular wavefunction Ψ energy is given as

$$E = \int \Psi H \Psi d\tau \quad (1)$$

Molecular wavefunctions computed in this research are based on spin-restricted molecular orbital theory, with the $2n$ -electron wave function Ψ considered as a Slater determinant of the molecular orbitals ψ_i

$$\Psi = |\psi_1(1)\bar{\psi}_1(2)\psi_2(3)\bar{\psi}_2(4)\cdots\psi_n(2n-1)\bar{\psi}_n(2n)| \quad (2)$$

The molecular orbitals are individually expanded as linear combinations of atomic orbitals (LCAO) ϕ_{μ} centered on constituent atoms

$$\psi_i = \sum_{\mu} c_{\mu i} \phi_{\mu} \quad (3)$$

where the $c_{\mu i}$ are linear expansion coefficients. The calculation of the molecular wavefunction reduces to the determination of the coefficients by matrix Hartree-Fock self-consistent field procedures. The total energy of the system at a given geometry is given by the expression

$$E = \sum_{\mu\nu} \sum_{\mu'\nu'} (H_{\mu\nu} + G_{\mu\nu}) + \sum_{A<B} \sum_{R} \sum_{AB} Z_A Z_B R_{AB}^{-1} \quad (4)$$

where the summations over greek and latin letters refer to orbitals and atoms respectively. The first term on the right hand side of equation 4 is the electronic energy of the system and involves $H_{\mu\gamma}$, the one-electron matrix elements between atomic orbitals ϕ_{μ} and ϕ_{γ} , and is representative of the kinetic and nuclear attraction operators. The $G_{\mu\gamma}$ are elements of the matrix representative of electron repulsion operators. The density matrix elements $P_{\mu\gamma}$ are defined in terms of the LCAO coefficients as

$$P_{\mu\gamma} = 2 \sum_i^n c_{\mu i} c_{\gamma i} \quad (5)$$

and specify the distribution of electronic charge in the system. The second term on the right side of equation 4 accounts for internuclear repulsions, and involves the core charges Z_A , Z_B and the internuclear separation between atoms A and B, R_{AB} .

Theoretical studies of neurotransmitter structure have used methods ranging from empirical pairwise potential functions to a variety of approaches based on molecular quantum mechanics. The quantum mechanical methods currently being used treat σ and π electrons explicitly, and fall into four basic categories: approximate independent molecular orbital theory, approximate self consistent field molecular orbital theory, approximate configurational interaction (CI) methods and ab initio SCF-MO methods.

In calculating electronic wavefunctions, one considers simultaneously the attractive between electrons and atomic nuclei of a molecule and the interelectron repulsions in the framework of molecular orbital theory. However, the size of the mathematical problem goes up as least as N^4 , where N is the number of electrons.

Thus for large bio-organic molecules the calculation of precise wavefunctions is beyond the time limitations of our present generation of computers. In view of this, considerable effort has been devoted to developing molecular orbital methods capable of treating large organic and bio-organic molecules with sufficient accuracy to provide the information necessary for the treatment of scientific problems in chemistry and molecular biology. The quantum mechanical methods which are currently being used are mentioned above, and these methods as well as those used in early work are discussed in the following paragraphs.

Approximate molecular orbital theories began with methods limited to pi-electrons of unsaturated molecules such as in Hückel theory, which has been extensively applied to problems in biochemistry by Pullman and collaborators. Methods of this type have often been criticized on the grounds of giving too many approximations to be a basis for reliable theory, since inter-electron repulsions are neglected. A more refined approach to pi-electron theory including inter-electron repulsion in a self-consistent field manner was introduced by Pariser, Parr and Pople and has been highly successful in accounting especially for the wavelengths of electron absorption bands in ultraviolet spectra. The consideration of all chemically effective electrons in a molecule in approximate molecular orbital theory was developed in the form of Extended Hückel Theory by Hoffman but is subject to criticism with regard to inter-electron repulsions, just as was simple Hückel theory. EHT falls into the category of approximate independent electron molecular orbital theory and has been widely used by Hoffman in innovative studies of organic reaction mechanisms. The quantitative application of this method to conformational

problems has proved less successful, with bond lengths sometimes unreliable, and bond angles and dihedral angles giving some reasonable agreement with experiment in certain systems. The well known limitations of independent electron molecular orbital theory in treating heteroatomic systems is a special disadvantage for neurotransmitter structures, as evidenced in the molecular electronic charge distributions computed using EHT.¹⁹

Self-consistent field molecular orbital theory has provided a framework for the development of a series of approximate methods for theoretical studies of polyatomic molecules. The principle approximations are the neglect of differential overlap in two-electron repulsion integrals, and a semi-empirical parameterization of certain one electron integrals. Valence electron SCF theories involving complete neglect of differential overlap (CNDO) and intermediate neglect of differential overlap (INDO), where differential overlap is neglected only in polycentric electron repulsion integrals were developed by Pople, Segal, Santry, Beveridge and Dobosh,^{59,60} and parameterized for elements of the first row of the periodic table. Generally these methods produce good electronic charge distributions as evidenced by the agreement between theory and experiment for electric dipole moments,⁵³ and they are among the best approximate molecular orbital methods currently available for treating large organic and bio-organic molecules. Bond lengths and angles are reasonably well accommodated,⁵³ with certain exceptions. The agreement between theory and experiment to be expected for rotational barriers and dihedral angles has been well documented.⁶¹ The methods have shown success tempered with significant inadequacies, such as failure to reproduce the planar geometry of unsaturated polyenic hydrocarbons.⁶² Bond ionization

excitation energies are poorly reproduced by INDO and CNDO, but a modification of INDO due to Dewar (MINDO) has proved to accommodate bond energies and ionization energies. Jaffe and del Bene have reworked the CNDO method for excitation energies. Extension of the methodology to second row elements and transition metals has proved to be quite complicated, although some progress has been recently achieved.

An alternative approach to the quantum mechanical calculation of conformational energy is the PCILO method, where the energy is developed using perturbative configuration interaction methods on a localized molecular orbital basis. A wide range of applications of the PCILO method to biological molecules has been reported by Pullman and coworkers, using atomic integrals evaluated in the CNDO approximation. This approach has some basic theoretical and technical advantages for conformational problems, since with the perturbation expansion carried to third order some representation of electron correlation is introduced, and since there is no iterative matrix eigenvalue problem to solve, the calculations are relatively fast even for large molecules. Energy variation with respect to dihedral angles in PCILO/CNDO calculations is significantly less than that for SCF/CNDO calculations due to a natural tendency of configuration interaction to depress higher energy regions relatively more than lower energy regions, and rotational barriers may be too low. The PCILO localized orbital basis may be designed using basic chemical intuition, and as chosen appears to correct for tendencies in the approximate SCF methods to overestimate intramolecular effects such as hydrogen bonding.

Molecules the size of chemical neurotransmitters are just coming within the reach of ab initio molecular quantum mechanical calculations. The molecular fragments approach of Christofferson, and ab initio SCF MO calculations (Port and Pullman) have been applied to acetylcholine.

With modest amounts of computer time available, however, molecular orbital theory with atomic integrals evaluated at the INDO level of approximation does provide a quantum mechanical computational vantage point tractable for extensive calculation of conformational energy maps of molecules of the size considered herein.

Using the INDO method, the total energy of the system is calculated using equation 4 with the appropriate integral approximations included. The net electrical charges Δq_A associated with each of the atoms A in the molecule is given by

$$\Delta q_A = Z_A - \sum_{\mu}^A P_{\mu\mu} \quad (6)$$

where the summation includes all $P_{\mu\mu}$ for orbitals centered on atom A. The electric dipole moment μ at the INDO level is given by the expression

$$\mu = \mu_{\text{chg}} + \mu_{\text{hyb}} \quad (7)$$

where

$$\mu_{\text{chg}} = 2.546 \sum_A \Delta P_{AA} R_{AA} \quad (8)$$

and, e.g.

$$(\mu_{\text{hyb}})_x = -14.674 \sum_{A(\neq H)} \zeta_A^{-1} P_{2S_A 2P_{XA}} \quad (9)$$

where ζ is the orbital exponent of the orbitals centered on atom A.

In computing conformational stability, the total energy E is calculated as a function of the appropriate internal displacement coordinates, and the calculated energy E can be partitioned into monoatomic and diatomic contributions E_A and E_{AB} respectively such that

$$E = \sum_A E_A + \sum_{A<B} E_{AB} \quad (10)$$

and the variation of individual terms examined separately. The expressions for E_A and E_{AB} are:

$$E_A = \sum_{\mu}^A P_{\mu\mu} [2U_{\mu\mu} + .25P_{SS} F^0 + P_{SS} (P_{SX} + P_{SY} + P_{SZ}) (F^0 - .167G^1) \\ + .5(P_{XX}^2 + P_{YY}^2 + P_{ZZ}^2) (.5F^0 + (4/50)F^2) + 2(P_{XX}P_{YY} + P_{XX}P_{ZZ} + P_{YY}P_{ZZ}) (F^0 - 7F^2) \\ + .5(P_{SX}^2 + P_{SY}^2 + P_{SZ}^2) (G^1 - F^0) + (P_{XY}^2 + P_{XZ}^2 + P_{YZ}^2) ((11/50)F^2 - (1/2)F^0)] \quad (11)$$

$$E_{AB} = \sum_{\mu}^A \sum_{\gamma}^B P_{\mu\gamma} [(\beta_A^0 + \beta_B^0) S_{\mu\gamma} - (1/2) P_{\mu\gamma} \chi_{AB}] \\ + (1/2) [P_{AA} (P_{BB} - 2Z_B) + P_{BB} (P_{AA} - 2Z_A)] \chi_{AB} \quad (12)$$

where $U_{\mu\mu}$ is a monoatomic core integral; F^0 , F^2 and G^1 are Slater-Condon notation for one-center radial atomic integrals; γ_{AB} is a two center repulsion integral; β_A^0 and β_B^0 are bonding parameters; and $S_{\mu\gamma}$ is an overlap between atomic orbitals ϕ_μ and ϕ_γ . Values for these quantities are assigned as described in Ref. 53. Elucidation of the factors responsible for the conformational stability of the gauche O-C-C-N⁺ grouping is approached by examining the variation in E and individual E_A and E_{AB} for choline and norcholine as a function of $\tau(01-C5-C4-N)$. A significant variation in an E_A term may be ascribed to charge redistribution and rehybridization effects, while a variation in E_{AB} signals a change in bonding.

The fortran routines which have the capability of performing SCF-MO calculations at the INDO level of approximation require as input total molecular charge, indication if the calculation is to be carried out in the ground state or an excited state (ground state for all calculations presented herein), and atomic number and cartesian coordinates for each atom in the molecule. Once these data are provided, the INDO wavefunction and the properties calculatable therefrom are uniquely defined, and thus are obtainable through an automatic computational procedure. This system is conveniently interfaced with the model builder system (SUBROUTINE ZMAT in Appendix C) which accepts as input intramolecular bond lengths and angles, and four atom torsions, and generates cartesian coordinates in an arbitrary frame. Thus the completion of INDO calculations reduces to a problem of geometrical input. For the calculations presented herein, great value has been placed upon the results of crystal structure determinations for input. Although this approach has possible limitations, it has the advantage

of keeping the input to the MO calculation well in contact with physical reality, and obviates the extensive preliminary setting of numerous geometrical parameters. A fortran routine XTAL was specifically developed for convenient workup of crystallographic data. A part of this program frequently employed in the work presented herein is SUBROUTINE UNZMAT which accepts cartesian coordinates (derived directly from the crystal unit cell) and generates input to model builder. A listing of XTAL is presented in Appendix A.

Intramolecular steric interactions have the capability of significantly influencing INDO calculated potential energy surfaces. Thus it is advantageous to have access to a computationally inexpensive method of evaluating intramolecular steric interactions before the relatively more expensive MO calculations are undertaken. Accordingly a routine SZMAT was developed which accepts input to model builder, and also parameters for systematic incrementing of crucial bond lengths or angles, or more frequently, four atom torsions. The routine preserves on peripheral storage devices the interatomic distance arrays of all pairs of atoms which anywhere in the conformations considered have an interatomic distance of less than 3\AA . Toward completion of the routine these arrays are printed with a summary steric grid which clearly defines sterically permitted and forbidden regions in conformational space. These steric grids can have significant correlation with INDO calculated potential energy surfaces. A listing of SZMAT is provided in Appendix B.

During the course of thesis research modifications were inserted into the INDO routines which reduced the requirement for computer central memory from $57,000_{10}$ 60 bit words to $16,000_{10}$ 60 bit words, (for 35 atoms and 80 basis functions). This was

effected by use of peripheral devices for storing the core hamiltonian, and other coding changes. The smaller version does not require significantly greater amounts of computer time than the original routine, and is presented in Appendix C.

Data acquired in the course of quantum mechanical calculations as described above must be reduced to a form suitable for developing a detailed understanding of each individual system and for cross-comparison of each system with others. In this regard, extensive use is made of computer graphics for display of potential energy surfaces and conformations of molecules. Here reliance is placed on two programs: CONSURF and ORTEP.

CONSURF is a fortran program for graphic display of contour lines representative of a function of two variables. This routine is used to contour potential energy surfaces as functions of atomic internal displacement coordinates. An example of CONSURF output is presented in Fig. 8 .

ORTEP is a modification of the fortran coded Oak Ridge ⁷² Thermal Ellipsoid Plot program which was developed by C.K. Johnson. This routine provides for automatic drawing of molecular geometries on an incremental plotter. Input of cartesian or crystallographic coordinates of a molecular system is accepted, and output like that presented in Fig. 2 is produced. Accurate display of molecular geometry in this manner substantively aids in the elucidation of common structural features of sets of compounds.

D. Results:

As noted in sections A.3 and B, prior to the calculations of a $\Psi(01-C5-C4-N)$ vs. $\Psi(C6-01-C5-C4)$ potential energy surface for Ach or other cholinergic substances, it is valuable to know the minimum energy configurations of the trimethylammonium group's methyl hydrogens. Accordingly calculations were carried out on the model compound tetramethylammonium (TMA), which is a structural analogy of Ach's cationic head, and has 1% of Ach's nicotinic activity. A priori, it is expected that due to steric factors the minimum energy configuration is the one where all methyl hydrogens are staggered, i.e. maximally distant from one another as depicted in Fig. 5. Prior to studying $\Psi(H-C-N-C)$, a minimization of the total energy as a function of the N-C bondlengths was carried out and the result is presented in Fig. 6, (hydrogens were held staggered). The energetically preferred N-C bondlength is calculated to be 1.44⁰Å. Using this datum, an energy was calculated for TMA with the hydrogens eclipsed, as shown in Fig. 7, and the result shows that the staggered form is favored over the eclipsed by ~25 kcal/mol. This steric placement of trimethylammonium methyl hydrogens is readily demonstratable in choline and Ach, and is thus applied to the calculations on cholinergic substances described herein.

The potential energy surface for acetylcholine as a function of $\Psi(01-C5-C4-N)$ and $\Psi(C6-01-C5-C4)$ as calculated from INDO molecular orbital theory is presented in Fig. 8. This conformational energy map was traced from a computer generated contour surface based on 144 calculated grid points with

contour levels spaced at intervals of 0.22 kcal/mol. The minima on the surface are labelled A,B,C...G in order of increasing energy and are summarized in Table 1. Other extrema in the surface are potential energy maxima.

The absolute minimum on the surface, labeled A on Fig. 8, is located at $\{50^\circ, 270^\circ\}$ and a local minimum at $\{50^\circ, 50^\circ\}$, point B, is calculated to be 3.68 kcal/mol above $\{50^\circ, 270^\circ\}$. The $\{50^\circ, 270^\circ\}$ and $\{50^\circ, 50^\circ\}$ conformers are closely related in that both positive and negative synclinal minima in the $\tau(\text{C6-O1-C5-C4})$ would be required by symmetry if $\tau(\text{O1-C5-C4-N})$ were synplanar. With $\tau(\text{O1-C5-C4-N}) = 50^\circ$, a residual tendency toward the paired synclinal energy minima remains, showing up as points A and B on the surface.

The conformation associated with the calculated minimum at $\{50^\circ, 50^\circ\}$ can be identified with the $\{77^\circ, 79^\circ\}$ geometry observed for Ach in the bromide crystal. While this is not the absolute minimum in the surface, a comparison of molecular models of the $\{50^\circ, 50^\circ\}$ and $\{50^\circ, 270^\circ\}$ geometries reveals the $\{50^\circ, 50^\circ\}$ would be more favorable for closest packing of molecules in the crystalline solid. This rationale is tempered, however, by the fact that the conformation of Ach in the salt of the chloride is {sc,app}.

Local minima D and H at $\{40^\circ, 180^\circ\}$ and $\{180^\circ, 180^\circ\}$, respectively, can be identified with conformations relevant to biological functions of Ach. The $\{40^\circ, 180^\circ\}$ conformation corresponds closely to the geometry of Ach implicated in muscarinic and nicotinic aspects of cholinergic action by Chothia and Pauling.^{33,36} The $\{180^\circ, 180^\circ\}$ geometry corresponds to the staggered, extended conformer considered by Chothia and Pauling to be complementary

to the Ach receptor of acetylcholinesterase and the nicotinic
 conformer discussed by Martin-Smith, Small, and Stenlake.⁷³

The existence of a number of local minima calculated from quantum mechanical considerations as described above may be readily understood on the basis of fundamental principles of structural chemistry and organic stereochemistry. With $\tau(01-C5-C4-N)$ held in a positive synclinal position, the calculated minima in $\tau(C6-01-C5-C4)$ shown in Fig. 9 correspond roughly to the minima of 60° , 180° and 300° expected in a potential energy profile for rotation of tetrahedrally hybridized atoms about an essential single bond. With $\tau(C6-01-C5-C4)$ held in an antiplanar position, analogous considerations apply to the minima in $\tau(01-C5-C4-N)$ shown in Fig. 10. The local minima at points E and F correspond to conformations wherein both $\tau(01-C5-C4-N)$ and $\tau(C6-01-C5-C4)$ fall near 60° , 180° or 300° , and thus, all the minima on the surface with the exception of point C can be accounted for on this basis. The local minimum at point C appears to arise from an interaction of methyl hydrogens of the trimethylammonium group and a methylene hydrogen of C4. This interaction stabilizes $\tau(01-C5-C4-N)$ at 120° . No experimental data with regard to the conformations of points A, C, E or F have been reported.

For both $\tau(01-C5-C4-N)$ and $\tau(C6-01-C5-C4)$, the synclinal conformations are calculated to be more stable than the other accessible conformations; cf. Figs. 9 and 10. An understanding of the forces stabilizing the synclinal positions of both torsional angles can be developed in terms of intramolecular hydrogen bonding. Intramolecular hydrogen bonding is most commonly found in circumstances involving an A-H...X structure, where A and X are both electronegative with respect

to hydrogen; the structure is stabilized by a combination of Coulomb,
van der Waals, and charge-transfer forces. In C-H bonds, the bond
polarity is ordinarily very small, leading to little propensity for
hydrogen bonding. However, for C-H bonds incorporated into a
trimethylammonium cationic head, the electronegative quarternary
nitrogen may effectively withdraw electrons from all the methyl C-H
groups, activating the methyl hydrogens for hydrogen bonding. An
accurate account of hydrogen bonding energies is somewhat beyond
the capability of the level of calculations presented herein, since
van der Waals forces are not accommodated in the orbital approximation
and since the semiempirical nature of the INDO methodology introduces
considerable uncertainty in the calculated energies and energy
differences. Nevertheless, a contribution from Coulomb forces
should appear, and the corresponding trends in the relative
energies and calculated charge distributions should be recognizable.
This is significant in that the Coulomb energy is generally held to
be the dominant attractive contribution to weak hydrogen bonds.

The calculated net atomic charges for Ach in the
conformations $\{180^\circ, 180^\circ\}$, $\{40^\circ, 180^\circ\}$, $\{50^\circ, 270^\circ\}$, and $\{50^\circ, 50^\circ\}$ are shown
in Figs. 11 - 14 . The extended totally antiplanar $\{180^\circ, 180^\circ\}$ conformer
serves as a convenient reference for a discussion of general aspects
of Ach charge distributions, since secondary intramolecular interactions
are minimal in this geometry. As expected, the positive charge
associated with the quarternary nitrogen in the principal valence
structure is delocalized over the entire cationic head, and the
nitrogen atom due to its intrinsic electronegativity is in fact the
least negative of the heavy atoms in the trimethylammonium group. The

methyl carbons and hydrogens carry net positive charges of +.12 and +.03, respectively. The net atomic charges of all the atoms in the $-\text{CH}_2\text{N}(\text{CH}_3)_3$ cationic head grouping sum to +.91. The ester oxygen and carbonyl oxygen both carry net negative charges, and the high net positive charge of the carbonyl carbon is consistent with the electrophilicity attributed to this atom from infrared and reaction kinetic investigations.⁷⁶ The ester linkage is not dipositive and, to the extent these calculated net atomic charges are correct, the hydrolysis of Ach by acetylcholinesterase must be considered an exception to Pullman's dipositive bond theory of enzymatic hydrolysis.

The electronic charge distributions of Ach in other conformations corresponding to energy minima may be best understood in terms of perturbations on the distribution for the $\{180^\circ, 180^\circ\}$ geometry. In the $\{40^\circ, 180^\circ\}$ conformer the synclinal orientation of $\tau(\text{O1-C5-C4-N})$ is marked by a charge-redistribution involving the ester oxygen and a methyl hydrogen H_a . The net negative charge of the ester oxygen O(1) and the positive net charge of H_a are both increased from their respective values at $\{180^\circ, 180^\circ\}$. The net charges in the cationic head still sum to +.91, indicating that there is a charge polarization within the cationic head without significant charge transfer to other regions of the molecule. This polarization occurs in such a way as to increase Coulombic attraction between the ester oxygen and proximal methyl hydrogens, and correlates with a potential energy minimum. The $\text{H}_a \cdots \text{O}(1)$ distance at $\{40^\circ, 180^\circ\}$ is 1.88Å, well within the van der Waals contact distance. The results are all consistent with an interpretation of the stabilization of $\{40^\circ, 180^\circ\}$ in terms of intramolecular hydrogen bonding.

In the paired $\{50^\circ, 50^\circ\}$ and $\{50^\circ, 270^\circ\}$ forms of Ach, the

charge polarization effects characteristic of intramolecular hydrogen bonding show up for the trimethylammonium group and both the ester oxygen and the carbonyl oxygen. In $\{50^\circ, 50^\circ\}$, the ester oxygen interaction involves two hydrogens of the same methyl group with the critical interatomic distances $O(1)\cdots H_a$ and $O(1)\cdots H_c$ being 1.98 and 2.65Å, respectively. A methylene hydrogen of C(5) is also proximal to O(2) and carries a correspondingly high net positive charge. In the $\{50^\circ, 270^\circ\}$ geometry O(1) interacts with H_a at a distance of 1.98Å and O(2) interacts with H_d at a distance of 2.1Å. The net charges of the atoms of the cationic head in $\{50^\circ, 270^\circ\}$ sum to +.92, indicating slight electronic charge transfer out of this region.

Thus, a characteristic feature of synclinal geometries associated with energy minima in acetylcholine's potential energy surface is charge polarization expected to be concomitant with the formation of weak intramolecular hydrogen bonds. The combination of energy stabilization, charge polarization, and intermediate distances within the van der Waals contact value indicate that the synclinal stabilization of $\gamma(O1-C5-C4-N)$ and $\gamma(C6-O1-C5-C4)$ in calculations at the INDO level of approximation is due to intramolecular hydrogen bonding. More detailed theoretical considerations are in order on this point and will be presented below.

Subsequent to the calculation of Ach's potential energy surface which was presented in the paragraphs immediately preceding, two other Ach conformational energy maps were generated. The first of these tests our assumption that $\gamma(C7-C6-O1-C5)$ is antiplanar for all variations in $\gamma(C6-O1-C5-C4)$. The INDO calculated potential energy

surface of Ach as a function of $\tau(\text{C6-01-C5-C4})$ and $\tau(\text{C7-C6-01-C5})$ with $\tau(\text{01-C5-C4-N})$ held antiplanar is given in Fig.15. There are three minima on the surface, all with $\tau(\text{C7-C6-01-C5}) = 180^\circ$. Rotations of the latter coordinate out of the antiplanar configuration is accomplished by an increase in energy to 20 kcal/mol, consistent with the expected double bond character of the C6-01 bond as discussed by Baker et al. This coordinate is maintained antiplanar in all subsequent calculations.

In order to obtain more detail, a second SCF-INDO conformational energy map of Ach as a function of $\tau(\text{01-C5-C4-N})$ and $\tau(\text{C6-01-C5-C4})$ with a closer grid of 20° on the full range of 360° in both variables was generated. The results are relevant to succeeding discussion and are given in Fig.16. The global minimum on the surface is in the $\{-sc,sc\}$ region, and local minima D and H can be identified with the bromide and chloride crystal geometries, respectively. The qualitative features are in accord with chemical intuition as described above. On a more detailed level the SCF-INDO calculations place the synclinal minima of both coordinates somewhat inside the experimentally observed values, with in some cases non-bonded atoms coming within van der Waals contact distances. Using the wavefunctions generated in the latter calculation, the dipole moment of Ach was calculated to be 1.5 to 9.8 debye, depending on the conformation. An experimentally observed value for Ach in chloroform was estimated to be 2.65 debye. While a number of assumptions on structure and polarizabilities are involved in reduction of the experimental data, this relatively low value suggests that the structure of Ach in chloroform may resemble the crystalline bromide

geometry rather than the crystalline chloride geometry also observed for Ach in D₂O.

Since the publication of the SCF-INDO conformational energy map for Ach, analogous calculations have been reported³⁰ by Pullman, Courriere and Coubeils using the PCILO-CNDO method. Studies on acetylcholine at the SCF-CNDO level have been reported⁷⁸ by Savran and Govil. The pairwise potential function method was elaborated to include a coulombic term and applied to Ach by Ajo,⁴⁸ Bossa, Damiani, Fidenzi, Oigli, Lanzi and Lapiccinella. Net atomic charges were adopted from EHT and CNDO calculations on a single conformer.⁴⁹ Froimowitz and Gans reported similar calculations based on the net atomic charges computed in the INDO approximation. The only non-empirical theoretical studies reported to date are the⁵⁰ SCF-FSGO molecular fragment calculation by Genson and Cristofferson, and the SCF-MO study by Port and Pullman.⁵¹

There is considerable but not total accord in the results on Ach from these diverse theoretical points of view. The SCF-CNDO should and do give results identical to those obtained at the INDO level. The corresponding PCILO-CNDO surface is somewhat flatter, with a total variation of 6 kcal/mol in sterically permitted regions, (11 kcal/mol for SCF-INDO). Pullman and Courriere have studied the sensitivity of the results to the geometrical input of the calculations and have found that calculations based on the bromide geometries give low-energy {sc,sc} minima, and calculations based on the chloride geometry give low energy {sc,ap} minima. Froimowitz and Gans have provided a detailed comparison between the pairwise potential function methods and the quantum mechanical

studies, showing similar results to those of Fig. 8. A slight tendency of the INDO method to allow non-bonded atoms to come within van der Waals radii of one another was empirically adjusted in their repulsive potentials. This problem is probably avoided in the PCILO calculations by the choice of localized molecular orbital basis functions.

50 The non-empirical calculation of Ach by Genson and Cristoffer-son produced significantly different results, with a considerably wider variation in energy with respect to both coordinates, and minima synperiplanar and antiperiplanar in $\tau(01-C5-C4-N)$. The experimentally observed synclinal value is near an energy maximum, with a variation in energy with respect to $\tau(01-C5-C4-N)$ with $\tau(C6-01-C5-C4) = 180^\circ$ of 50 kcal/mol, vs. 5 kcal/mol for INDO and 3 kcal/mol for PCILO. The synclinal minimum is developed by non-covalent intramolecular bonding interactions, and this questions the ability of the molecular fragments procedure to describe this effect with functions positioned in covalent bonding regions, although evidence from calculations on other systems indicate no special problems on this point. Recent thoughts relate the problem to the limited basis set. The ab initio SCF calculation at the STO-3G level gives a synclinal minimum in $\tau(01-C5-C4-N)$ with a barrier to the antiperiplanar form of 3 kcal/
51 mol.

Most of the theoretical and experimental studies of conformation in cholinergic substances presented above indicated a synclinal stabilization of $\tau(01-C5-C4-N)$. In order to quantitatively determine the stabilizing force on the O-C-C-N group,

a partitioning on the model compound choline of the INDO total energy into individual monoatomic and diatomic contributions was carried out. Calculations on choline are compared with those obtained for electrically neutral norcholine, where activation of hydrogens by Sutor's mechanism is precluded. Fig. 17 presents the structure of choline. 85

The calculated total energies of choline and norcholine are displayed as a function of $\phi(OL-C5-C4-N)$ in Fig. 18. Norcholine shows synclinal and antiplanar minima in the range displayed. The pattern is characteristic of the torsional potential expected in rotation about saturated carbon atoms, with all minima falling in a range of 1 kcal/mol. Analogous minima can be identified on the choline curve, but here the synclinal minimum is preferentially stabilized to the extent of 4-5 kcal/mol. The $O\cdots H$ distance in the synclinal minimum of choline (40°) is 2.07\AA .

The electronic charge distribution calculated for choline is given in Figs. 19, 20. The antiplanar conformer serves as a convenient point of reference, since intramolecular interactions are minimal in this geometry. As expected, the positive charge associated with the quarternary nitrogen in the principal valence structure is delocalized over the entire cationic head, and the methyl carbons and hydrogens carry net positive charges of 0.12 and 0.03, respectively. The nitrogen atom, consistent with its intrinsic electronegativity is the least positive (0.0907) of the heavy atoms in the trimethylammonium group. The charge on the acyloxy oxygen is -0.279, and the net charge on the atoms $-\text{CH}_2-\text{N}(\text{CH}_3)_3$ comprising the cationic head sum to 0.901.

The principal change in charge density from the antiplanar to synclinal geometries of choline is the increased net positive

charge (0.048) found on the methyl hydrogen proximal to the oxygen, and increased net negative charge on the oxygen (-0.311). The nitrogen also has a small increase in net positive charge, from 0.091 to 0.094. The net charges of the cationic heads for the antiplanar and synclinal conformers are 0.907 and 0.906, respectively.

The calculated electronic charge distribution for norcholine is presented in Fig. 21, 22. In the antiplanar conformer, the dimethylammonium group is nearly electrically neutral. The nitrogen and methyl hydrogens are net negative, and the methyl carbons show net positive charges; a charge alternation effect discussed more generally by Pople and Gordon.⁷⁹ The oxygen net charge is -0.302. Going over to the synclinal conformer, there is a decrease in negative charge on the oxygen and an increase in negative charge on the nitrogen, directly opposite to the trend calculated for choline. As in choline, there is a decrease in negative charge on the methyl hydrogen proximal to the oxygen.

Before proceeding to a detailed consideration of the results of Fig. 26, it is useful to consider the extent to which the minima are sensitive to the specific orientation of the trimethylammonium hydrogens assumed for calculation. To consider the orientation of the methyl groups, an energy surface for each compound was generated as a function of $\angle(OL-C5-C4-N)$ and $\angle(H-Cl-N-C2)$, with the other methyl hydrogens geared for minimal steric repulsions. The results for choline and norcholine are given in Figs. 23 and 24, respectively. The minima for both synclinal and antiplanar conformers occur for $\angle(H-Cl-N-C2) = 60^\circ$ in both compounds; furthermore the synclinal and antiplanar conformers

are minimal for any slice of $\tau(\text{H-C1-N-C2})$. The results of Fig. 18 are thus independent of methyl group orientation.

At this point a more detailed characterization of the factors contributing to the variation in energy as a function of $\tau(\text{O1-C5-C4-N})$ is in order. For each value of $\tau(\text{O1-C5-C4-N})$ considered, the calculated total energy was partitioned into monoatomic and diatomic contributions. The variation in many individual contributions exceeded the variation in the calculated total energy, emphasizing the extent to which the total energy is a subtle balance of widely varying terms. Each E_A and E_{AB} was individually examined as a function of $\tau(\text{O1-C5-C4-N})$, and the significant results are collected in Figs. 25 and 26. All relevant contributions decreasing in the synclinal region of $\tau(\text{O1-C5-C4-N})$ are represented in these figures, as are particularly interesting contributions on the increase.

Selected monoatomic contributions to the total energy of choline are plotted together with the total energy as functions of $\tau(\text{O1-C5-C4-N})$ in Fig. 25, and the analogous plots for selected diatomic contributions are given in Fig. 26. The calculated net stabilization of syn conformers over anti conformers is correlated with stabilizing contributions from the monoatomic oxygen term, the monoatomic contribution of the methyl carbon proximal to the oxygen and the diatomic oxygen-hydrogen term for the methyl hydrogen proximal to the oxygen. The diatomic oxygen-nitrogen term shows only a small variation over the range of τ studied. For the stabilization of the synclinal conformer with respect to the synplanar, the stabilization contributed by the oxygen-methyl hydrogen interaction

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is dominant, acting in concert with the monoatomic nitrogen term. Thus the calculated stabilization of the energetically preferred conformation with respect to $\tau(01-C5-C4-N)$ is directly associated with the interaction between the oxygen and the cationic head, with the interaction between the oxygen and the proximal methyl hydrogen indicated as a significant factor.

An important point to consider is the comparison between the calculated results and experimental observation. Theory and experiment concur on the existence of a preferred conformation in the synclinal region of $\tau(01-C5-C4-N)$. The calculated energy minimum falls at $\tau(01-C5-C4-N) = 40^\circ$, as compared to the experimentally observed value of 84° . In view of the fact that the energy curve is rather flat (total calculated variation of the order of 5 kcal/mol), this can be considered reasonable accord between approximate molecular orbital theory and experiment. A point of contention arises in the consideration of the nature of the $O \cdots H-C-N$ interaction. At $\tau = 40^\circ$, $R_{O \cdots H} = 2\text{\AA}$, well within the sum of the van der Waals radii of hydrogen and oxygen. At $\tau = 84^\circ$, $R_{O \cdots H} = 2.5\text{\AA}$, just beyond the sum of the van der Waals radii and just beyond the $O \cdots H$ distance expected for hydrogen bond formation. The $O \cdots H$ interaction plays a significant role in the stabilization of the INDO calculated synclinal energy minimum, but the possibility that this interaction is overestimated by the INDO method must not be excluded. The INDO calculations indicate that a hydrogen bonding interaction would go smoothly over to an electrostatic interaction as the $O \cdots H$ distance increases in choline, and thus the question here is more one of degree than of

fundamental character.

With the structural chemistry of acetylcholine and the cholinergic O-C-C-N grouping well characterized by molecular quantum mechanics at the INDO level of approximation, study at this level of approximation was addressed to the important cholinergic agonists: muscarine, nicotine, acetyl- α -methylcholine, acetyl- β -methylcholine and acetyl- α, β -dimethylcholine. The result of this work is presented in the following paragraphs.

Muscarine. Muscarine has been studied from a theoretical viewpoint by a variety of methods with no substantive disagreement.^{18,19,30} A conformational study of muscarine reduces to a one parameter problem, with $\tau(C6-O1-C5-C4)$ constrained to 144° by the intramolecular five membered ring. Calculations were carried out on the C6(S),C9(R), C5(S) isomer shown in Fig.3, and for the related compounds C6(S),C9(S),C5(S) epi-muscarine, C6(R),C9(S),C5(S) allo-muscarine and C6(R),C9(R),C5(S) epiallo-muscarine. The INDO conformational energy of muscarine plotted as a function of $\tau(O1-C5-C4-N)$ is presented in Fig.27. The calculations show a global minimum at 60° in accord with the observed crystal geometry. A local minimum appears at 160° in $\tau(O1-C5-C4-N)$ at an energy 7 kcal/mol above the local minimum. The results for epi-muscarine, allo-muscarine, and epiallo-muscarine are essentially identical; these compounds differ from muscarine only in the absolute configuration of the methylated and hydroxylated ring carbon atoms and in their biological activities to be discussed in the next section. The calculated net atomic charges for muscarine in the $\{60^\circ, 144^\circ\}$ conformation are given in Fig. 3. The calculated electric dipole moment is 8.05 debye.

Nicotine. The crystal geometry for nicotine dihydro-
 iodide as determined by Koo and Kim is shown in Fig. 4. Here
 $\angle(C8-C7-C2-N)$ is analogous to $\angle(O1-C5-C4-N)$ in Ach, and $\angle(C9-C8-C7-C2)$
 holds some analogy to $\angle(C6-O1-C5-C4)$. With the latter coordinate
 constrained antiplanar by the pyridine ring, the crystal geometry
 can be represented as $\{-60^\circ, 180^\circ\}$. Rotation of the pyridine
 ring by 180° places N2 in a position analogous to the carbonyl
 oxygen of Ach in the $\{60^\circ, 180^\circ\}$ conformation. The pyrrolidine
 ring deviates somewhat from planarity, with $\angle(C5-C2-N1-C3) = 17^\circ$
 and $\angle(N1-C3-C6-C5) = 14^\circ$. Simple steric considerations indicate
 that interactions between pyridine hydrogens and hydrogens attached to
 the pyrrolidine ring and N-methyl group may strongly influence the
 conformational energy about $\angle(C8-C7-C2-N1)$.

While rapid inversion of the absolute configuration around
 nicotine's pyrrolidine nitrogen is likely in solution, the the 1(R), 2(S)
 configuration of nicotine is studied here since crystal data is
 available for this epimer.

In the initial SCF-INDO calculations on nicotine, a conformational
 energy map was generated as a function of $\angle(C8-C7-C2-N1)$ and
 $\angle(H_a-C4-C2-N1)$, the latter coordinate specifying the orientation of
 the N-methyl hydrogens. Two energy minima were found, differing in
 energy by less than 1 kcal/mol and both corresponding to $\angle(H_a-C4-N1-C3)$
 $= 80^\circ$. The calculated energy vs. $\angle(C8-C7-C2-N1)$ with $\angle(H_a-C4-N1-C3) =$
 80° is shown Fig. 28. The energy minima correspond to $\angle(C8-C7-C2-N1) =$
 0° and 160° , both somewhat removed from the observed value of -60° .
 In an attempt to understand the discrepancy between the calculated and
 observed values, we explored the effect of deviations in hydrogen
 positions on the calculated result. The coordinates specifying the

hydrogen positions were adjusted slightly in the direction expected to reduce steric effects and calculation of conformational energy vs. $\angle(\text{C8-C7-C2-N1})$ was repeated. The resulting plot is also presented in Fig. 28. The barrier heights were reduced by 1.5 to 2 kcal/mole, but the positions of the minima were essentially unchanged. Superimposed on the same plot are the interatomic distances of hydrogen atoms coming within van der Waals contact distance of one another. At $\angle(\text{C8-C7-C2-N1}) = 40^\circ$ to 80° , the $\text{H}_a\text{-H}_d$ distance and the $\text{H}_b\text{-H}_c$ are very low resulting in an increased conformational energy. At $\angle(\text{C8-C7-C2-N1}) = 220^\circ$ to 260° the $\text{H}_a\text{-H}_c$ and $\text{H}_b\text{-H}_d$ distances are close, also destabilizing the system. Our calculated minima correspond roughly to regions where all these interatomic distances are simultaneously maximal. Thus in spite of the lack of a calculated energy minimum in the region of the observed geometry, our results are understandable, and represent the degree of agreement to be achieved assuming the crystal geometry for non-hydrogen atoms. Conformations of nicotine with $\angle(\text{C8-C7-C2-N1})$ from 100° to 200° and from -40° to 20° are energetically removed from the absolute minimum by less than 2.5 kcal/mole. The calculated charge distribution for nicotine at the crystal geometry is recorded in Fig. 4, and the calculated dipole moment ranged from 7.4 to 8.9 debye.

The calculations on nicotine reported by other investigators leave the relation between calculated and observed geometries incompletely resolved. The study reported by Kier using extended Hückel theory gave good agreement with experiment but assumed a planar pyrrolidine ring and computed energies on a 60° grid. INDO calculations performed on 1(R), 2(S) nicotine with the pyrrolidine ring planar yield minima in $\angle(\text{C8-C7-C2-N1})$ at -40° and 140° . However, it is difficult to justify

comparison of this result with that of the crystallographic study.

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Pullman et al. using the PCILO method and an unspecified 1(R), 2(S) standard geometry obtained minima at $\tau(\text{C8-C7-C2-N1}) = -40^\circ$ and 120° , in improved agreement with the crystal geometry.

Acetyl- α -methylcholine. The SCF-INDO conformational energy map of $\alpha(\text{R})$ -methyl acetylcholine is presented in Fig.²⁹. The conformational map for $\alpha(\text{S})$ -methyl acetylcholine, the enantiomer, can be generated through the transformation $\{x,y\} \rightarrow \{x,-y\}$. The global minimum for the $\alpha(\text{R})$ derivative occurs in the vicinity of $\{80^\circ, 240^\circ\}$. The nine other local minima are listed in Table ². The crystal geometry at $\{90^\circ, 170^\circ\}$ is calculated to be 4 kcal/mole above the absolute minimum, and the $\{212^\circ, 176^\circ\}$ crystal result can be identified with a local minimum at $\{180^\circ, 180^\circ\}$. In the latter case, with $\tau(\text{O1-C5-C4-N}) = 180^\circ$ the shape of the surface indicates considerable lability in $\tau(\text{C6-O1-C5-C4})$ from 80° to 240° . Steric interference of the $\alpha(\text{R})$ methyl group with the acetate carbonyl group precludes conformations with $\tau(\text{O1-C5-C4-N})$ and $\tau(\text{C6-O1-C5-C4})$ simultaneously in the range of 40° to 200° , and -40° to 60° , respectively. The calculated magnitudes of angles of the $\{sc,sc\}$ minima are increased over that calculated for Ach, but comparison of Fig.¹⁶ and Fig.²⁹ show that the overall effect of α -methyl substitution of the conformational energy map is relatively minor. None of the local minima on the Ach potential surface are energetically precluded for the α -methyl derivative. The α -methyl surface is slightly flatter than that of Ach, consistent with the results indicated in NMR studies.

The calculated net atomic charges for the $\{80^\circ, 240^\circ\}$ conformation of $\alpha(\text{R})$ -methyl acetylcholine are presented in Fig.³⁰. Comparison of Fig.³⁰ with the charge distribution reported for acetylcholine in Fig.²

show that there is a charge redistribution induced by α -methyl substitution. There is a decrease in positive charge on N, C1 and C6, and a decrease and an increase in negative charge on O1 and O2, respectively. The calculated dipole moment ranges from 0.5 to 9.1 debye.

Acetyl- β -methyl acetylcholine. The conformational energy map computed for β (S) methyl acetylcholine using the INDO method is given in Fig.31. The surface may be viewed in marked contrast to that of Ach, with 50% of the conformational space sterically excluded. The primary source of the steric effect is the interaction between the β -methyl group and the trimethylammonium methyl groups, important for all values of τ (O1-C5-C4-N) above 180° . The global minimum on the surface is located at $\{60^\circ, 30^\circ\}$, with a local minimum at $\{60^\circ, 240^\circ\}$ computed to be about 4.8 kcal/mole higher in energy. The latter local minimum may be identified with the crystal geometry at $\{85^\circ, 203^\circ\}$.

The calculated charge distribution for the $\{60^\circ, 240^\circ\}$ conformer of β (S)methyl Ach is given in Fig.32. A comparison with the calculated charge distribution for Ach show that the effect of β -methyl substitution is to decrease positive charge on N, C1 and C6, and to decrease and increase negative charge on O1 and O2, respectively. These charge redistributions are directly analogous to those which occur on α -methyl substitution. The calculated dipole ranges from 1.4 to 11.4 debye in the sterically allowed region of space.

Acetyl- α,β -dimethylcholine. The SCF-INDO conformational map calculated for threo- α (R), β (R)-dimethylacetylcholine is presented in Fig. 33. Here 87% of the surface is sterically unfavored. All conformers with τ (O1-C5-C4-N) between 40° and 200° are excluded due to interactions between β -methyl and trimethylammonium hydrogens, and

conformers with $\angle(C6-O1-C5-C4)$ between 200° and 260° have unfavorable interactions between the β -methyl group and the carbonyl oxygen. The global minimum on the surface is at $\{280^\circ, 140^\circ\}$, with a local minimum at about the same energy at $\{220^\circ, 60^\circ\}$, separated by a barrier computed to be less than 2 kcal/mole. A second local minimum is present at $\{280^\circ, 300^\circ\}$, separated from the first by a barrier of some 25 kcal/mole. The experimentally observed crystal geometry for the threo- $\alpha(R)$, $\beta(R)$ derivative is $\{217^\circ; 95^\circ\}$. Figure 34 presents the computed net atomic charges for the $\{80^\circ, 220^\circ\}$ conformer of threo- $\alpha(S)$, $\beta(S)$ -dimethylacetylcholine. In comparison with the calculated net atomic charge densities for acetylcholine, there is a decrease in positive charge on N, an increase on C6, and an increase in negative charge on O1. Charges on other atoms are essentially unchanged from those of acetylcholine. The calculated electric dipole moment ranges from 0.9 to 8.8 debye.

The conformational energy map for erythro- $\alpha(S)$, $\beta(R)$ -dimethylacetylcholine is given in Fig. 35. Steric interactions analogous to those described above exclude above 86% of the conformers on this surface. In the remaining area, the global minimum is located at $\{280^\circ, 120^\circ\}$, with a local minimum at $\{240^\circ, 80^\circ\}$ and $\{280^\circ, 280^\circ\}$ at relative energies of 1.91 and 3.34 kcal/mole, respectively. The latter two minima are separated by a computed barrier of 6 kcal/mole. The crystal geometry is $\{280^\circ, 160^\circ\}$, a point computed to be 1.7 kcal/mole above the global minimum. The charge distribution for erythro- $\alpha(R)$, $\beta(S)$ -dimethylacetylcholine, as presented in Fig. 36, is similar to that presented for the threo derivative except that C6 does not evidence an increase in positive charge over the analogous atom in Ach. The calculated dipole ranges from .9 to 9.0 debye.

E. Discussion:

The results of the preceding section can be used together with the biological activity data to approach a deeper understanding of the role of α - and β -methyl substituents in cholinergic action, and to gain perspective on general aspects of the structural chemistry of cholinergic transmission. Since the methyl derivatives of Ach have all of the functional groups necessary for either muscarinic or nicotinic activity, the present data may be used to examine the role of molecular conformation vis-a-vis the direct interaction of the methyl groups with the cholinergic receptor. To the extent molecular conformation is a dominant factor, compounds in this series with a particular type of activity should have the appropriate functional groups disposed in three dimensional space in a common pattern. In terms of structural parameters, this disposition is specified by sterically permitted or energetically preferred values of $\tau(O1-C5-C4-N)$ and $\tau(C6-O1-C5-C4)$, and any common pattern should be revealed by a comparison of allowed regions or energy minima in the $\{\tau(O1-C5-C4-N), \tau(C6-O1-C5-C4)\}$ conformational maps.

The conformational data presented in the preceding section has been reduced to tabular form and collected with the biological activity data in Table 2. Each compound considered is represented by a row of the table, containing from left to right its muscarinic activity, nicotinic activity and enzymatic hydrolysis rate; each given as percentages with respect to available data on Ach. The biological data represent results from a variety of preparations and experimental conditions, and the relative activities listed are thus of qualitative or semi-quantitative significance at best.

Further to the right of Table 2, the positions of energy minima calculated for the substance are enumerated. The columns of the table in this region are organized with respect to the calculated energy minima for Ach given in the top row; entries in the same column down the table indicate corresponding energetically preferred conformations in different substances. All preferred conformations energetically within 20kcal/mole of the global minimum of each compound are included.

In examination of the data for compounds with significant muscarinic activity, it is again evident that the geometry common to muscarinic agonists is {sc,ac-ap}, consistent with ideas proposed by Pauling and co-workers. For Ach and muscarine this geometry (column 2 in the conformational energies of Table 2) corresponds to a calculated energy minimum and is thus energetically preferred. For the active $\beta(S)$ -methyl derivative and the erythro- $\alpha(R)$, $\beta(S)$ -dimethyl derivative (probably the active erythro-dimethyl enantiomer), this geometry does not correspond to local energy minima but is not sterically excluded. Beyond this, it appears that $\beta(S)$ -methyl or methylenic substitution actually enhances the muscarinic activity of an agonist. Bioassay data (see Table 2) for muscarine, acetyl- $\beta(S)$ -methylcholine and erythro- $\alpha(R)$, $\beta(S)$ -dimethylacetylcholine show these compounds to have 270%, 133% and 14% of the muscarinic activity of Ach, respectively. The muscarinic activities of erythro- $\alpha(R)$, $\beta(S)$ -dimethylacetylcholine and $\alpha(R)$ -methylacetylcholine are 14% and .6% relative to Ach. Examination of the conformational maps and calculated electronic charge distributions for these molecules shows no outstanding detail which could explain the enhancement of muscarinic activity for a $\beta(S)$ substituent simply in terms of molecular

conformation and other molecular properties. Therefore it appears that the variation in the level of muscarinic activity in these compounds may involve a direct interaction of the methyl substituents with the muscarinic receptor.

Table ² also lists a number of compounds which have calculated energetically preferred conformations in the vicinity of {sc,-ac} yet have low muscarinic activity. Both α (R)- and α (S)-methyl derivatives fall into this category, with α (S)-methyl substitution diminishing muscarinic activity by a factor of 10 more than α (R)-methyl substitution. Since no significant portion of the Ach conformational map is sterically precluded for the α (R)- or α (S)-methyl derivative, simple conformational effects cannot be responsible. A direct interaction of the α -methyl substituents with the receptor, contributing destructively to agonist activity, can explain the observed reduction in muscarinic potency. The loss of muscarinic activity upon α -methyl substitution is also seen in the dimethyl derivatives. Erythro- α (R), β (S)-dimethylacetylcholine has an energetically preferred conformation at {sc,-ac} and a muscarinic activity in the racemate of 14% relative to Ach, compared to 133% for β (S)-methylacetylcholine. The greater reduction in muscarinic activity for α (S)-methyl substitution as compared with α (R) substitution is evidenced again by the lack of activity in threo- α (S), β (S)-dimethylacetylcholine whereas the erythro- α (R), β (S) derivative elicits small but significant muscarinic activity.

Analogous conclusions can be drawn from a consideration of the calculated energy profiles of muscarine, given in Fig. 27, as compared with those for epi-muscarine, allo-muscarine and epiallo-muscarine. The energy profiles are similar while the observed activities

as listed in Table 2 are quite different. Neither conformational effects or a variation in electronic charge distribution can explain the variance in activity, and a direct interaction of functional groups with the receptor is indicated. The observed activities appear to implicate muscarine's hydroxyl oxygen and ring methyl group in positions analogous to the carbonyl oxygen and acetate methyl of Ach in muscarinic action.

Consideration of the data for compounds with significant nicotinic activity leads to additional information on the role of conformational effects in nicotinic action. As noted by others, nicotinic activity is clearly less stereospecific than muscarinic action, but a {sc, ac-ap} conformation has been implicated. Both $\alpha(R)$ - and $\alpha(S)$ -methyl derivatives are nearly as active at nicotinic sites as Ach. Methyl substitution at either $\beta(R)$ - or $\beta(S)$ - positions significantly reduces the nicotinic activity of an agonist. In consideration of the widely different effects of $\beta(R)$ and $\beta(S)$ substitution on conformational preferences, and that the {sc, -ac} is permitted if not preferred in the $\beta(S)$ derivative, a direct interaction of methyl groups with the nicotinic receptor is indicated.

Consideration of the relative rates of cholinesterase mediated hydrolysis for the various compounds alongside the calculated results on structure and properties for methyl Ach derivatives points also towards some direct interaction of the methyl groups with the active site of the enzyme. Both $\alpha(R)$ - and $\alpha(S)$ -methylacetylcholine can achieve any point on the { $\pi(O1-C5-C4-N)$, $\pi(C6-O1-C5-C4)$ } conformational map accessible to Ach, and have no significant differences in charge distributions. Thus the observed decreased hydrolysis rate of the $\alpha(R)$ derivative compared to the $\alpha(S)$ derivative of Ach does not appear to be dependent upon conformational effects,

and may likely involve methyl groups directly. For the β -methyl derivatives, β (R) substitution reduces the hydrolysis rate to zero whereas β (S) substitution shows 54% the hydrolysis of Ach. This indicates positive synclinal and anticlinal values of τ (O1-C5-C4-N) lead to conformations complementary to the cholinesterase receptor. The calculated conformational map for β (S)-methylacetylcholine shows local minima for (+)-synclinal values of τ (O1-C5-C4-N), but none for ac to ap values. The $\{150^\circ, 180^\circ\}$ geometry implicated by Pauling et al. in enzymatic hydrolysis lies 12 kcal/mole above the global minimum.

For hydrolysis, the effects of α - and β -substitution may again be extrapolated to the α , β -dimethyl derivatives. The decreased hydrolysis rate for an α (R) derivative explains the negligible rate observed for erythro- α (R), β (S)-dimethylacetylcholine. We predict the hydrolysis rate for threo- α (S), β (S)-dimethylacetylcholine to be higher.

Overall, we can ascertain from these results that structures implicated in various aspects of cholinergic action can be identified with regions of conformational energy sterically permitted but not necessarily energetically preferred in the isolated molecule. This seems reasonable since a change in membrane permeability is probably a structural adaptation to agonist-receptor interaction, and a conformational effect on the agonist is certainly possible. Structural modifications in both enzyme and substrate are evident from spectral studies of enzymatic reactions.

In comparing theory and experiment, the structural detail presented in the results section must be considered in the perspective of a physiochemical system. At physiological and room temperatures

many conformations will be thermally populated, and in solid and solution, environmental effects are surely important. Intramolecular hydrogen bonding and the various conformations of Ach in the $\{\Gamma(01-C5-C4-N), \Gamma(C6-01-C5-C4)\}$ surface would be influenced significantly by solvent polarity. The bromide crystal geometry B and the related conformation A in Fig 16 have both the acetoxy and acyloxy oxygen atoms in the interior of a roughly spheroidal structure with C-H bonds on the exterior. In solution these geometries would likely be favored by low solvent polarity, although Ach as a cation has proved sparingly soluble in such solvents. Geometries such as D and G exposing one or both oxygens could be preferentially stabilized by highly polar, intermolecularly hydrogen bonding solvents.

The natural selection of acetylcholine as a chemical neurotransmitter has been attributed in part to its relatively non-substituted structure and subsequent conformational flexibility; being adaptable to nicotinic, muscarinic and possibly many other receptor sites. In light of the possible solvent effects on Ach's conformational flexibility, local biological environments could also serve to preferentially stabilize conformations complementary to specific receptor sites, and thus contribute to optimum biological function.

F. Summary and Conclusions:

The INDO molecular orbital calculations on acetylcholine reveal a number of energy minima with respect to the torsional angles $\tau(O1-C5-C4-N)$ and $\tau(C6-O1-C5-C4)$. Certain of the minima can be closely identified with the Ach crystal geometries, the geometries implicated in muscarinic and nicotinic aspects of cholinergic action, and the geometry considered favorable for hydrolysis by cholinesterase. The energy stabilization of synclinal values of both $\tau(O1-C5-C4-N)$ and $\tau(C6-O1-C5-C4)$ in Ach is attributed to intramolecular hydrogen bonding as evidenced by an electronic charge redistribution in a manner consistent with polarization effects expected for hydrogen bonding structures.

Thus a number of proposed structural aspects of the neurobiological action of Ach can be understood and unified on the basis of quantum mechanical calculations, considering local minima in the potential energy surface and corresponding molecular electronic properties.

The conformational energy maps and electronic charge distributions for muscarine, nicotine, the α and β methyl, and dimethyl derivatives of Ach have been considered in terms of physiochemical studies, the available bioassay data on cholinergic substances, and current theories of the structural chemistry of cholinergic transmission. Geometries observed from crystallographic and solution spectral studies for each compound may be identified with energetically preferred geometries (local minima) on the calculated conformational energy maps. General aspects of

cholinergic activity are seen to be related to regions of conformational space sterically allowed, but are not always directly associated with energetically preferred geometries. The variance in bioassay data for active compounds cannot be explained in terms of simple conformational effects and distributions of electronic charge, and direct interactions of methyl substituents with cholinergic receptors are indicated.

Table 1

Identification on Figure 8	Relative energy, kcal/mol	Geometry		Physiochemical or biological significance
		Calcd	Exptl	
A	0.00	{50°, 270°}		See text
B	3.68	{50°, 50°}	{77°, 79°}	Observed in crystalline acetylcholine bromide
C	4.98	{120°, 300°}		See text
D	6.27	{40°, 180°}	{75°, 180°} {60°-120°, 144°-213°}	Implicated in nicotinic action Implicated in muscarinic action
E	7.72	{200°, 330°}		See text
F	7.84	{160°, 30°}		See text
G	9.98	{180°, 180°}	{180°, 150°}	Implicated in nicotinic action and hydrolysis by cholinesterase

Key for Table 2:

- a. Guinea pig ileum, Ref. 81.
- b. Cat blood pressure, Ref. 81.
- c. Frog rectus muscle, Ref. 44 and Ref. 82.
- d. Blood pressure rise with atropine, and cat gastrocnemius stimulation, Ref. 83.
- e. Hydrolysis by a standard bovine erythrocyte acetylcholinesterase homogenate, Ref. 41.
- f. Guinea pig ileum, Ref. 44.
- g. Hydrolysis by true acetylcholinesterase from the electric organ of the eel, Ref. 44.
- h. Cat blood pressure, Ref. 25.
- i. Blockage of cat superior cervical ganglion, Ref. 25.
- j. Curariform action on cat gastrocnemius muscle, Ref. 25.
- k. Guinea pig ileum during anoxia, Ref. 84.
- l. Cat superior cervical ganglion, Ref. 7.

*Bio-assay data are given as percentages relative to Ach.

**
x - sterically forbidden conformations.
y - sterically allowed conformations.

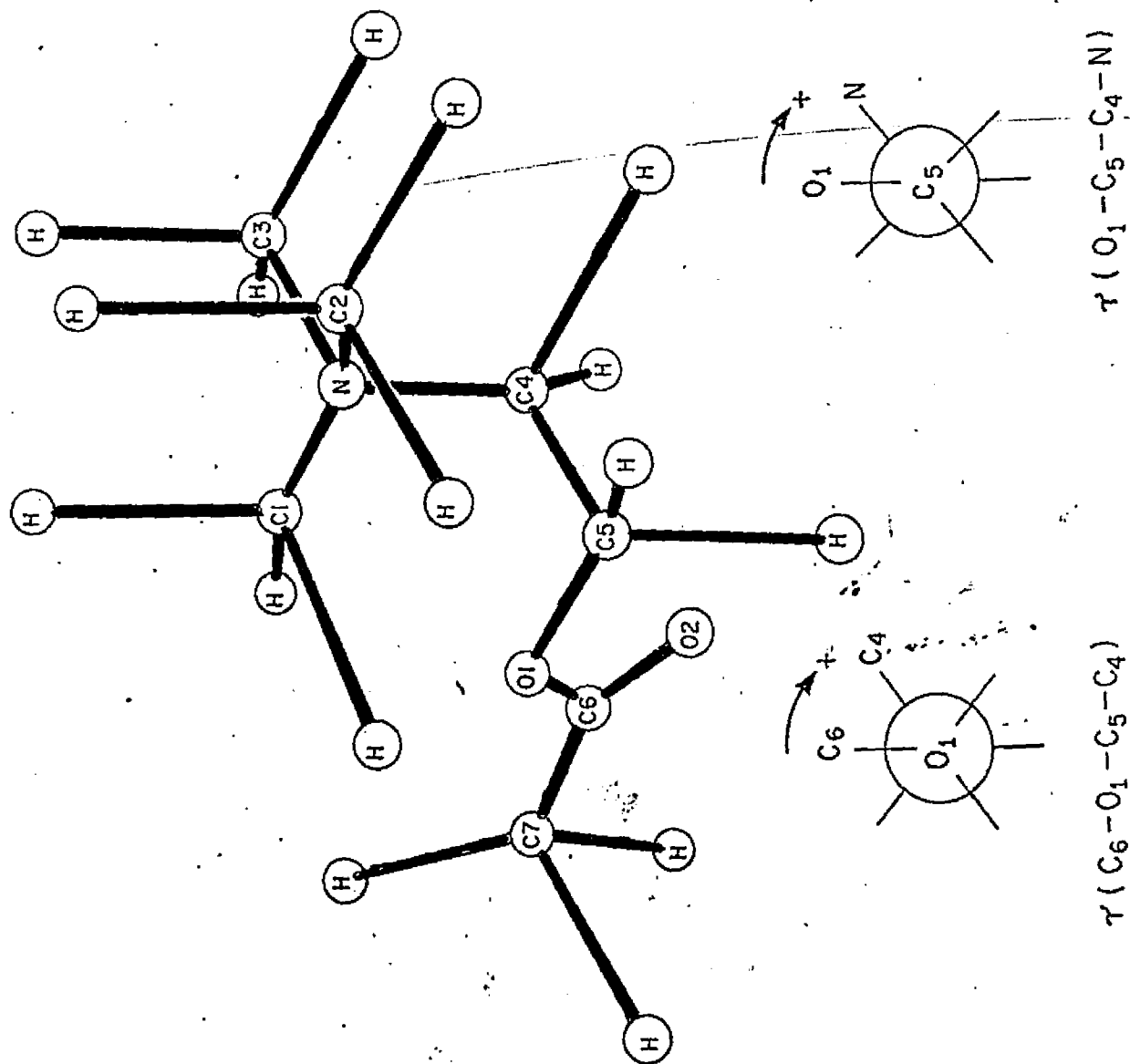


Figure 1

Figure 2

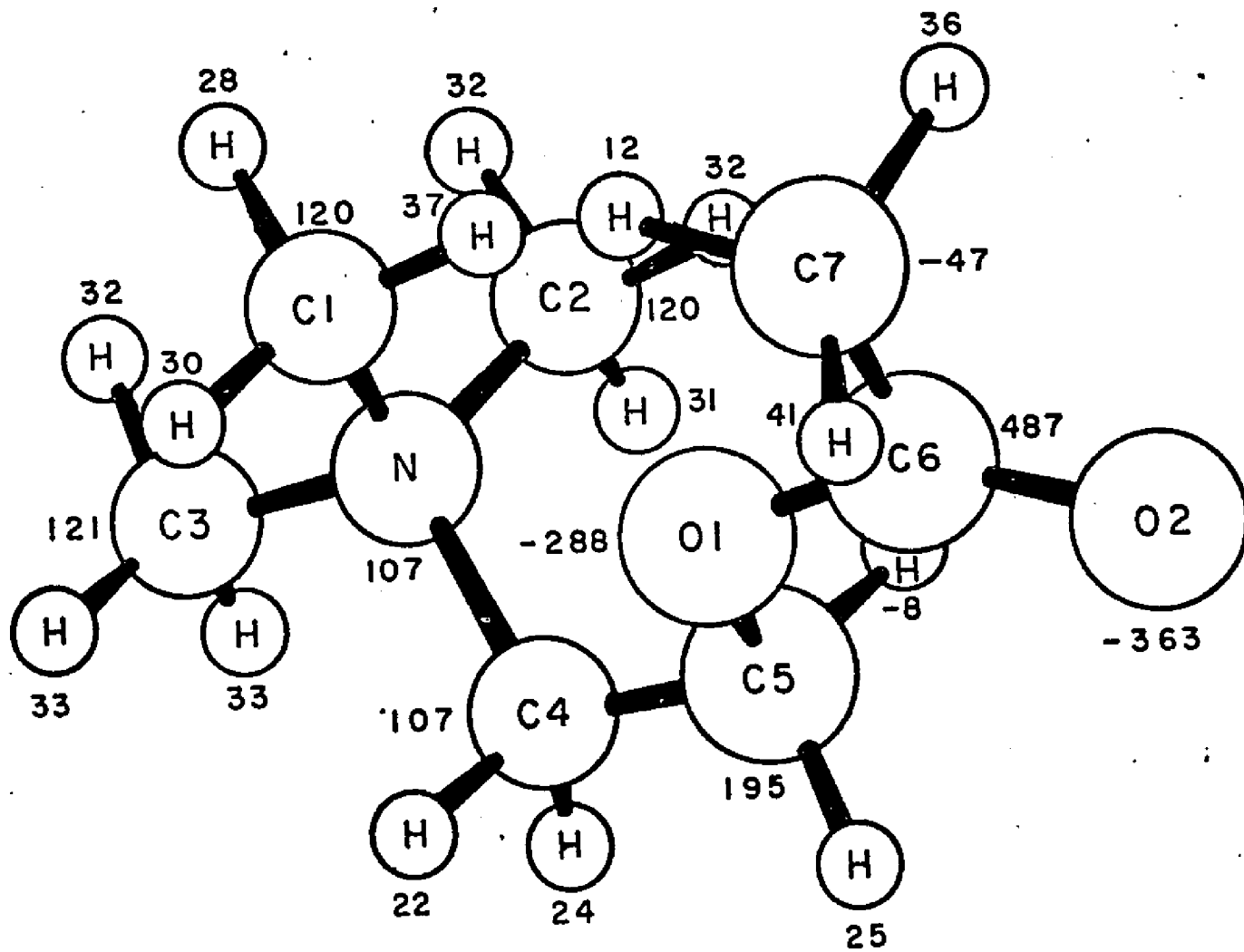


Figure 3

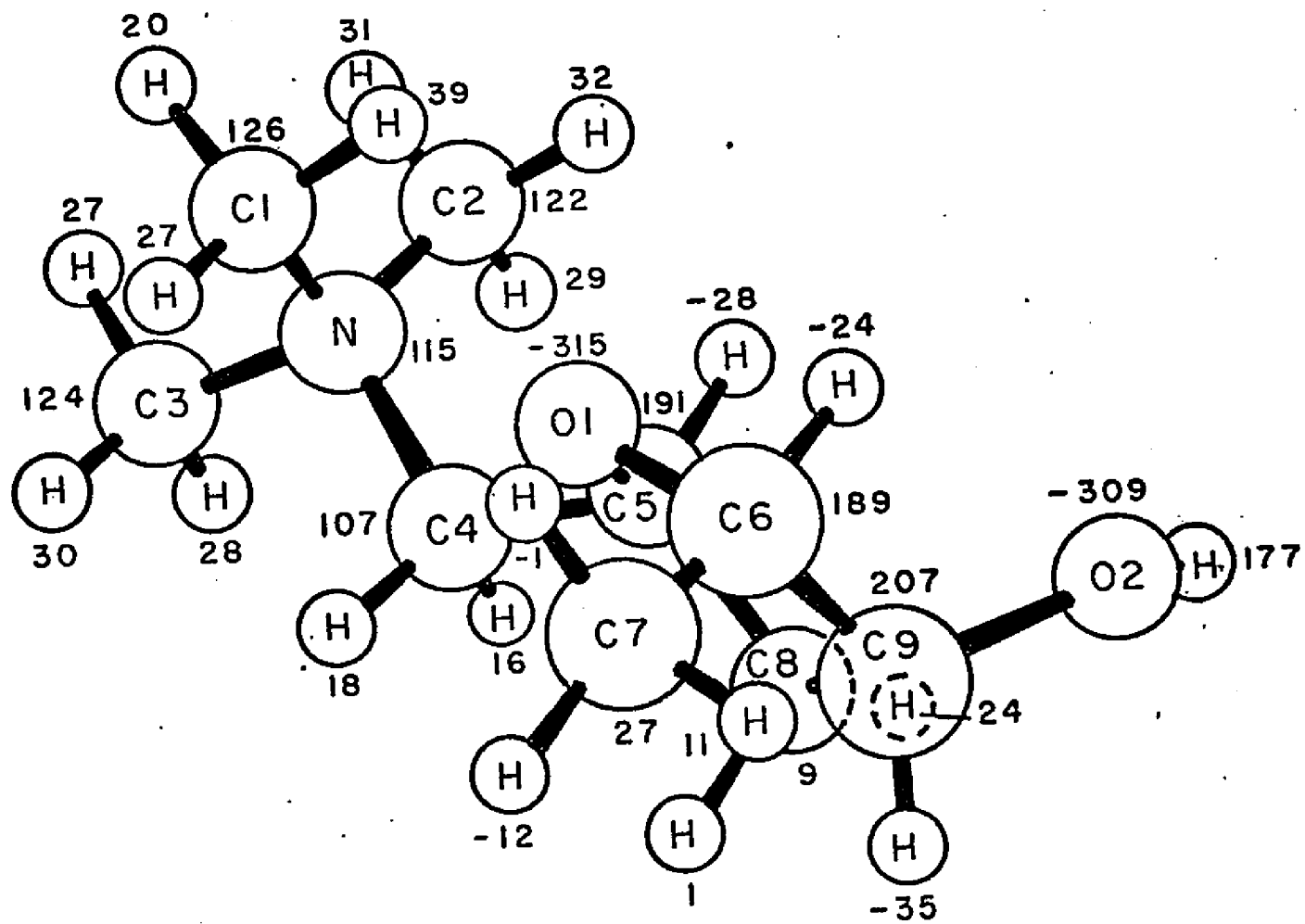
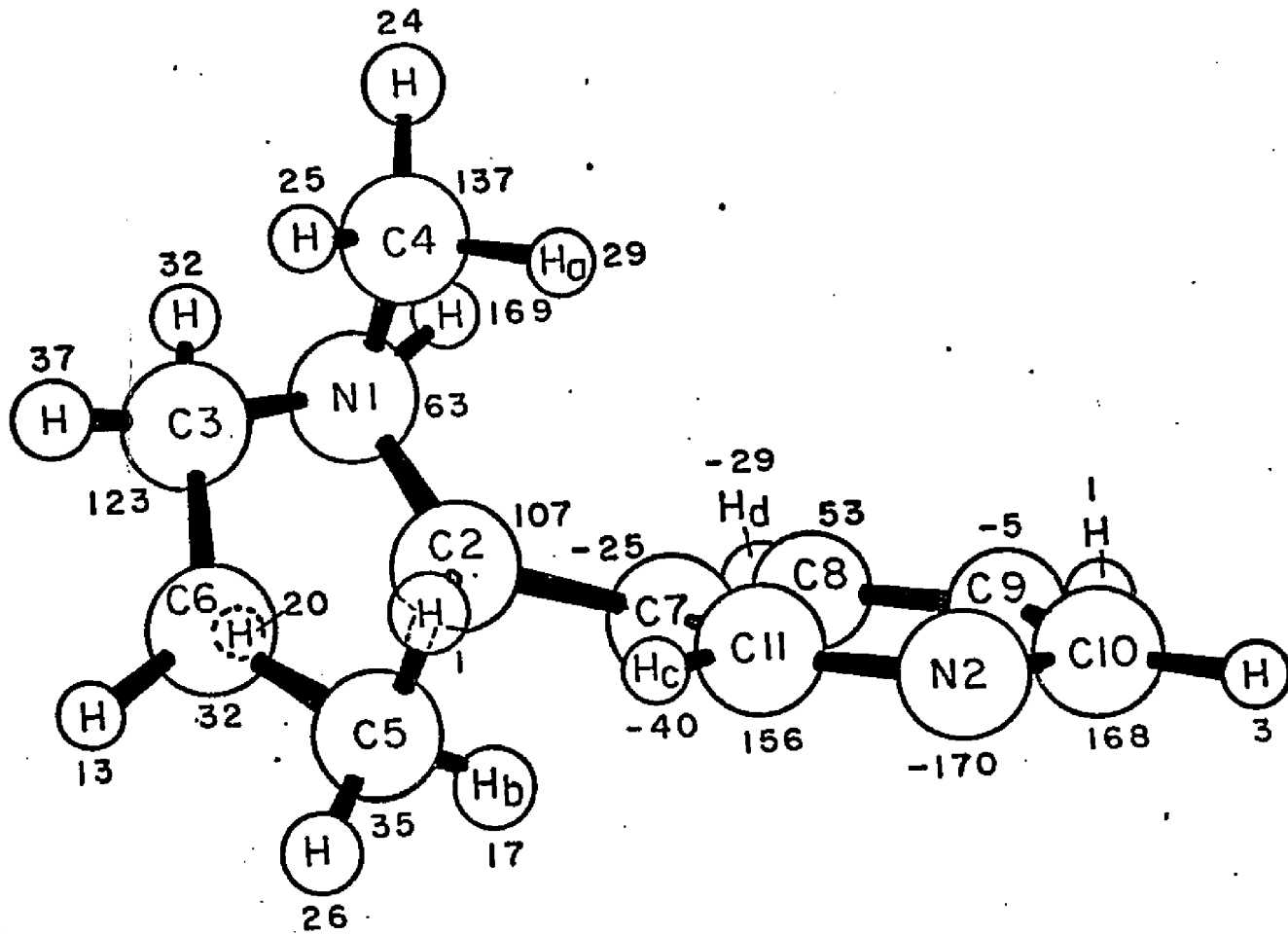


Figure 4
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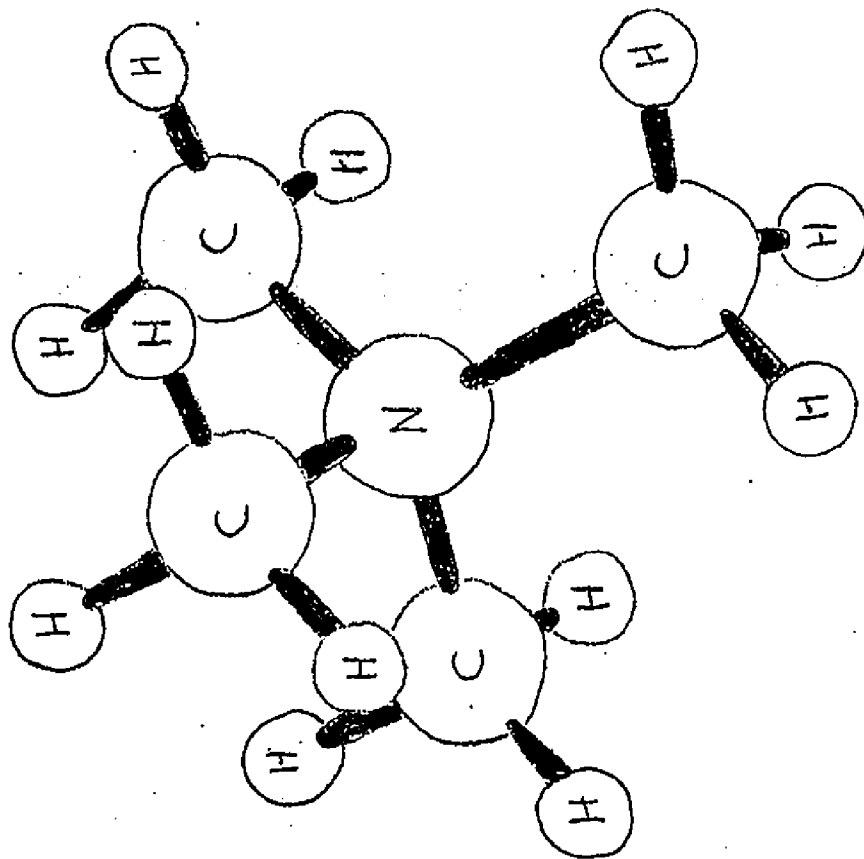


Figure 5

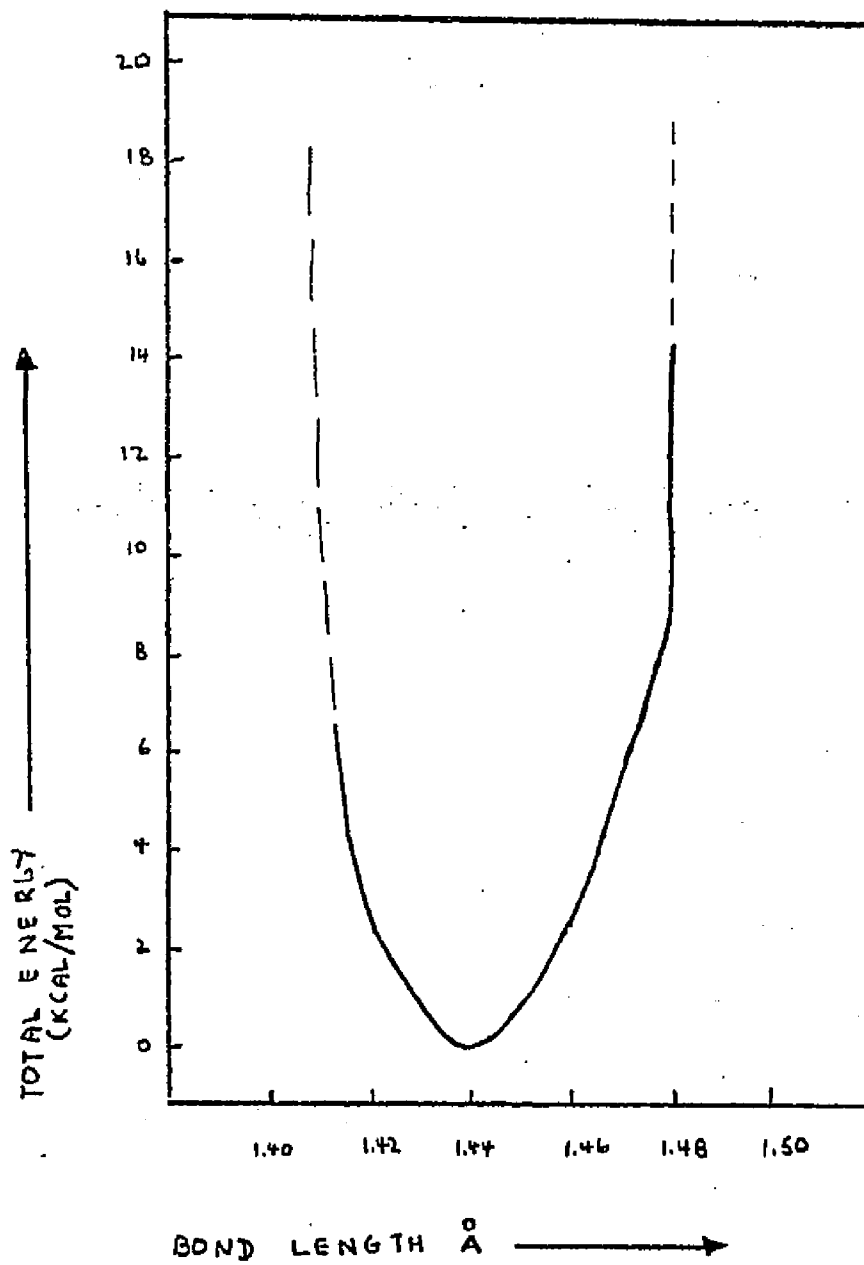


Figure 6

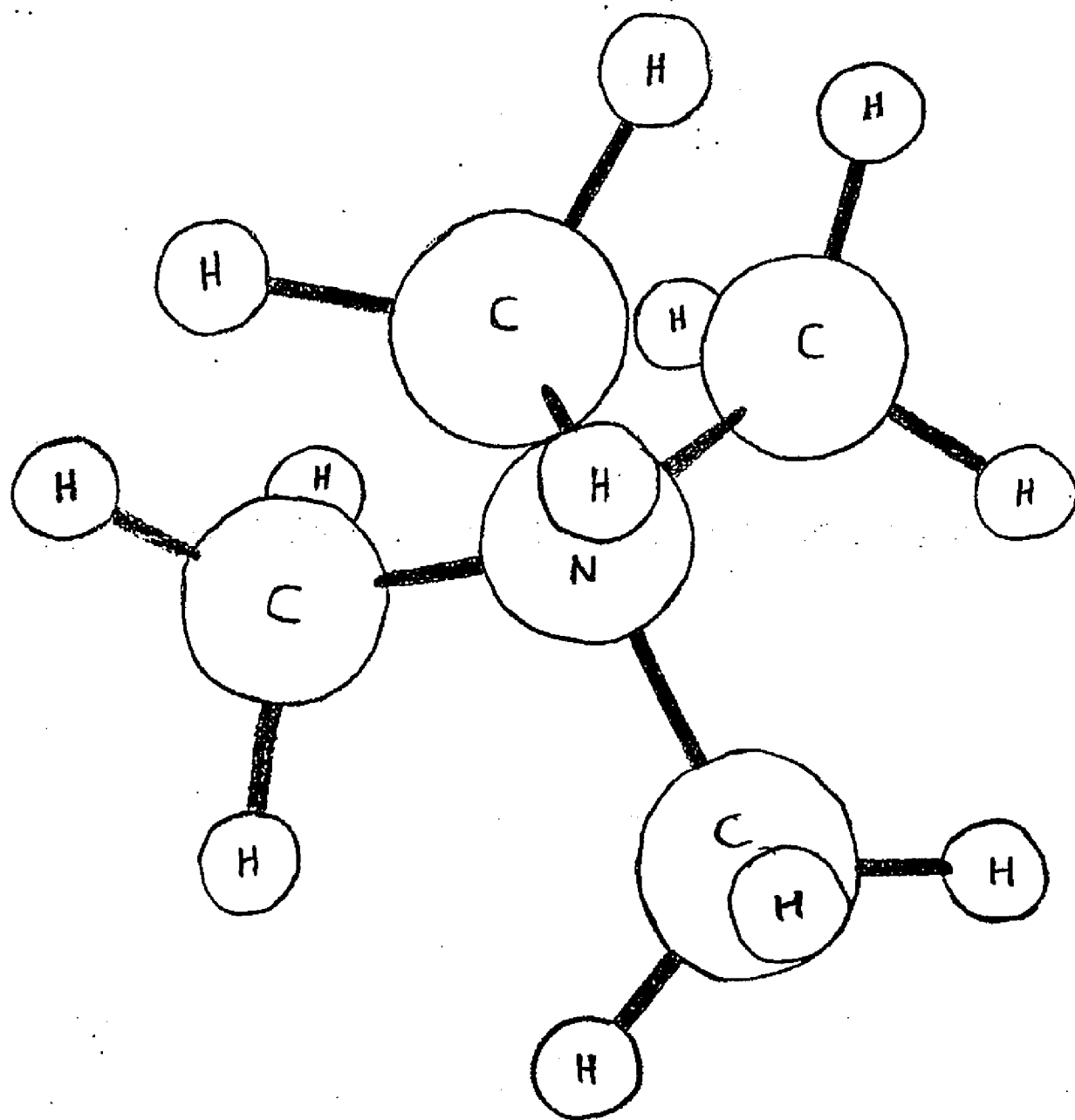
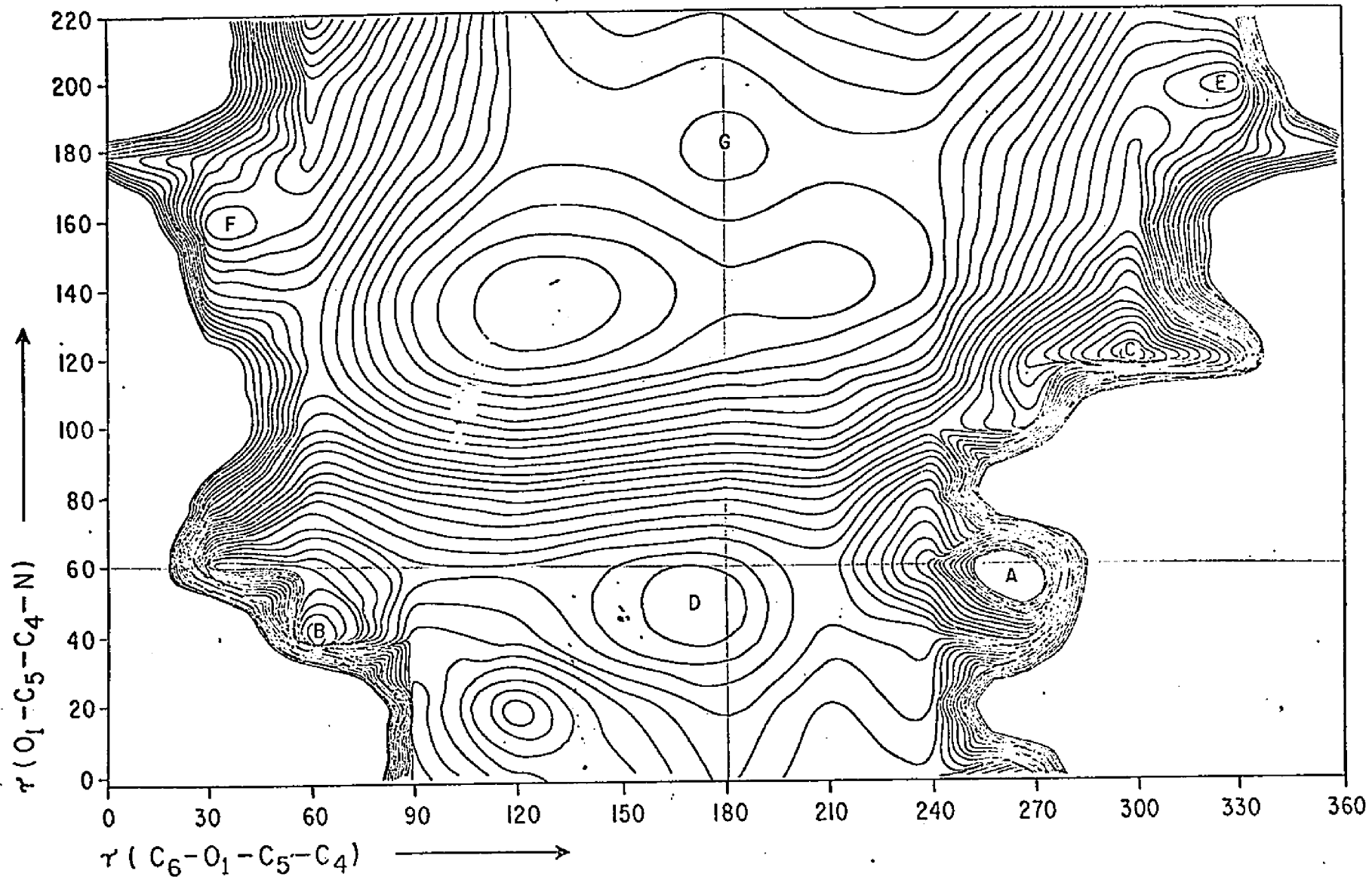


Figure 7

Figure 8



64
Figure 9

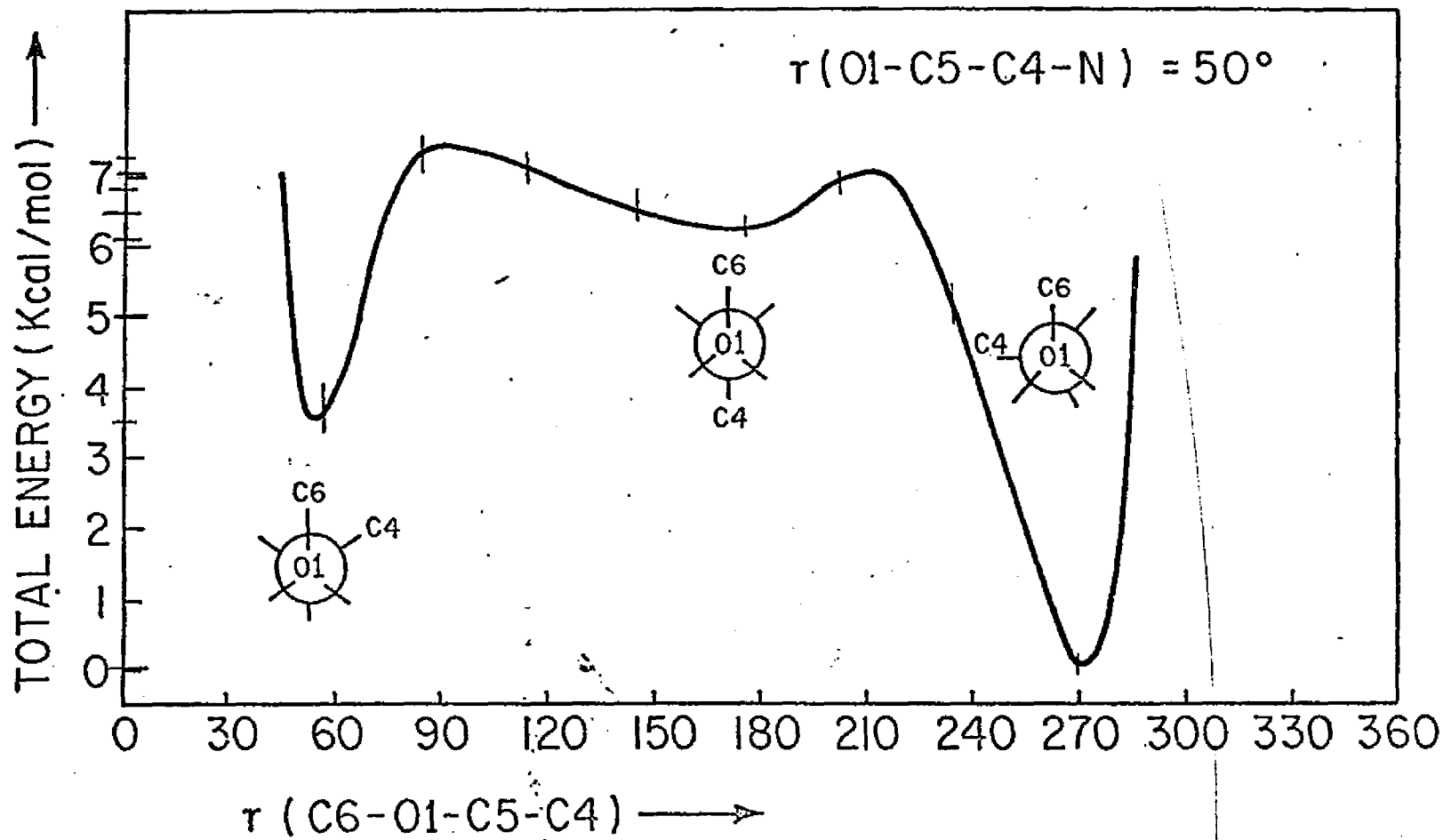
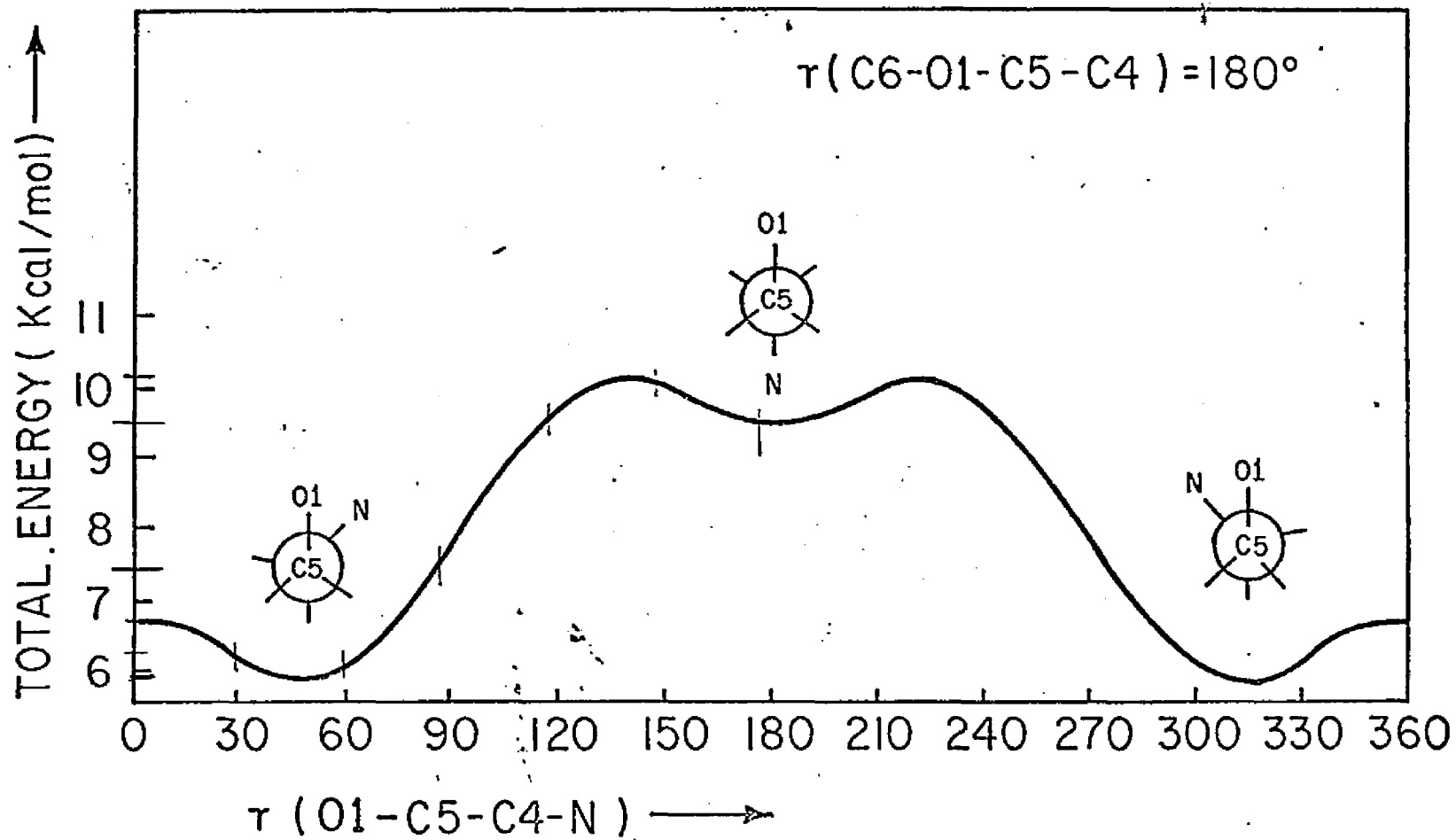


Figure 10



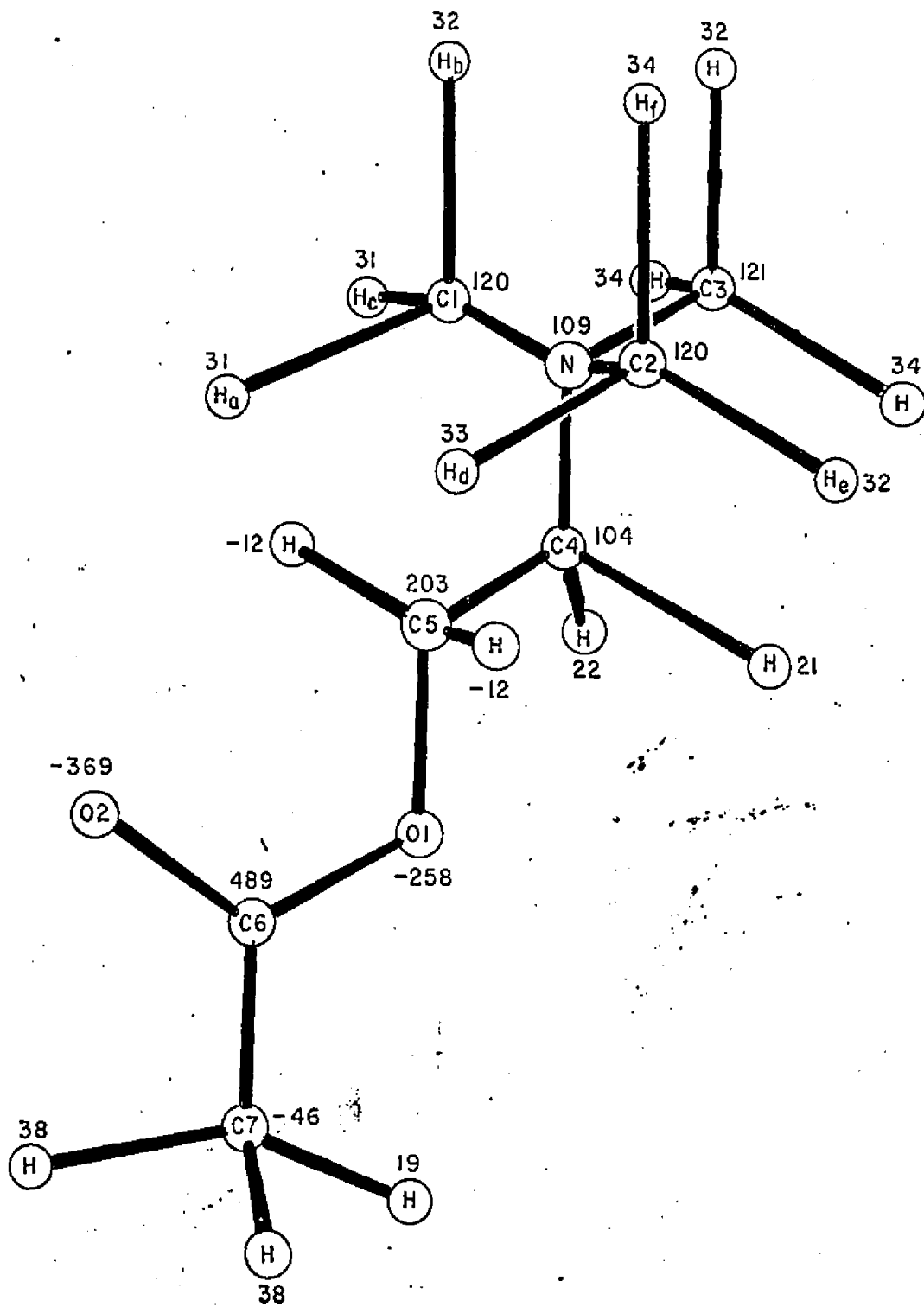


Figure 11

Figure 12

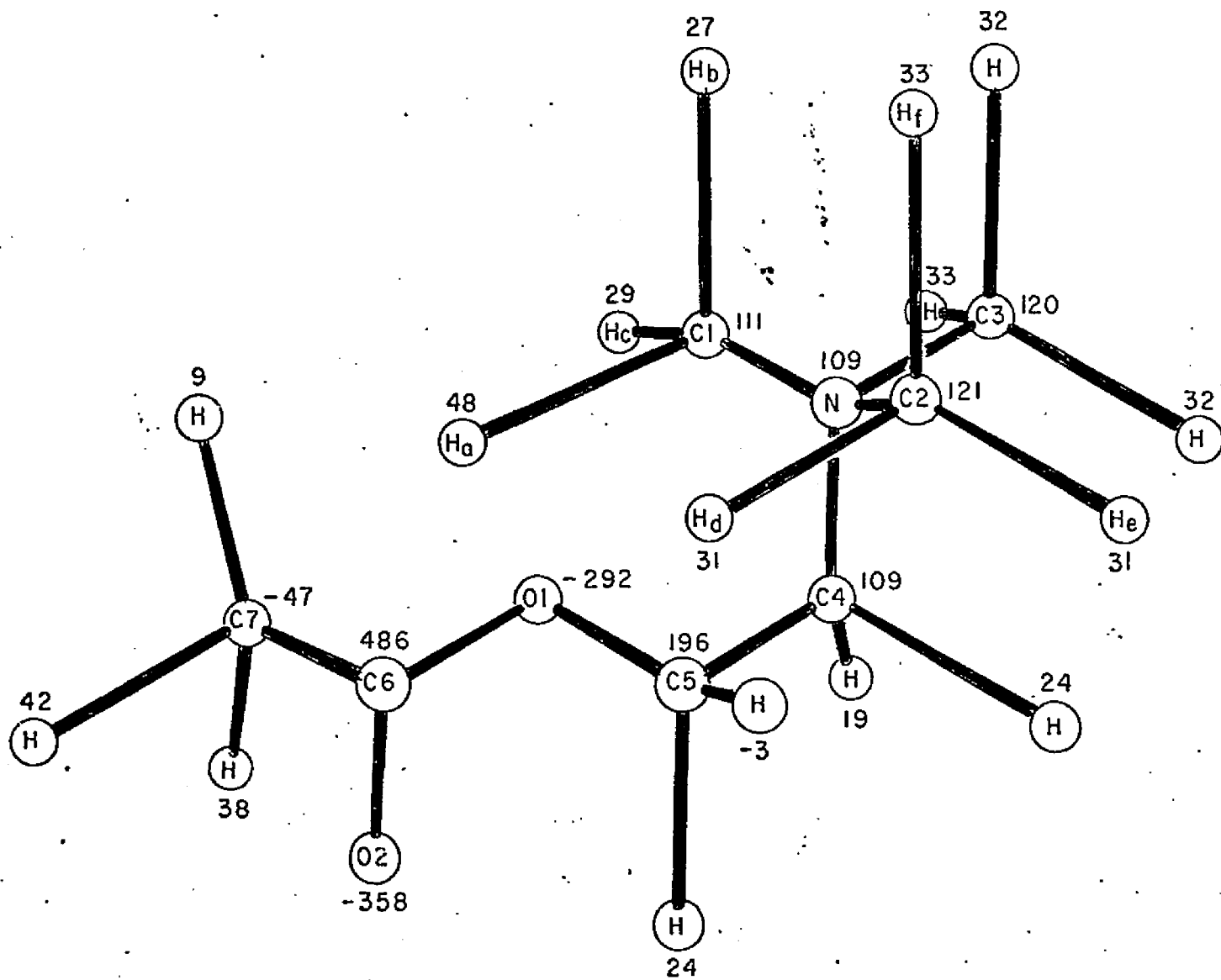


Figure 13

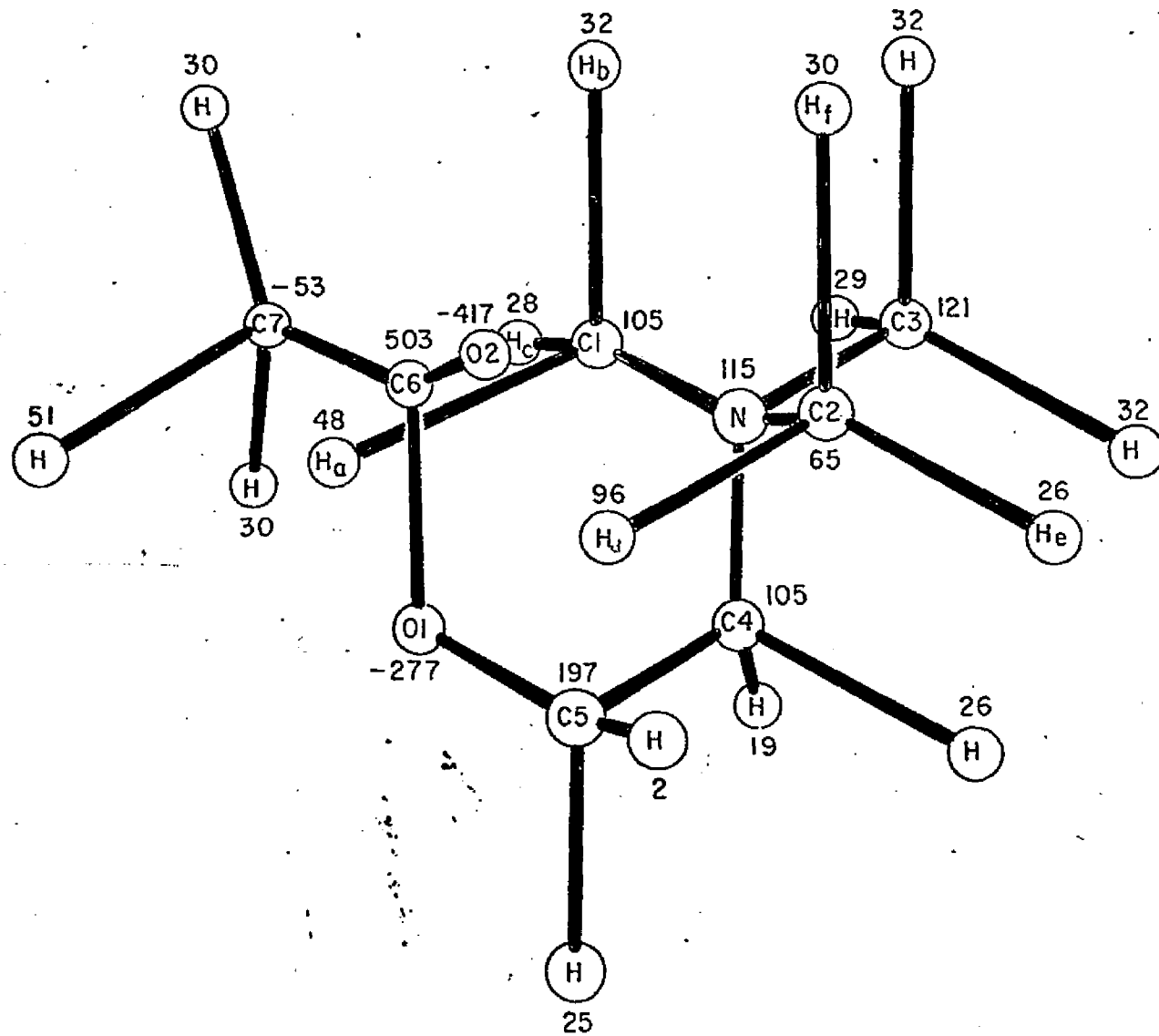
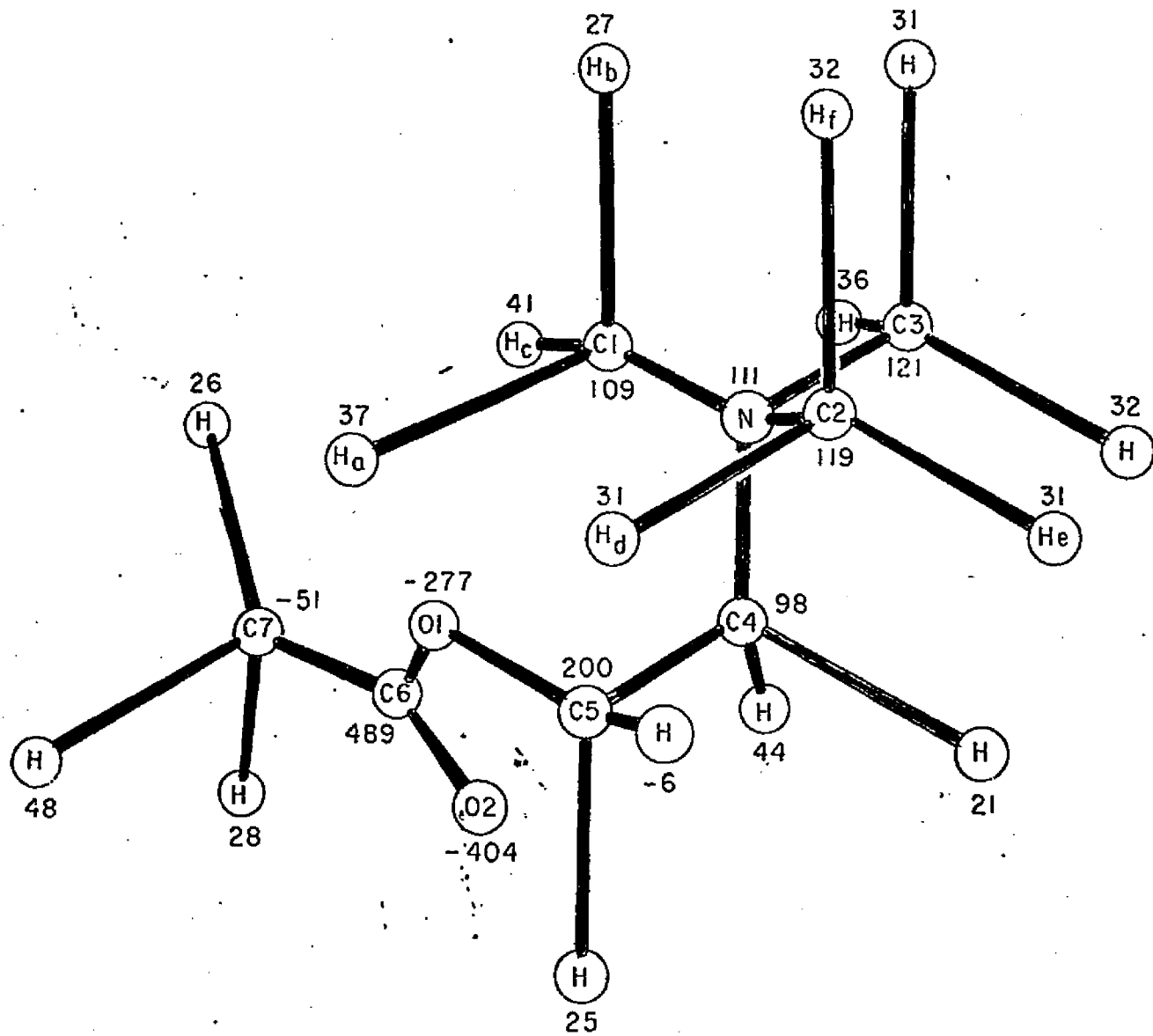


Figure 14



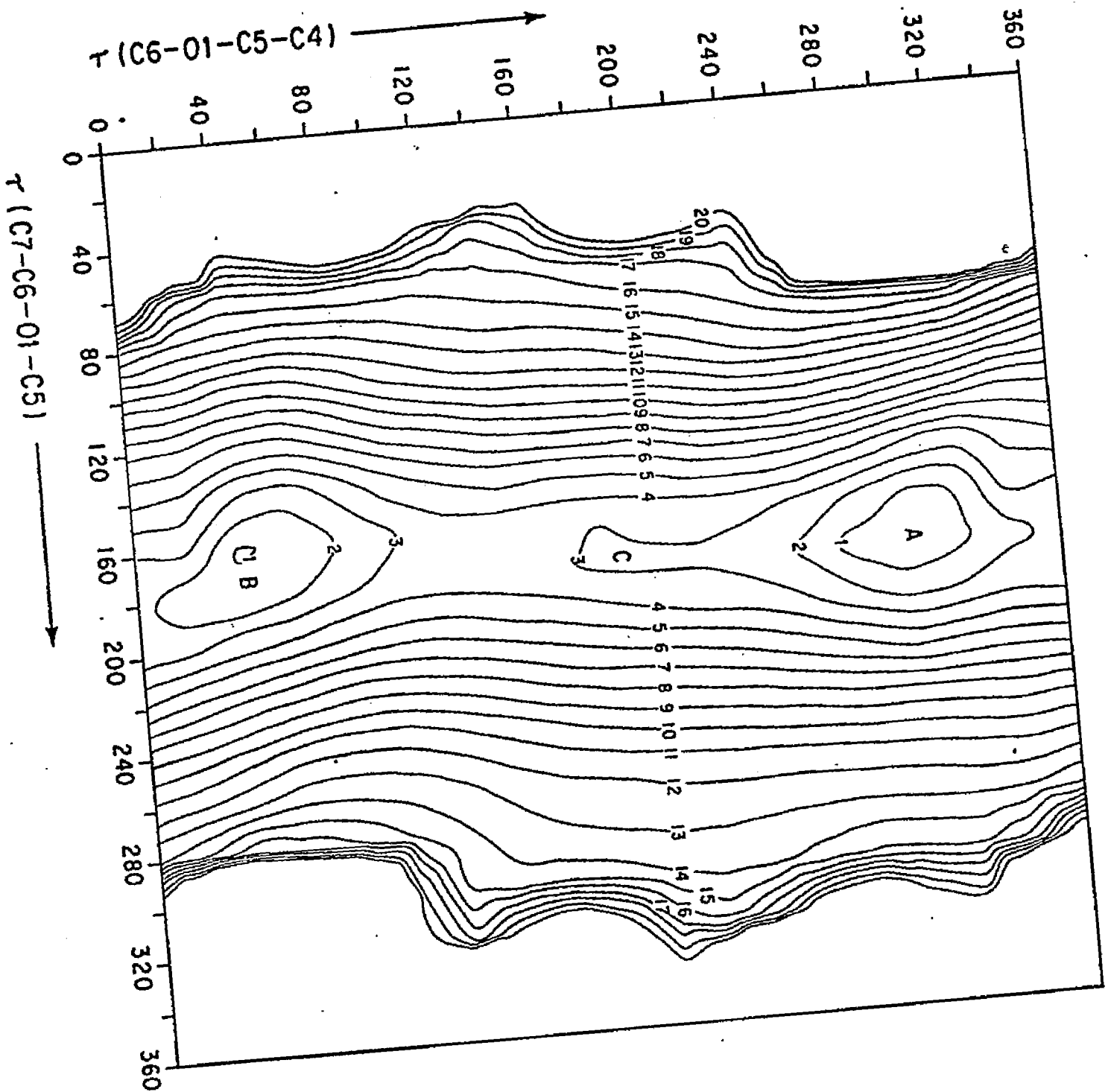


Figure 15

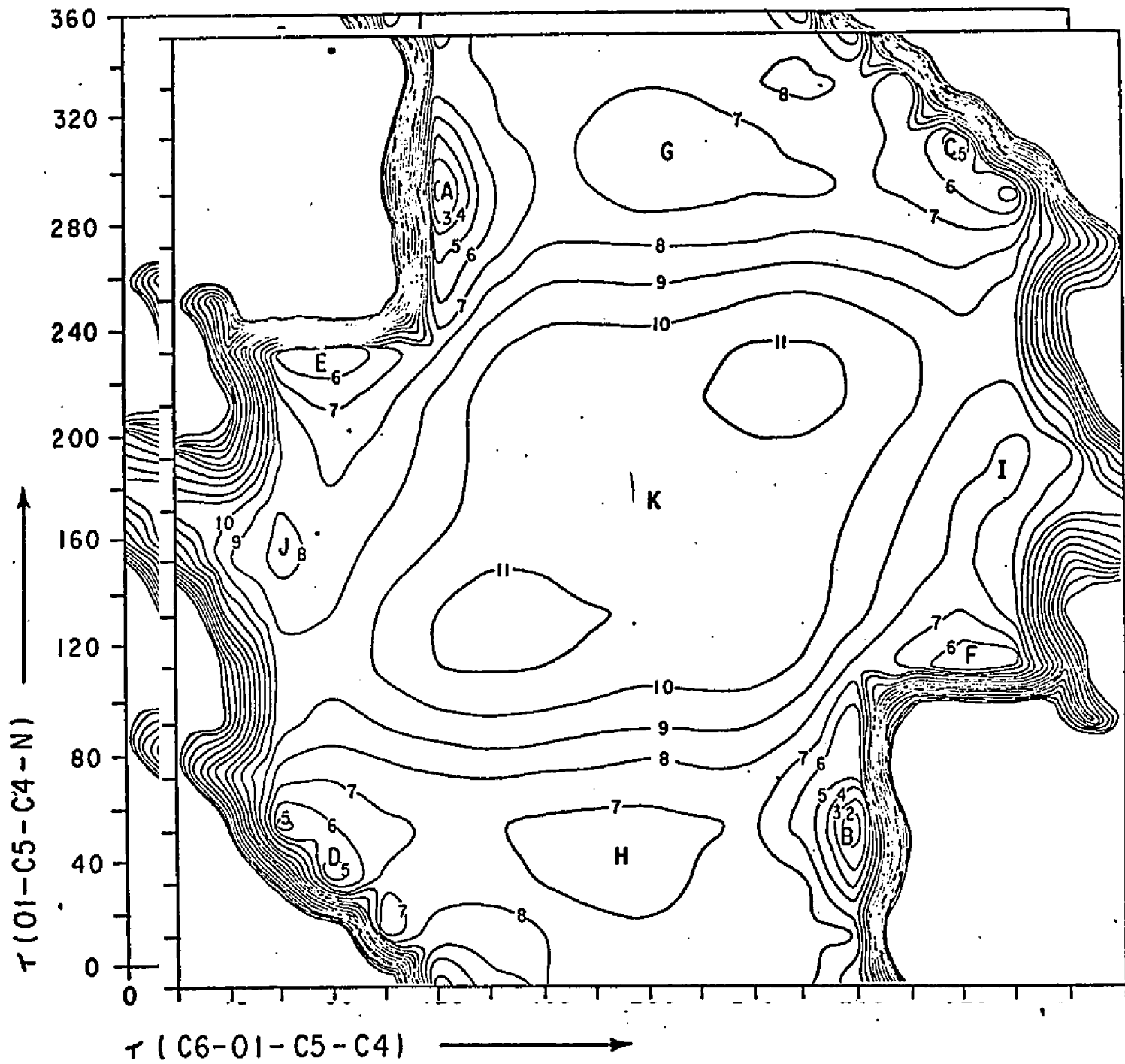


Figure 16

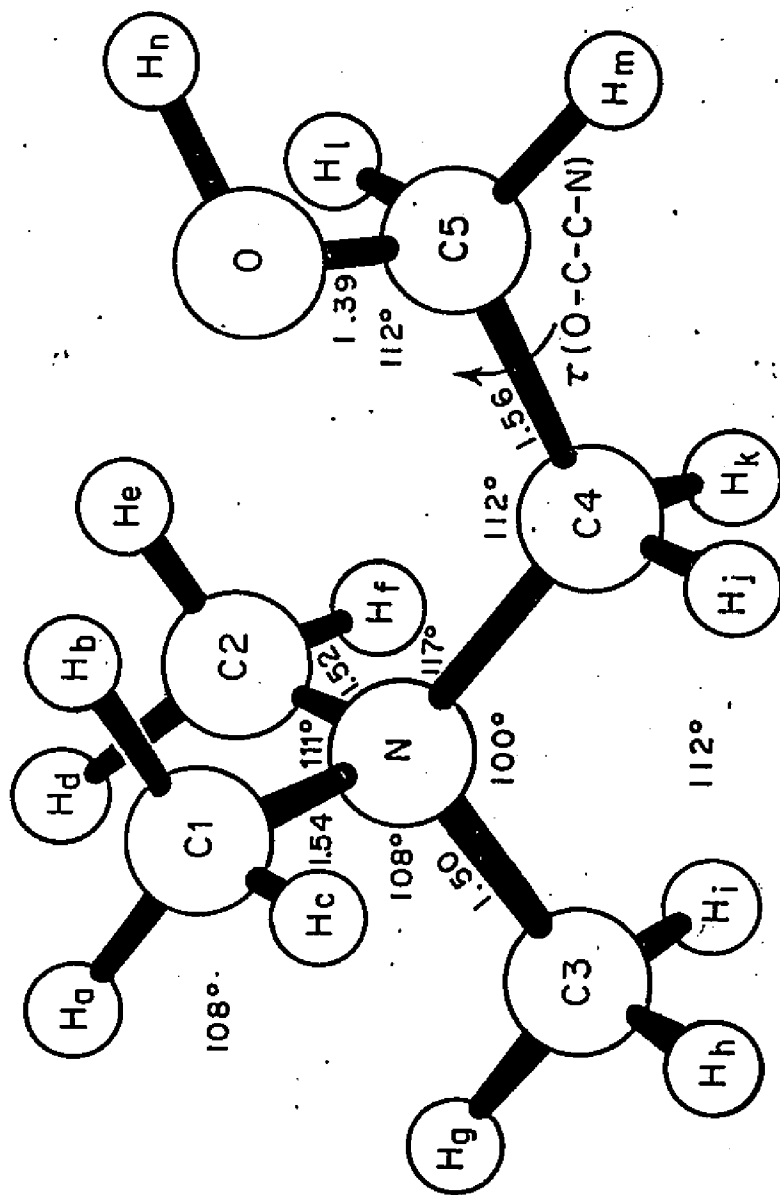


Figure 17

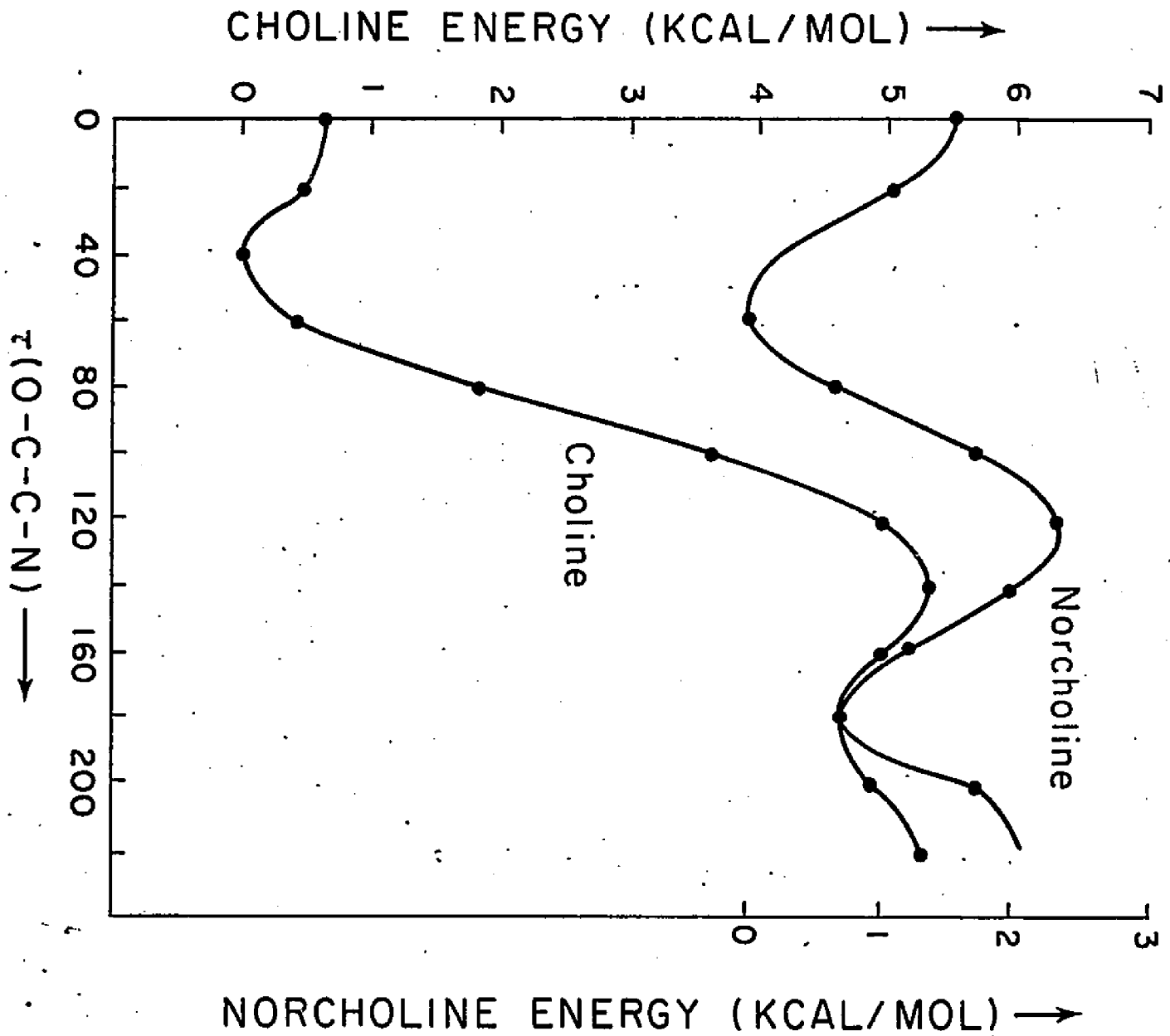
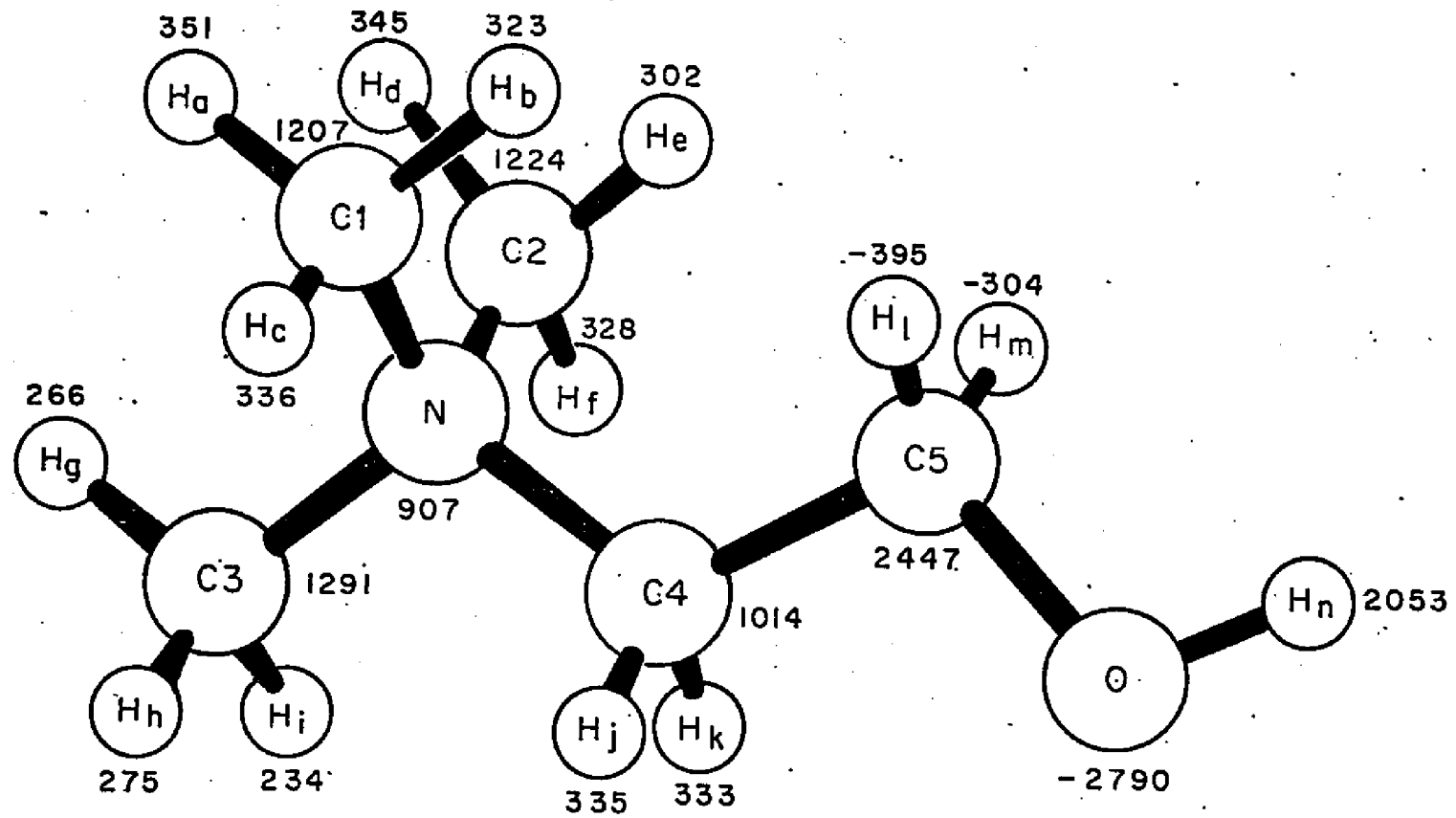
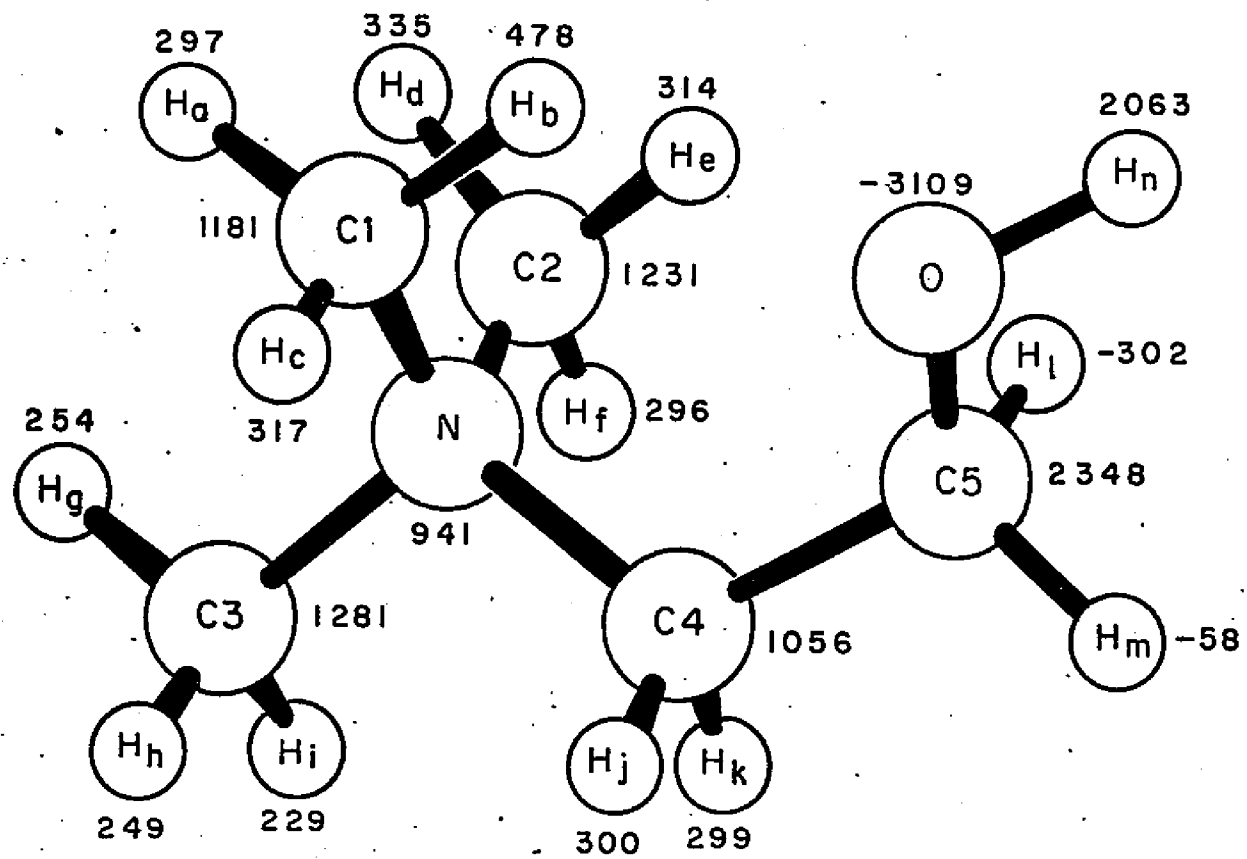


Figure 18

Figure 19
74



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Figure 20



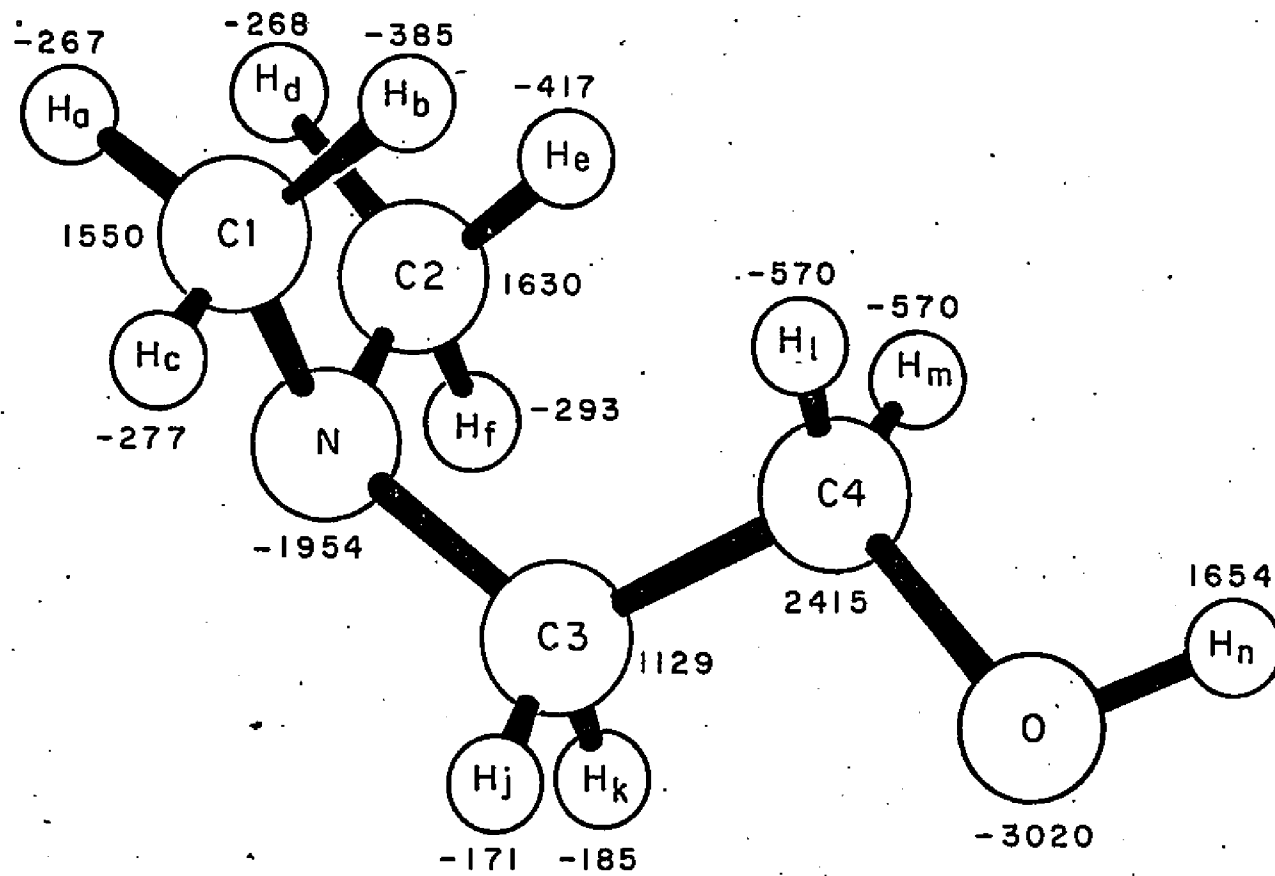


Figure 21

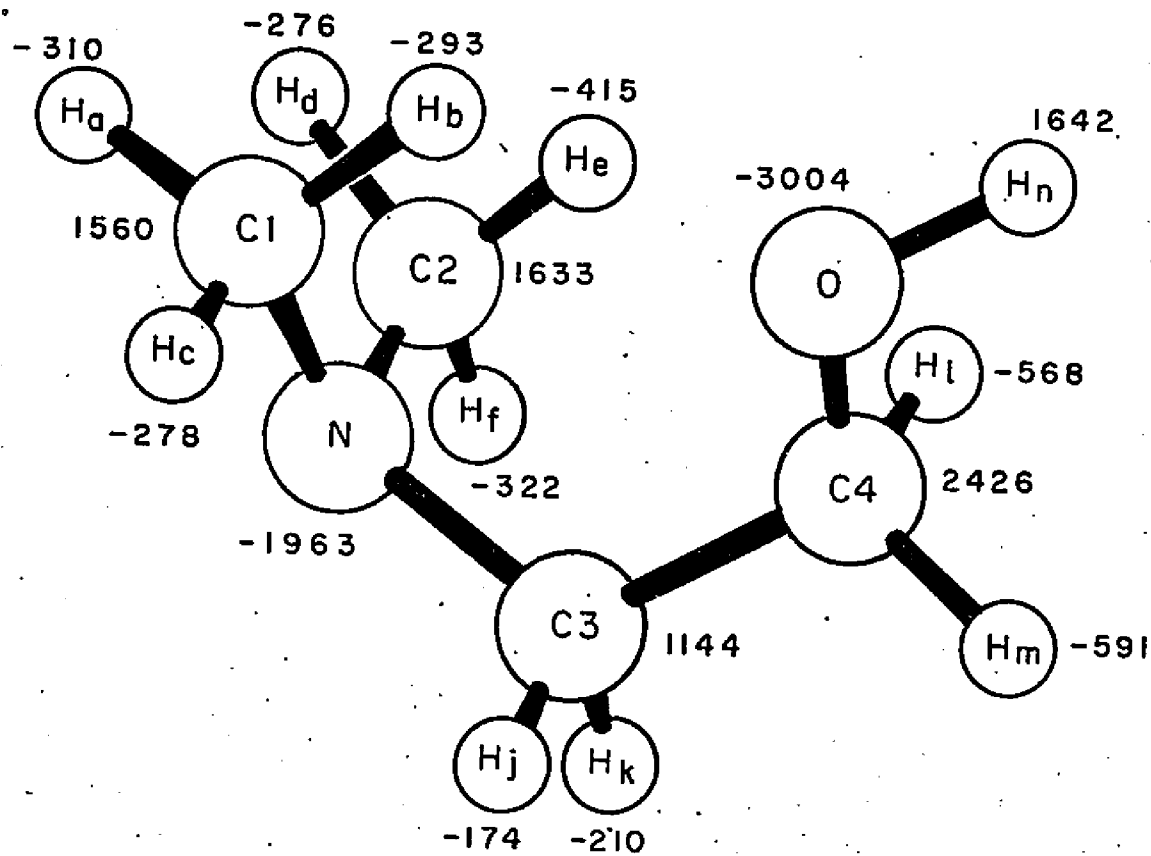


Figure 22

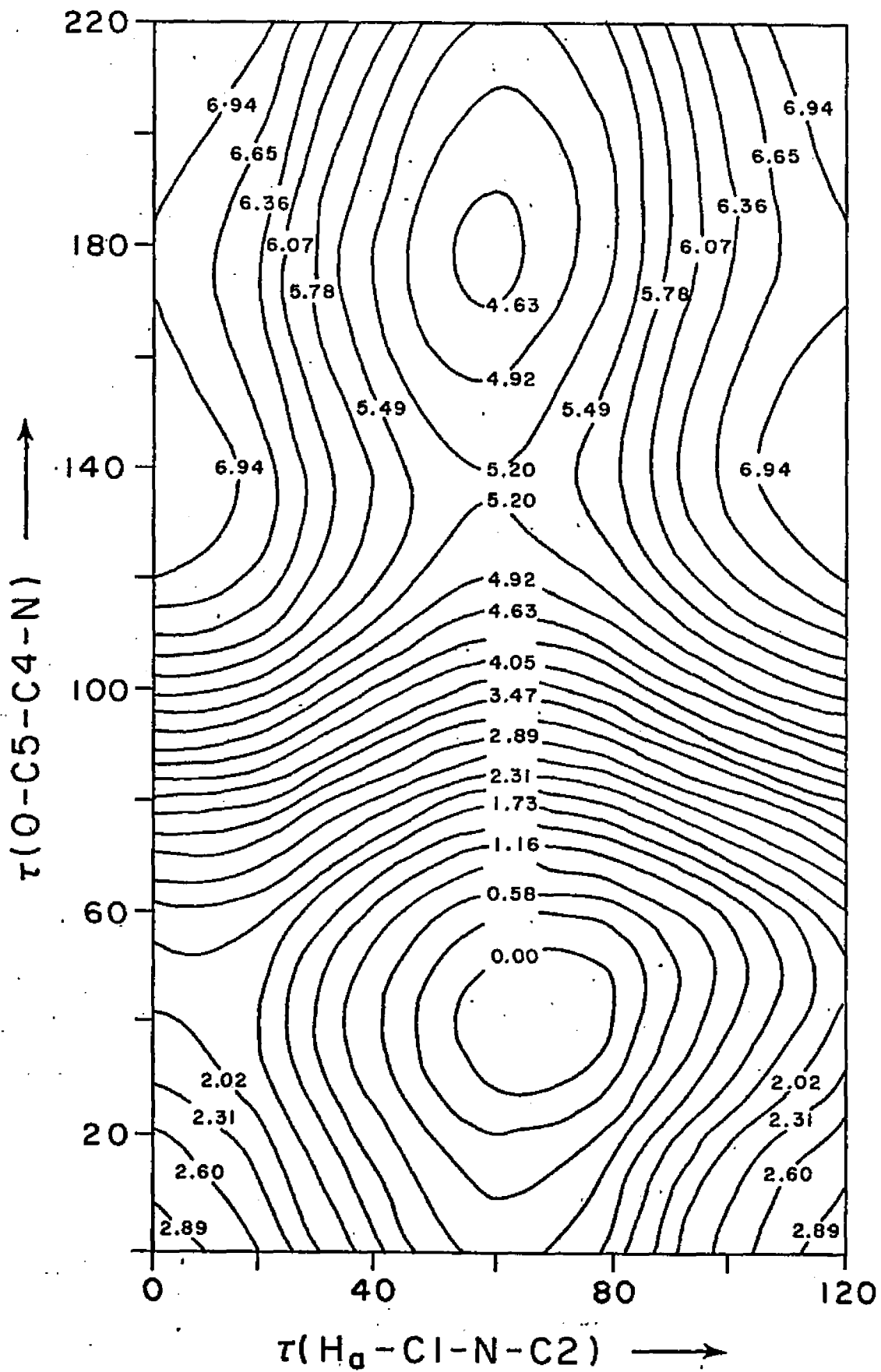


Figure 23

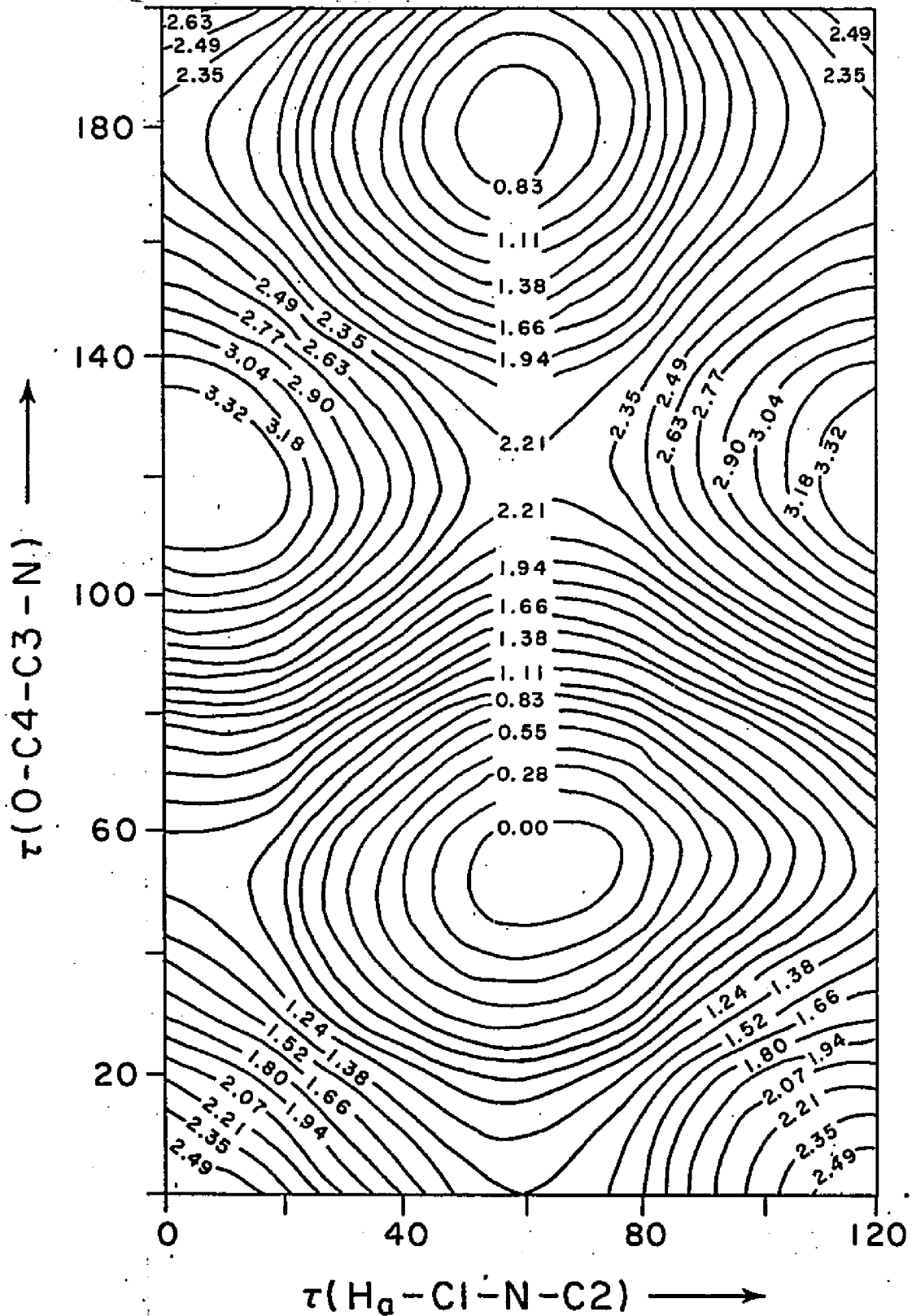


Figure 24

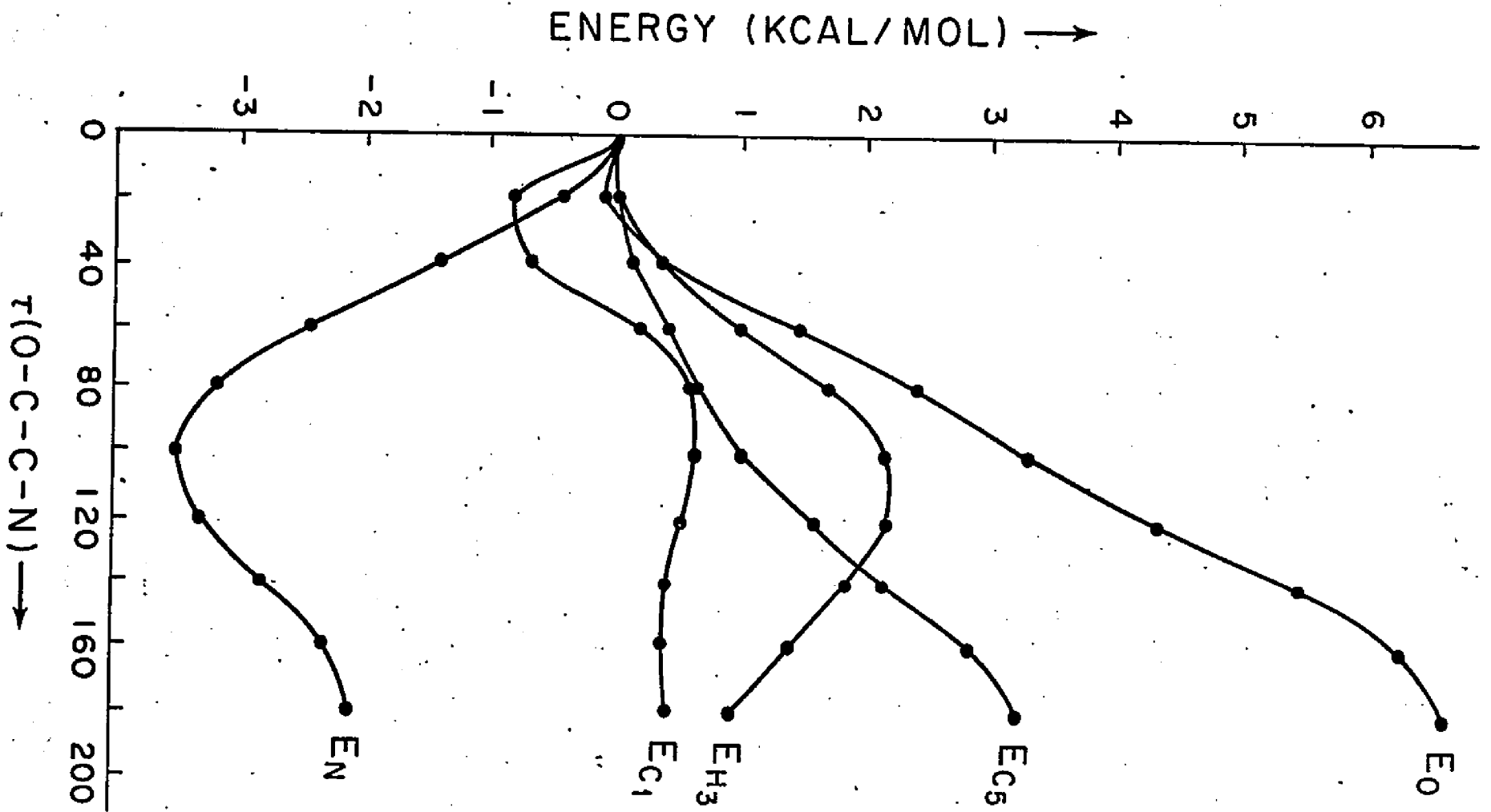


Figure 25
80

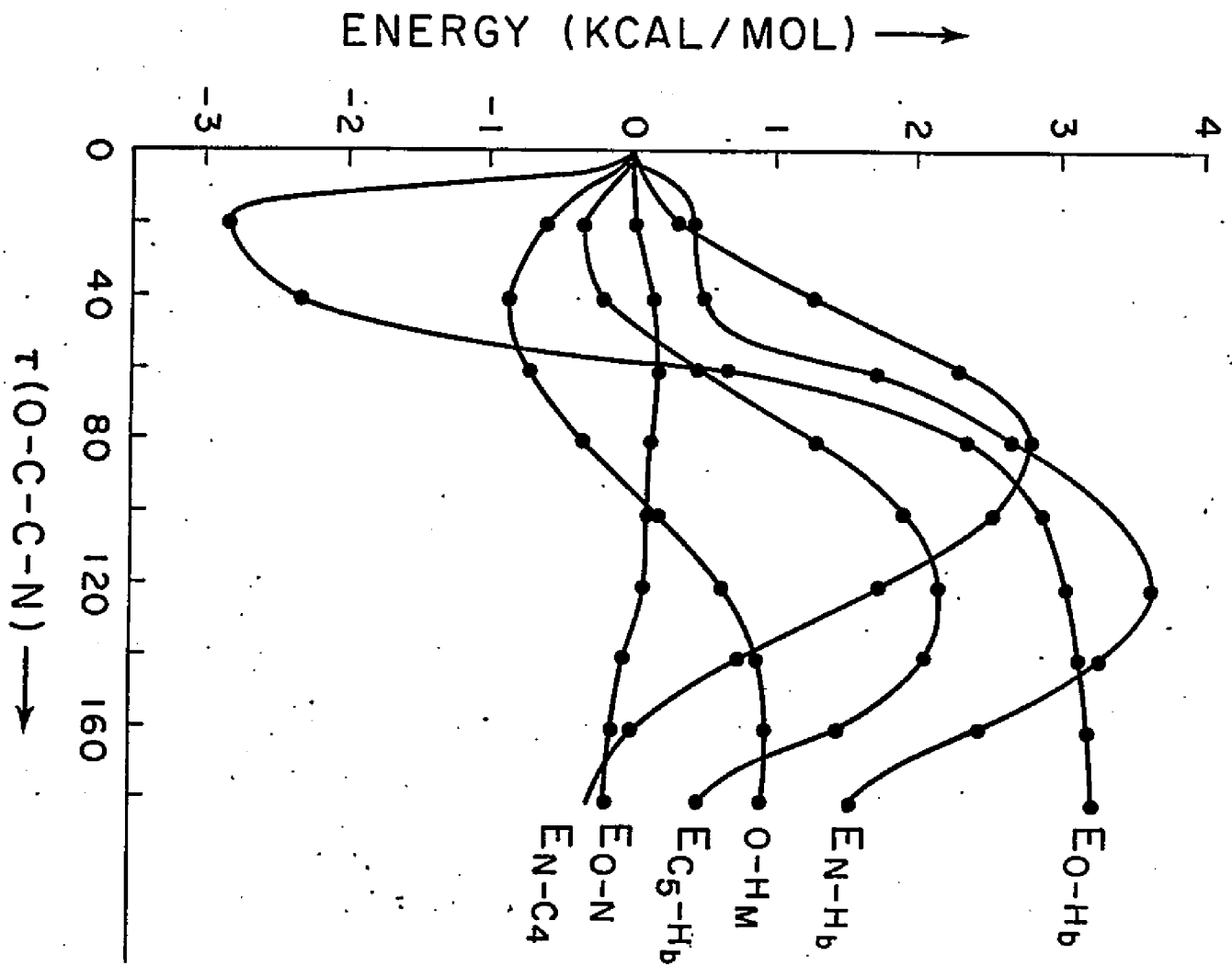


Figure 26

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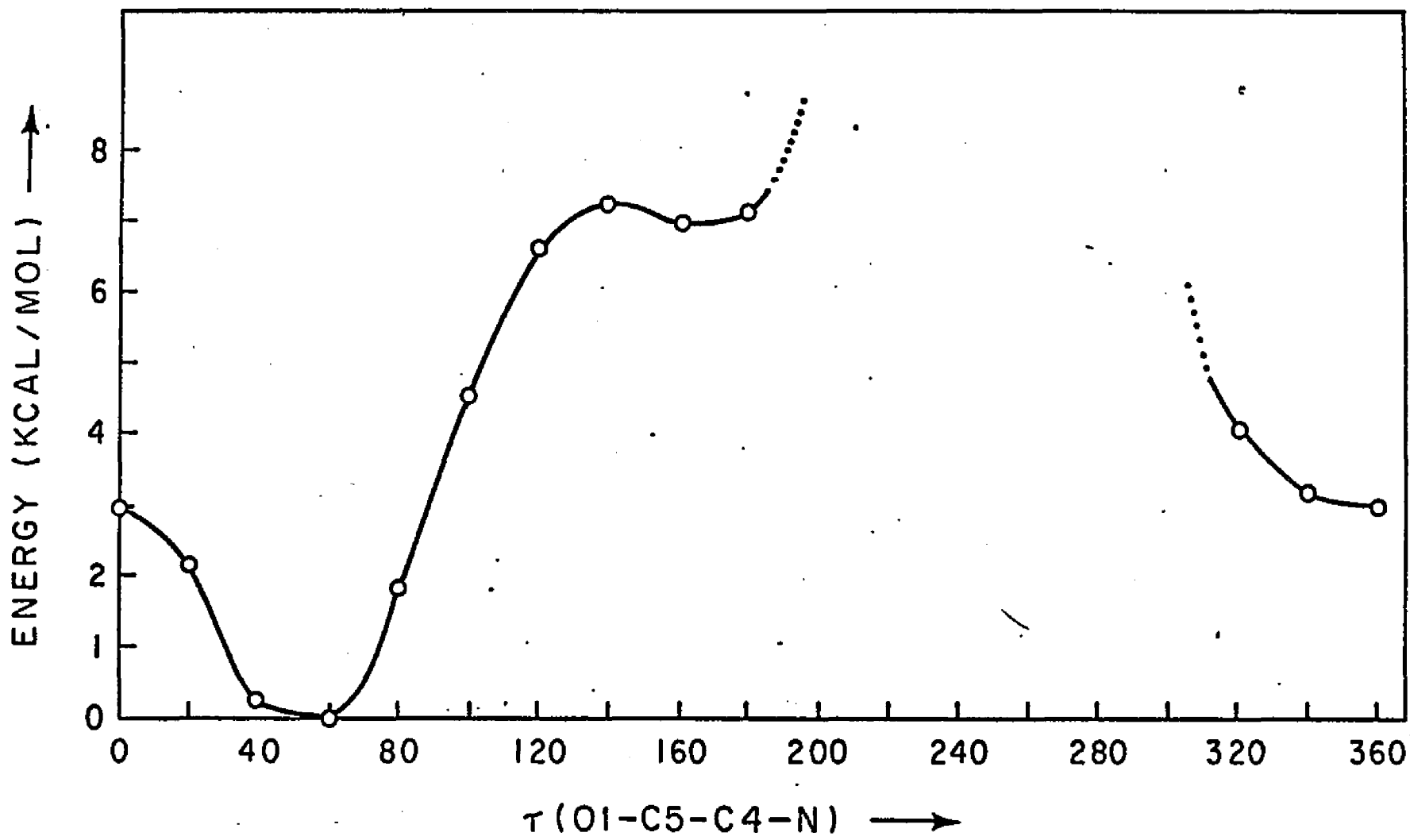
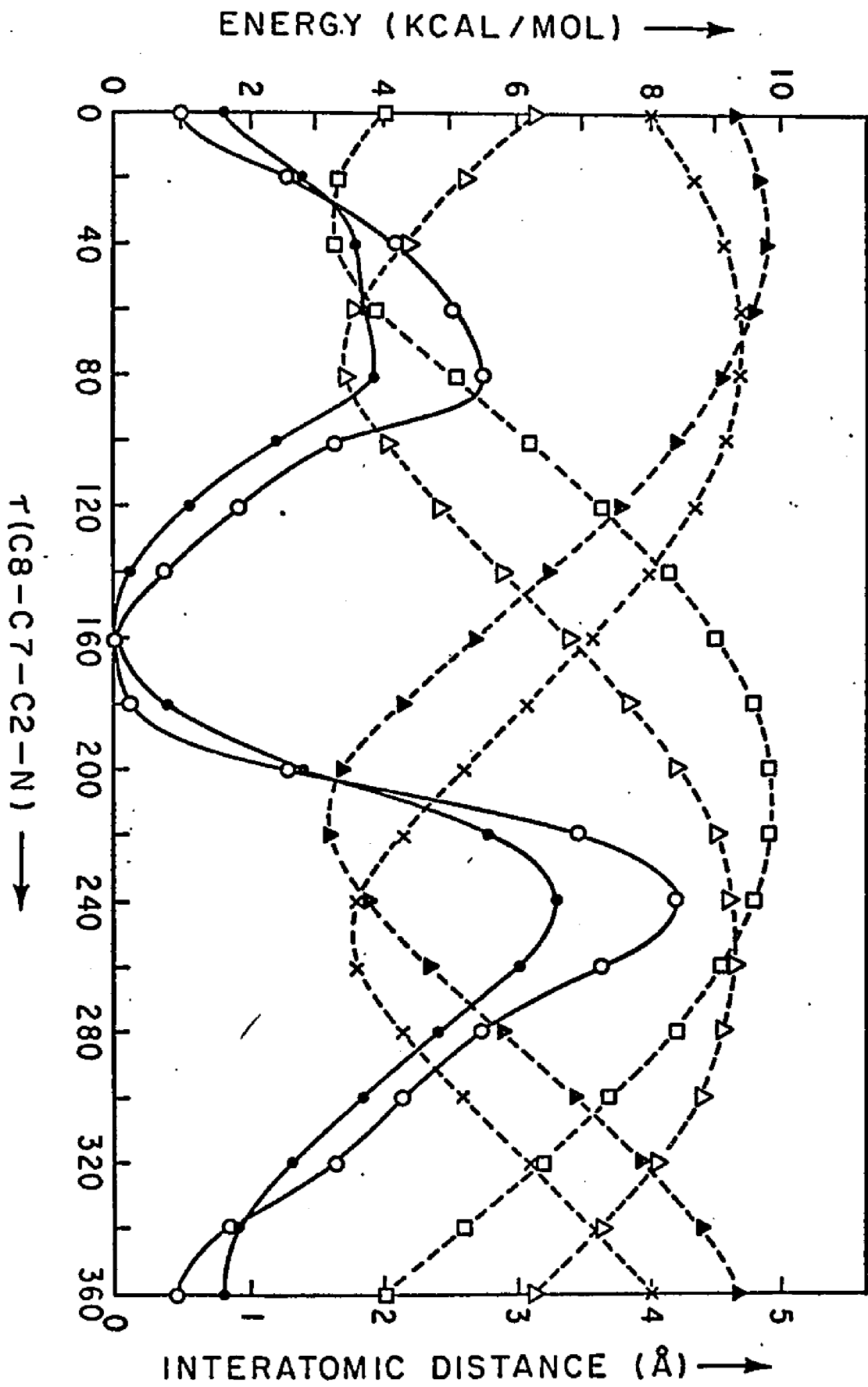


Figure 27

Figure 28

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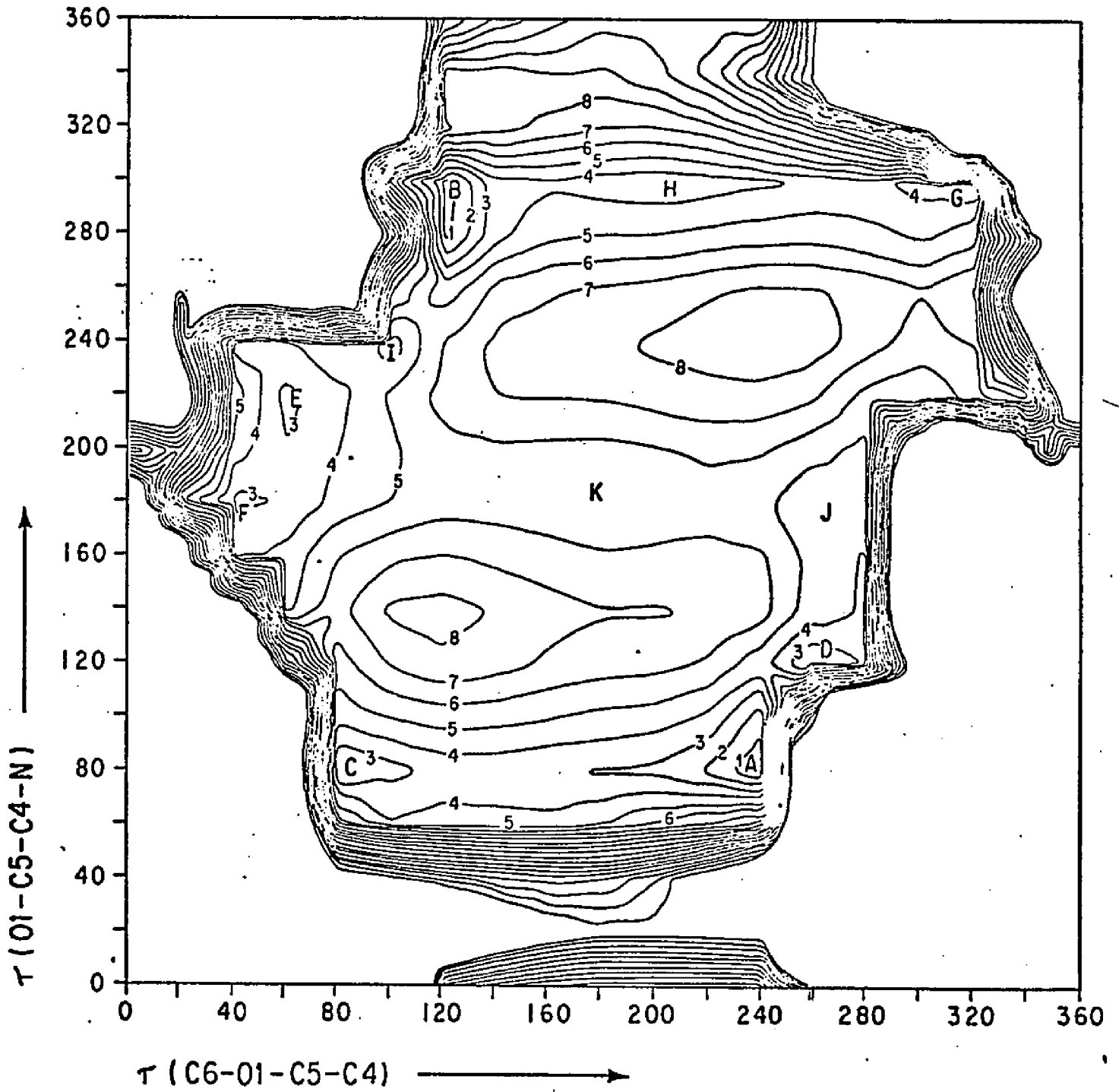


Figure 29

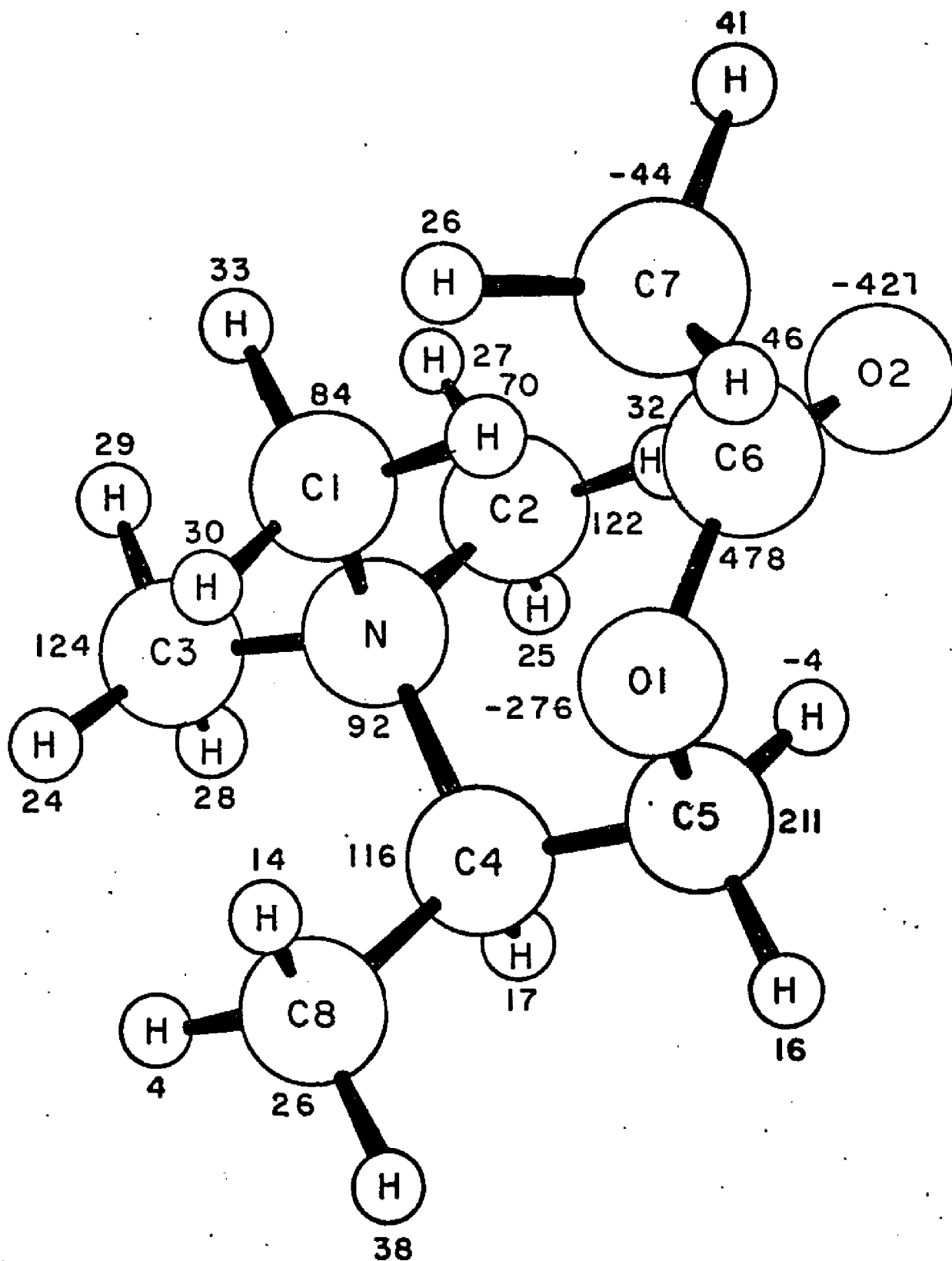


Figure 30

Figure 31
87

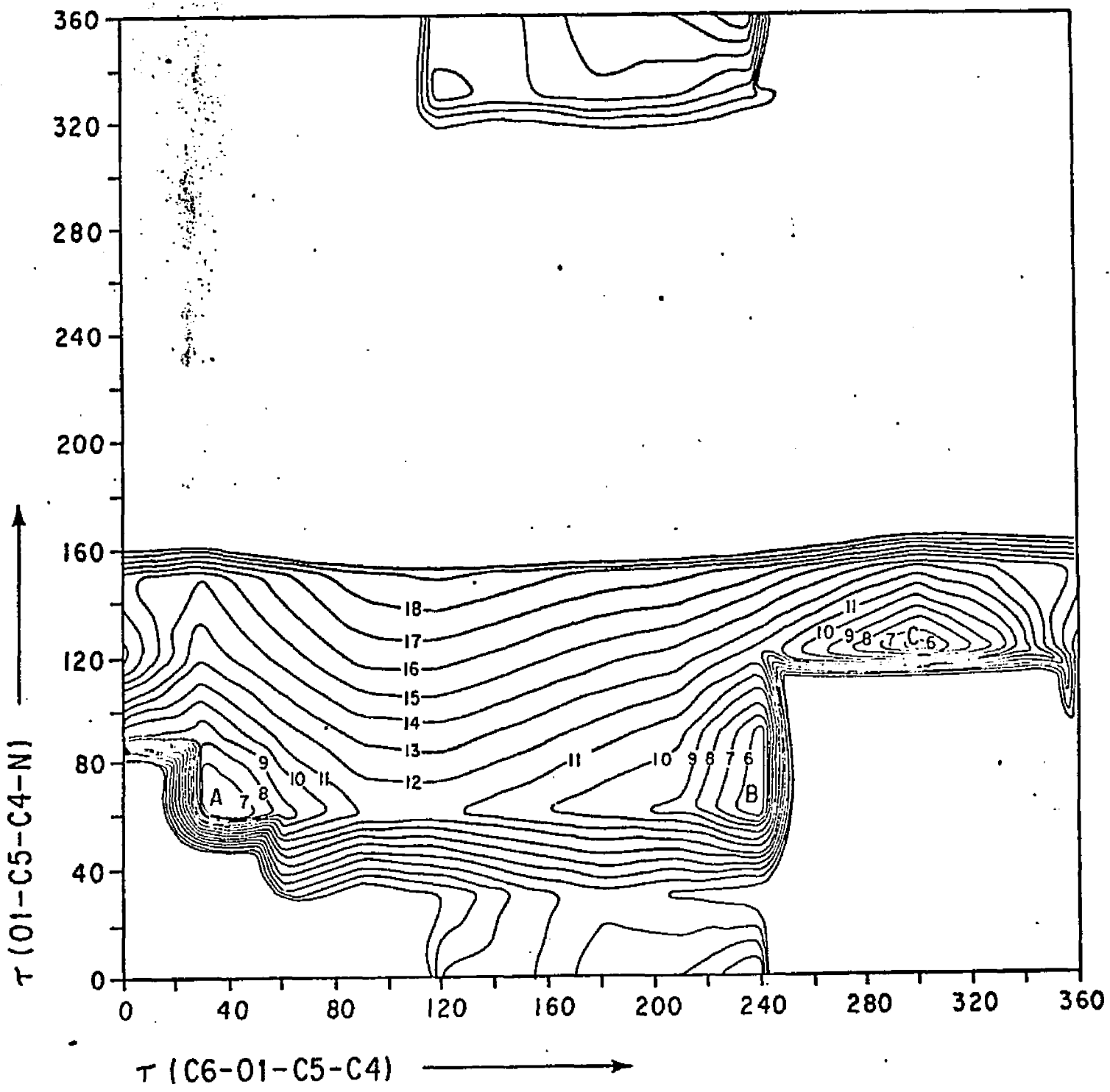
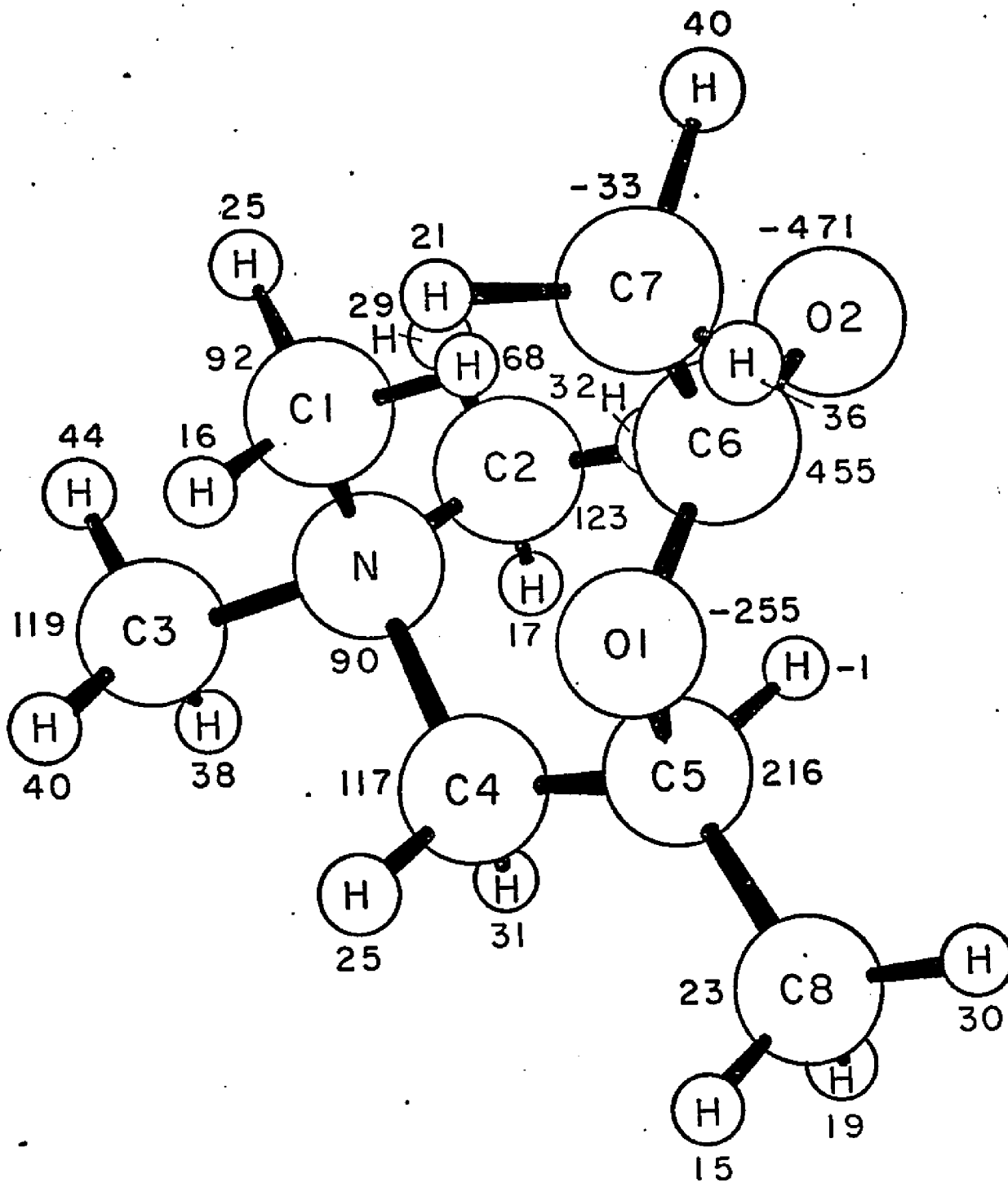


Figure 32
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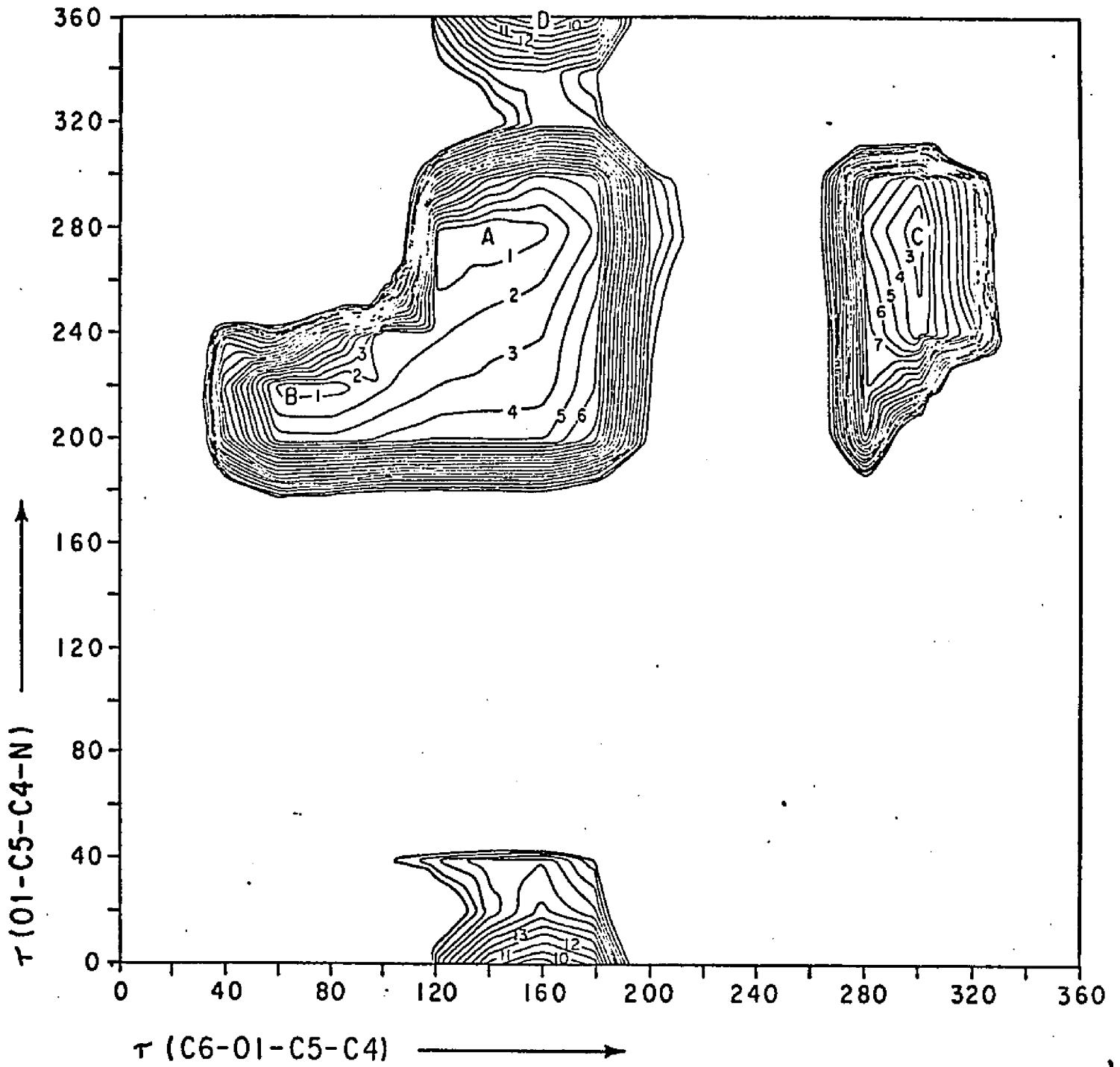
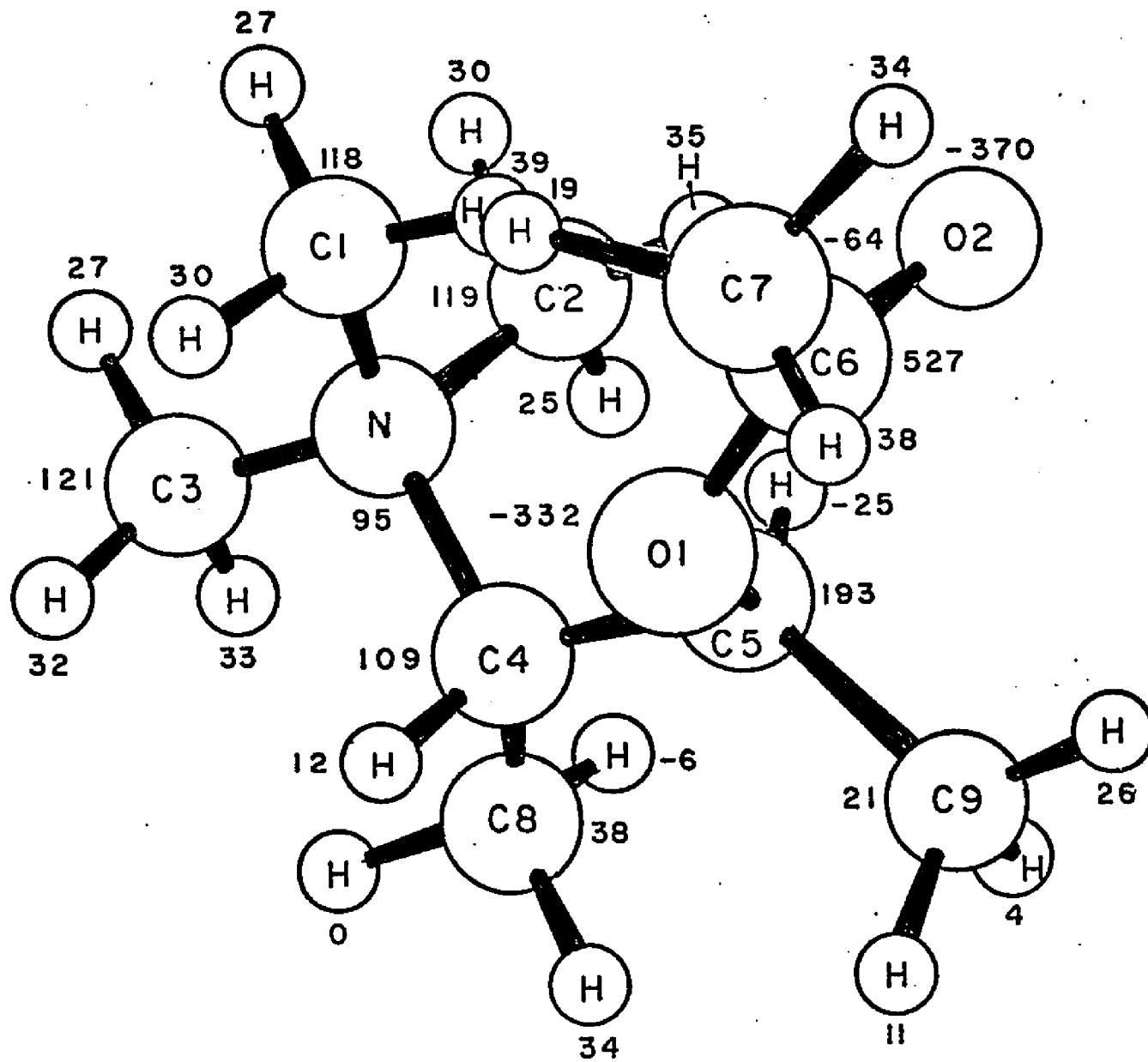


Figure 33

Figure 34



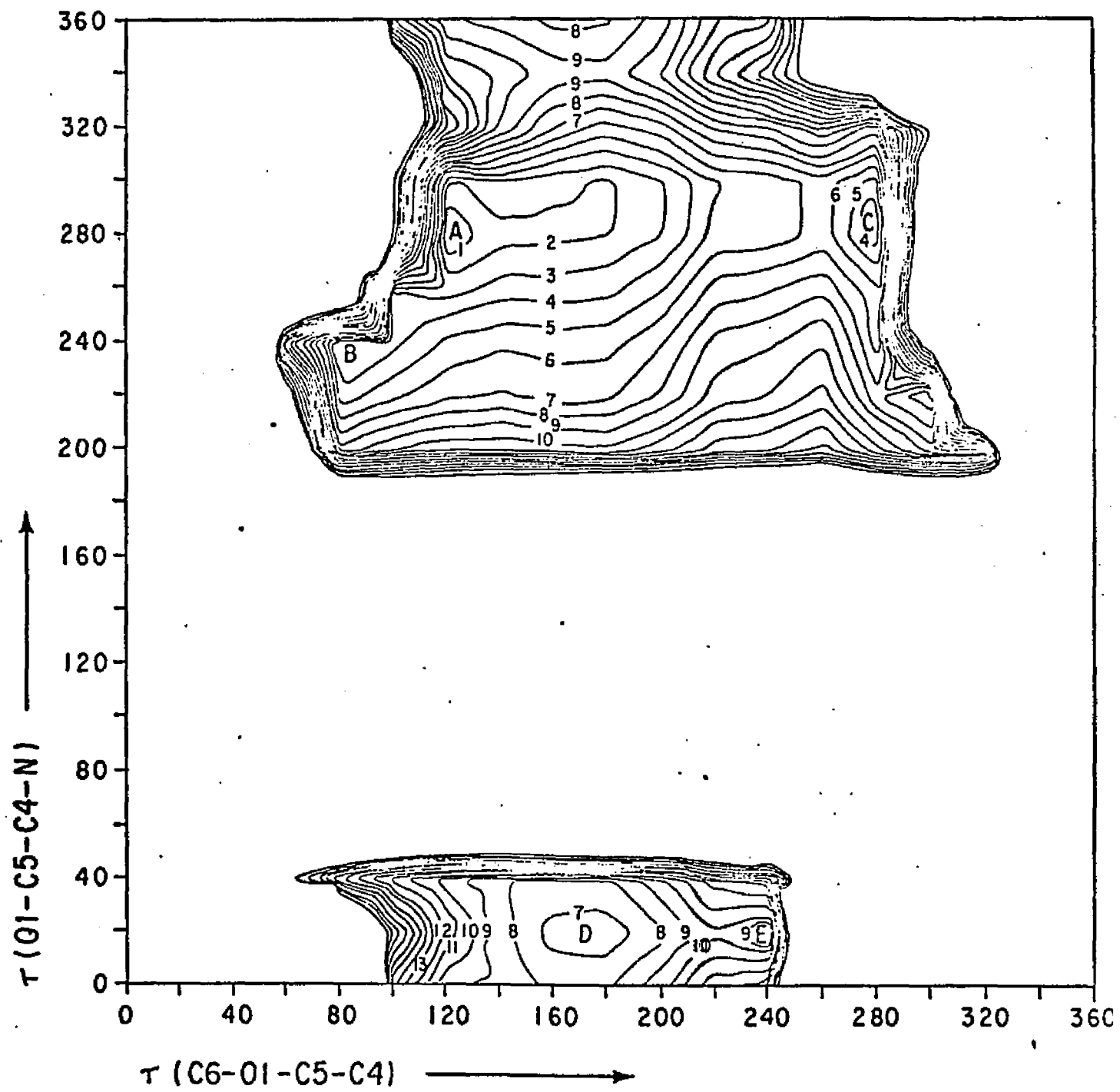
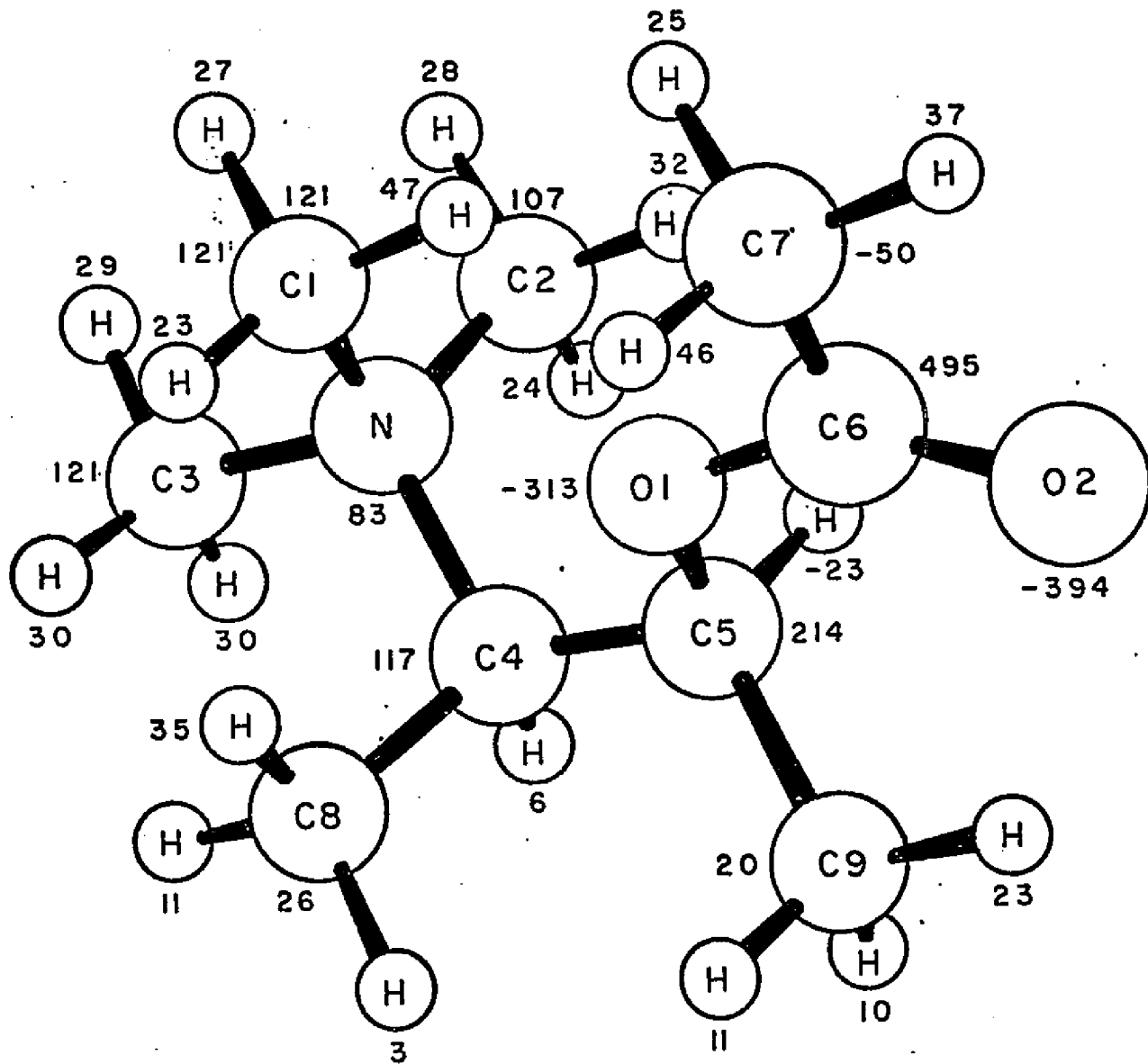


Figure 35

Figure 36



Appendix A:

XTAL accepts the coordinates of an orthorhombic crystal unit cell, and the dimensions of the unit cell. From this data it generates the cartesian coordinates of the system, and an interatomic distance array. The cartesian coordinates are transformed into the model builder frame where the first atom is at the origin of a right handed coordinate system, the second atom lies on the Z axis, and the third atom lies in the X-Z plane. XTAL then calls SUBROUTINE UNZMAT which generates all bond angles and four atom torsions, and writes input to M. Gordon's model builder routine ZMAT. The generated input to ZMAT is tested by SUBROUTINE ZTEST which calls SUBROUTINE ZMAT. The latter routine generates an interatomic distance array from the UNZMAT generated input to ZMAT, and compares this new interatomic distance array to the one calculated from the input crystal data. The input format for the dimensions of the unit cell and unit cell coordinates is (3F20.10).

=RJR,LIST=ALL
=100,NEW1=100

```

PROGRAM XTAL(INPUT,OUTPUT,PUNCH)
C   REVISED ZMAT GENERATING VERSION
    DIMENSION                                YC(60,3)
C   TEST INSERTION
COMMON/ARAN/ZS(3,3)
DIMENSION CT(3,3),TZ(3,3)
DIMENSION CY(3,3)
INTEGER AN
COMMON/ATOM/AN
COMMON/BONDS/NCIM(40,40),NCIM
DIMENSION AN(40)
COMMON/TRANZ/ AFILL(3,3)
DIMENSION INTER(60)
COMMON/IIII/LTEST
COMMON/JJJJ/BONDBL
COMMON/INFO/ORS
DIMENSION ORS(60,3)
DIMENSION                                RR(60,3),HHHH(60),QQQQ(60),SSSS(60)
DIMENSION Z7(3,3),Z(60,3),AR12(60),AR23(60),AR31(60)
DIMENSION C(60,3),R(60,60),FF(3,3),                                F(3,3)
DIMENSION T(3,3),CCC(3,60),EE(3,60)
DIMENSION Y(60,60),TRANS(3,3)
DIMENSION E(60,3),TRANT(3,3)
DIMENSION BC(3,3)
DIMENSION DC(1,3)
DIMENSION IDENT(20)
199 CONTINUE
C   INPUT
READ 999, (IDENT(I),I=1,20)
PUNCH 999,(IDENT(I),I=1,20)
READ 8888, LFIN,LPUN,NCIM
8888 FORMAT(3I4)
IF(LFIN .EQ. 1) GO TO 765
999 FORMAT (20A4)
PRINT 998, (IDENT(I),I=1,20)
998 FORMAT(1H1,////,20A4,///)
READ 4538, APH, BET, GAM,ACCC,ADDD
4538 FORMAT (3F20.10,2F10.5)
PRINT 342, APH, BET, GAM
342 FORMAT (///,1X,6HAPH = ,F10.5,3X,6HBET = ,F10.5,3X,6HGAM = ,F10.5,C
*///)
READ 1, AA,BB,CC
1 FORMAT (3F20.10)
PRINT 2, AA,BB,CC
2 FORMAT (1H ,///,3X,23HDIMENSIONS OF UNIT CELL,5X,2HA=,2X,F10.5,5X,
*2HB=,2X,F10.5,5X,2HC=,2X,F10.5)
READ 3,NN,LIN,BONDBL
3 FORMAT (2I4,F10.5)
IF(BONDBL .EQ. 0) BONDBL = 1.65
4 FORMAT (//,3X,17HNUMBER OF ATOMS =,I4)

```

```

      PRINT 4, NN
      IF(LIN .NE. 0) GO TO 556
      DO 5 I =1,NN
5     READ 6,((C(I,J),J=1,3),AN(I),INTER(I))
6     FORMAT (3F20.10,15,A4)
      GO TO 557
556   CONTINUE
      DO 558 I=1,NN
558   READ 559, (AN(I),(C(I,J),J=1,3),INTER(I))
559   FORMAT (14,3(3X,F12.7),A4)
557   CONTINUE
      IF(NCIM .NE. 1) GO TO 1733
      DO 1734 IR = 1,NN
      READ 1735, (NNCIM(IR,JR),JR=1,NN)
1734  CONTINUE
1735  FORMAT (80I1)
1733  CONTINUE
      DO 4239 I=1,NN
      IF(AN(I) .EQ.0) AN(I) = 6
4239  CONTINUE
C*****
C*****GENERATE CARTESIAN COORDINATES
      PRINT 7
7     FORMAT (///,3X,21HUNIT CELL COORDINATES,///)
      CALL COUT(C,NN)
      DO 10 I =1,NN
      C(I,1) = AA*C(I,1)
      C(I,2) = BB*C(I,2)
      C(I,3) = CC*C(I,3)
10    CONTINUE
      PRINT 4513
4513  FORMAT(//,1X,57HCARTESIAN COORDINATES WITHOUT ORTHOGONALIZATION PRO
      *OCEDURE,/)
      CALL COUT(C,NN)
      CALL DIST(C,NN,R)
      CALL OUT(R,NN)
C     CALL REF(C,NN)
C     PRINT 457
457   FORMAT (//,1X,70HCARTESIAN COORDINATES WITHOUT ORTHOGONALIZATION RO
      *EFERRED TO THE ORIGIN,/)
C     CALL COUT(C,NN)
C     CALL DIST(C,NN,R)
C     CALL OUT(R,NN)
      DO 7174 IN = 1,3
      DO 7174 JN = 1,3
      CY(IN,JN) = C(IN,JN)
7174  CONTINUE
      CALL CLINT (CY,CT,TZ)
      CALL MULT(C,TZ,C,NN)
C     PRINT 898
898   FORMAT (//,1X,40HCARTESIAN COORDINATES SUBJECTED TO CLINT,/)
C     CALL COUT(E,NN)

```

```

C      CALL DIST(F,NN,R)
C      CALL OUT(R,NN)
      CALL REF(C,NN)
      PRINT 8743
8743  FORMAT(//,1X,95HCARTESIAN COORDINATES SUBJECTED TO CLINT AND REFERO
      *RED TO THE ORIGIN (WITHOUT ORTHOGONALIZATION),//)
      CALL COUT(C,NN)
      CALL DIST(C,NN,R)
      CALL OUT(R,NN)
C      PRINT 88
C      CALL COUT(C,NN)
      IF((APH .EQ. 90.0) .AND. (BET .EQ. 90.0) .AND. (GAM .EQ. 90.0))
      *GO TO 498
      DO 9134 IZ=1,3
        DO 9134 JZ = 1,3
          AFILL(IZ,JZ) = 0.
9134  CONTINUE
C      PRINT 1213
1213  FORMAT(//,1X,26HNON-ORTHOGONAL COORDINATES,//)
C      CALL COUT(C,NN)
C      CALL DIST(C,NN,R)
C      CALL OUT(R,NN)
      CALL CFIX(C,APH,BET,GAM,NN)
      CALL MULT(C,AFILL,E,NN)
      PRINT 327
327  FORMAT (//,1X,31HCFIX ORTHOGONALIZED COORDINATES,//)
      CALL COUT(E,NN)
      CALL DIST(E,NN,R)
      CALL OUT(R,NN)
      CALL DFIX(C,APH,BET,GAM,NN)
      CALL MULT(C,ZS,C,NN)
      PRINT 2861
2861  FORMAT (//,1X,31HDFIX ORTHOGONALIZED COORDINATES,//)
      CALL COUT(C,NN)
      CALL DIST(C,NN,R)
      CALL OUT(R,NN)
498  CONTINUE
      IF((APH .EQ. 90.) .AND. (BET .EQ. 90.) .AND. (GAM .EQ. 90.)) PRINTO
      *1015
1015  FORMAT (//,1X,24HTHE SYSTEM IS ORTHOGONAL,//)
      DO 8712 I = 1,NN
        DO 8712 J = 1,3
8712  YC(I,J) = C(I,J) + 1.0
      CALL UNZMAT(YC,R,NN,AN,INTER)
      CALL COUT(C,NN)
C*****
C*****CREATE ZMAT CONVENTION COORDINATES FOR FIRST THREE ATOMS
      COA = ((R(1,3)**2) + (R(1,2)**2) - (R(2,3)**2))/
      *(2*(R(1,3))*(R(1,2)))
      ALPH = ACOS(COA)
      SIA = SIN(ALPH)
      COAA = COS(ALPH)

```

```

      PRINT 135, ALPH, SIA, COA, COAA
135  FORMAT (//, 3X, 4F10.5)
C    CONVERSION TO DEGREES
      BLPH = ALPH * (180./3.141592654)
      PRINT 136, BLPH
136  FORMAT (//, 3X, 16HALPH IN DEGREES=, F10.5, //)
      DO 501 I = 1, 3
501  F(1, I) = 0.0
      DO 500 J = 1, 2
500  F(2, J) = 0.0
      F(2, 3) = R(1, 2)
      F(3, 1) = R(1, 3) * SIN(ALPH)
      F(3, 2) = 0.0
      F(3, 3) = R(1, 3) * COS(ALPH)
      DO 502 I = 1, 3
      DO 502 J = 1, 3
502  FF(J, I) = F(I, J) + 1.
C *****
      DO 85 I = 1, 3
      DO 85 J = 1, 3
      TRANS(I, J) = 0.0
85  T(I, J) = 0.0
      DO 81 I = 1, 3
      DO 81 J = 1, 3
81  BC(J, I) = C(I, J) + 1.
      CALL RRED(C, NN, TRANS)
      DO 2221 I = 1, 3
      DO 2221 J = 1, 3
2221 TRANT(I, J) = TRANS(I, J)
C    CALL TMAT(TRANT, FF, T)
      CALL TMAT(BC, FF, T)
C *****GENERATE ZMAT CONVENTION COORDINATES
C *****
      CALL MULT(C, T, E, NN)
      CALL REF(E, NN)
C *****
      PRINT 187
187  FORMAT (//, 3X, 40HCARTESIAN COORDINATES IN ZMAT CONVENTION, //)
      CALL COUT(E, NN)
      CALL DIST(E, NN, R)
      PRINT 888
      CALL OUT(R, NN)
888  FORMAT (///, 3X, 21HINTERATOMIC DISTANCES, ///)
      IF(LPUN .NE. 1) GO TO 199
      DO 1111 I = 1, NN
1111 PUNCH 6, (E(I, J), J=1, 3)
      GO TO 199
765  CONTINUE
      END
      SUBROUTINE DFIX(C, APH, BET, GAM, NN)
      COMMON/ARAN/ A(3, 3)
      COMMON/ARRAYS/ AB(3, 3), VT(3, 3), X(3, 3)

```

```

COMMON/1/GAMMA(3),BETA(3),BETASQ(3), D(3),W(3),XYZ(60)
DIMENSION C(6C,3)
PT=3.141592654/180.
SINA=SIN(APH*PT)
COXA=COS(APH*PT)
SINB=SIN(BET*PT)
COSB=COS(BET*PT)
SING=SIN(GAM*PT)
COSG=COS(GAM*PT)
DO 37 I=1,3
DO 37 J=1,3
AB(I,J)=0.0
37 CONTINUE
AB(1,1)=1.0
AB(2,1)=COSG
AB(3,1)=COSB
AB(2,2)=1.0
AB(3,2)=COXA
AB(3,3)=1.0
CALL EIGN(3,0.000001)
DO 38 J=1,3
DO 38 I=1,3
38 VT(I,J)=VT(I,J)/SQRT(D(J))
DO 39 I=1,3
DO 39 J=1,3
39 A(I,J)=VT(J,I)
RETURN
END
SUBROUTINE EIGN(NN,RHO)
C RHO= UPPER LIMIT FOR OFF-DIAGONAL ELEMENT
C NN= SIZE OF MATRIX
C A = F MATRIX (ONLY LOWER TRIANGLE IS USED + THIS IS DESTROYED)
C EIG = RETURNED EIGENVALUES IN ALGEBRAIC ASCENDING ORDER
C VEC = RETURNED EIGENVECTORS IN COLUMNS
C IND = ERROR RETURN INDICATOR
C 0 FOR NORMAL RETURN
C 1 SUM OF EIGENVALUES NOT EQUAL TO TRACE
C 2 SUM OF EIGENVALUES SQUARED NOT EQUAL TO NORM
C 3 BOTH OF THESE ERRORS
COMMON/ARRAYS/A(3,3),VEC(3,3),X(3,3)
COMMON/1/GAMMA(3),BETA(3),BETASQ(3),EIG(3),W(3),XYZ(60)
C THE FOLLOWING DIMENSIONED VARIABLES ARE EQUIVALENCED
DIMENSION P(80),Q(80)
EQUIVALENCE (P(1),BETA(1)),(Q(1),BETA(1))
DIMENSION IPOSV(80),IVPOS(80),ICRD(80)
EQUIVALENCE (IPOSV(1),GAMMA(1)),(IVPOS(1),BETA(1)),
1(ICRD(1),BETASQ(1))
ABSF(X) = ABS(X)
SORTF(X) = SORT(X)
RHOSQ=RHO*RHO
N=NN
C RESET ERROR RETURN INDICATOR

```

```

IND=0
IF (N .EQ. 0) 640,10
10 N1=N-1
   N2=N-2
C   COMPUTE THE TRACE AND EUCLIDIAN NORM OF THE INPUT MATRIX
C   LATER CHECK AGAINST SUM AND SUM OF SQUARES OF EIGENVALUES
ENORM=0.
TRACE=0.
DO 30 J=1,N
DO 20 I=J,N
20 ENORM=ENORM+A(I,J)**2
   TRACE=TRACE+A(J,J)
30 ENORM=ENORM-.5*A(J,J)**2
   ENORM=ENORM+ENORM
   GAMMA(1)=A(1,1)
IF(N2) 200,190,40
40 DO 180 NR=1,N2
   B=A(NR+1,NR)
   S=0.
   DO 50 I=NR,N2
50 S=S+A(I+2,NR)**2
C   PREPARE FOR POSSIBLE BYPASS OF TRANSFORMATION
A(NR+1,NR)=0.
IF (S) 170,170,60
60 S=S+B*B
   SGN=+1.
IF (B) 70,80,80
70 SGN=-1.
80 SORTS=SQRTF(S)
   D=SGN/(SORTS+SORTS)
   TEMP=SQRTF(.5+B*D)
   W(NR)=TEMP
   A(NR+1,NR)=TEMP
   D=D/TEMP
   B=-SGN*SORTS
C   D IS FACTOR OF PROPORTIONALITY. NOW COMPUTE AND SAVE W VECTOR.
C   EXTRA SINGLY SUBSCRIBED W VECTOR USED FOR SPEED.
DO 90 I=NR,N2
   TEMP=D*A(I+2,NR)
   W(I+1)=TEMP
90 A(I+2,NR)=TEMP
C   PREMULIPLY VECTOR W BY MATRIX A TO OBTAIN P VECTOR.
C   SIMULTANEDUSLY ACCUMULATE DOT PRODUCT WP,(THE SCALAR K)
WTAW=0.
DO 140 I=NR,N1
   SUM=0.
   DO 100 J=NR,I
100 SUM=SUM+A(I+1,J+1)*W(J)
   I1=I+1
   IF(N1-I1) 130,110,110
110 DO 120 J=I1,N1
120 SUM=SUM+A(J+1,I+1)*W(J)

```

```

130 P(I)=SUM
140 WTAW=WTAW+SUM*W(I)
C   P VECTOR AND SCALAR K NOW STORED. NEXT COMPUTE Q VECTOR
DO 150 I=NR,N1
150 Q(I)=P(I)-WTAW*W(I)
C   NOW FORM PAP MATRIX. REQUIRED PART
DO 160 J=NR,N1
   QJ=Q(J)
   WJ=W(J)
DO 160 I=J,N1
160 A(I+1,J+1)=A(I+1,J+1)-2.*(W(I)*QJ+WJ*Q(I))
170 BETA(NR)=B
   BETASQ(NR)=B*B
180 GAMMA(NR+1)=A(NR+1,NR+1)
190 B=A(N,N-1)
   BETA(N-1)=B
   BETASQ(N-1)=B*B
   GAMMA(N)=A(N,N)
200 BETASQ(N)=0.
C   ADJOIN AN IDENTIFY MATRIX TO BE POSTMULTIPLIED BY ROTATIONS.
DO 220 I=1,N
DO 210 J=1,N
210 VEC(I,J)=C.
220 VEC(I,I)=1.
   M=N
   SUM=0.
   NPAS=1
   GO TO 350
230 SUM=SUM+SHIFT
   COSA=1.
   G=GAMMA(1)-SHIFT
   PP=G
   PPBS=PP*PP+BETASQ(1)
   PPBR=SQRTF(PPBS)
DO 320 J=1,M
   COSAP=COSA
   IF(PPBS .NE. 0.) 250,240
240 SINA=C.
   SINA2=0.
   COSA=1.
   GO TO 290
250 SINA=BETA(J)/PPBR
   SINA2=BETASQ(J)/PPBS
   COSA=PP/PPBR
C   POSTMULTIPLY IDENTITY BY P-TRANSPOSE MATRIX
   NT=J+NPAS
   IF(NT .GE. N) 260,270
260 NT=N
270 DO 280 I=1,NT
   TEMP=COSA*VEC(I,J)+SINA*VEC(I,J+1)
   VEC(I,J+1)=-SINA*VEC(I,J)+COSA*VEC(I,J+1)
280 VEC(I,J)=TEMP

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290 DIA=GAMMA(J+1)-SHIFT
   U=SINA2*(G+DIA)
   GAMMA(J)=G+U
   G=DIA-U
   PP=DIA*COISA-SINA*COISAP*BETA(J)
   IF(J .NE. M) 310,300
300 BETA(J)=SINA*PP
   BETASQ(J)=SINA2*PP*PP
   GO TO 330
310 PPBS=PP*PP+BETASQ(J+1)
   PPBR=SORTF(PPBS)
   BETA(J)=SINA*PPBR
320 BETASQ(J)=SINA2*PPBS
330 GAMMA(M+1)=G
C   TEST FOR CONVERGENCE OF LAST DIAGONAL ELEMENT
   NPAS=NPAS+1
   IF(BETASQ(M) .GT. RHOSQ) 370,340
340 EIG(M+1)=GAMMA(M+1)+SUM
350 BETA(M)=0.
   BETASQ(M)=0.
   M=M-1
   IF(M .EQ. 0) 400,360
360 IF(BETASQ(M) .LE. RHOSQ) 340,370
C   TAKE ROOT OF CORNER 2 BY 2 NEAREST TO LOWER DIAGONAL IN VALUE
C   AS ESTIMATE OF EIGENVALUE TO USE FOR SHIFT
370 A2=GAMMA(M+1)
   R2=.5*A2
   R1=.5*GAMMA(M)
   R12=R1+R2
   DIF=R1-R2
   TEMP=SORTF(DIF*DIF+BETASQ(M))
   R1=R12+TEMP
   R2=R12-TEMP
   DIF=ABSF(A2-R1)-ABSF(A2-R2)
   IF(DIF .LT. 0.) 390,380
380 SHIFT=R2
   GO TO 230
390 SHIFT=R1
   GO TO 230
400 FIG(1)=GAMMA(1)+SUM
C   INITIALIZE AUXILIARY TABLES REQUIRED FOR REARRANGING THE VECTORS
   DO 410 J=1,N
   IPOSV(J)=J
   IVPOS(J)=J
410 IORD(J)=J
C   USE A TRANSPOSITION SORT TO ORDER THE EIGENVALUES
   M=N
   GO TO 450
420 DO 440 J=1,M
   IF (EIG(J) .GE. EIG(J+1)) 440,430
430 TEMP=EIG(J)
   EIG(J)=EIG(J+1)

```

```

      EIG(J+1)=TEMP
      ITMP=IORD(J)
      IORD(J)=IORD(J+1)
      IORD(J+1)=ITMP
440  CONTINUE
450  M=M-1
      IF(M .NE. 0) 420,460
460  IF(N1 .EQ. 0) 510,470
470  DO 500 L=1,N1
      NV=IORD(L)
      NP=IPOSV(NV)
      IF(NP .EQ. L) 500,480
480  LV=IVPOS(L)
      IVPOS(NP)=LV
      IPOSV(LV)=NP
      DO 490 I=1,N
      TEMP=VEC(I,L)
      VEC(I,L)=VEC(I,NP)
490  VEC(I,NP)=TEMP
500  CONTINUE
510  ESUM=0.
      FSSQ=0.
C     BACK TRANSFORM THE VECTORS OF THE TRIPLE DIAGONAL MATRIX
      DO 570 NRR=1,N
      K=N1
520  K=K-1
      IF(K .LE. 0) 560,530
530  SUM=0.
      DO 540 I=K,N1
540  SUM=SUM+VEC(I+1,NRR)*A(I+1,K)
      SUM=SUM+SUM
      DO 550 I=K,N1
550  VEC(I+1,NRR)=VEC(I+1,NRR)-SUM*A(I+1,K)
      GO TO 520
560  ESUM=ESUM+EIG(NRR)
570  ESSQ=ESSQ+EIG(NRR)**2
      TEMP=ABSF(128.*TRACE)
      IF((ABSF(TRACE-ESUM)+TEMP)-TEMP.NE.0.) 580,590
580  IND=IND+1
590  TEMP=256.*FNORM
      IF((ABSF(FNORM-ESSQ)+TEMP)-TEMP.NE.0.) 600,610
600  IND=IND+2
610  CONTINUE
C     REVERSE ORDER OF EIGENVALUES AND EIGENVECTORS
      NHALF=N/2
      DO 620 I=1,NHALF
      TEMP=EIG(I)
      EIG(I)=EIG(N+1-I)
620  EIG(N+1-I)=TEMP
      DO 630 I=1,N
      DO 630 J=1,NHALF
      TEMP=VEC(I,J)

```

```

      VEC(I,J)=VEC(I,N+1-J)
630  VEC(I,N+1-J)=TEMP
640  RETURN
      END
      SUBROUTINE CLINT (C,CC,T)
      DIMENSION C(3,3),CC(3,3),T(3,3),Z(3),ZUNI(3),A(3),Y(3),YUNI(3),
      *AX(3),BY(3),CZ(3)
      DIMENSION XUNI(3)
C     THIS ROUTINE ACCEPTS A (3,3) COORDINATE SYSTEM, AND GENERATES A (3,3)
C     TRANSFORMATION MATRIX WHICH IS USED TO TRANSFORM A (NN,3) COORDINATE
C     SYSTEM INTO THE ZMAT CONVENTION) HERE BL(1,2) LIES IN THE Z AXIS
C     AND THE FIRST THREE ATOMS LIE IN THE X-Z PLANE (Y=0).
      Z(1) = C(2,1) - C(1,1)
      Z(2) = C(2,2) - C(1,2)
      Z(3) = C(2,3) - C(1,3)
      ZMAG = SQRT (Z(1)**2 + Z(2)**2 + Z(3)**2)
      ZUNI(1) = Z(1)/ZMAG
      ZUNI(2) = Z(2)/ZMAG
      ZUNI(3) = Z(3)/ZMAG
      A(1) = C(3,1) - C(1,1)
      A(2) = C(3,2) - C(1,2)
      A(3) = C(3,3) - C(1,3)
      CALL VECPRD(Y,Z,A)
      YMAG = SQRT(Y(1)**2 + Y(2)**2 + Y(3)**2)
      YUNI(1) = Y(1)/YMAG
      YUNI(2) = Y(2)/YMAG
      YUNI(3) = Y(3)/YMAG
      CALL VECPRD (XUNI,YUNI,ZUNI)
      DO 993 II=1,3
      AX(II) = 0.
      BY(II) = 0.
      CZ(II) = 0.
993  CONTINUE
      AX(1) = 1.
      BY(2) = 1.
      CZ(3) = 1.
      T(1,1) = DOTPRD (XUNI,AX)
      T(1,2) = DOTPRD (XUNI,BY)
      T(1,3) = DOTPRD(XUNI,CZ)
      T(2,1) = DOTPRD(YUNI,AX)
      T(2,2) = DOTPRD (YUNI,BY)
      T(2,3) = DOTPRD (YUNI,CZ)
      T(3,1) = DOTPRD (ZUNI,AX)
      T(3,2) = DOTPRD (ZUNI,BY)
      T(3,3) = DOTPRD (ZUNI,CZ)
      PRINT 10
      DO 5 I=1,3
      PRINT 6, (T(I,J),J=1,3)
5     CONTINUE
      6     FORMAT (1X,F10.5,2X,F10.5,2X,F10.5)
      10    FORMAT (//,2X, 21HTRANSFORMATION MATRIX,//)
      RETURN

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```

      END
      FUNCTION DOTPRD (X,Y)
      DIMENSION X(3), Y(3)
      C=0.
      DO 1 I=1,3
      C=C + X(I)*Y(I)
1 CONTINUE
      DOTPRD = C
      RETURN
      END
      SUBROUTINE MULT(C,T,E,NN)
C      THIS ROUTINE USES A (3,3) TRANSFORMATION MATRIX TO TRANSFORM A
C      (3,NN) ARRAY (THE TRANSPOSE OF THE(NN,3) ) TO A RESULTANT
C      (3,NN) ARRAY, AND THEN TRANSPOSES THE (3,NN) BACK TO A (NN,3).
      DIMENSION C(60,3),T(3,3),E(60,3),CC(3,60),EE(3,60)
      DIMENSION CCC(3,3)
      DO 1 I=1,NN
      DO 1J=1,3
      CC(J,I) = C(I,J)
1 CONTINUE
      DO 83 I=1,3
      DO 83 J=1,NN
      EE(I,J) = 0.
      DO 83 K = 1,3
83 EE(I,J) = EE(I,J) + .T(I,K)*CC(K,J)
      DO 3 I=1,NN
      DO 3 J=1,3
      E(I,J) = EE(J,I)
3 CONTINUE
      RETURN
      END
      SUBROUTINE COUT(C,NN)
C      THIS ROUTINE PRINTS A (NN,3) ARRAY
      DIMENSION C(60,3)
      COMMON/ATOM/AN(40)
      DIMENSION EL(9)
      INTEGER AN
      DATA ((EL(I),I=1,9)=4H H,4H HE,4H LI,4H BE,4H B,4H C,
      *4H N,4H O,4H F)
      PRINT 1
1 FORMAT(21X,1HX,10X,1HY,10X,1HZ,///)
      DO 8 I =1,NN
      IND1 = AN(I)
8 PRINT 9, I,EL(IND1), (C(I,J), J=1,3)
9 FORMAT (3X,14,3X,A4,3X,3F10.5)
      RETURN
      END
      SUBROUTINE OUT(R,NN)
C      THIS ROUTINE PRINTS AN (NN,NN) ARRAY.
      DIMENSION R(60,60)
      KITE = 0
      20 IOW = KITE + 1

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KITE = KITE + 12
KITE = AMINO(KITE,NN)
PRINT 19,(I,I=LOW,KITE)
19 FORMAT (//,6X,12(19,1X),//)
DO 32 I =1,NN
32 PRINT 18,1,(R(I,J),J=LOW,KITE)
18 FORMAT (2X,14,3X,12F10.4)
IF(NN-KITE) 40,40,20
40 RETURN
END
SUBROUTINE TMAT(A,B,T)
C TO SOLVE MATRIX EQ B = T*A FOR T GIVEN A AND B
C DIMENSION A(3,3),B(3,3),C(3,3),D(3,3),T(3,3),E(3,3)
C DIMENSION AL(2),BL(2),CL(2),DL(2),EL(2),FL(2)
C DATA ((AL(I),I=1,2)=4HMATR,4HIX A)
C DATA ((BL(I),I=1,2)=4HMATR,4HIX B)
C DATA ((CL(I),I=1,2)=4HINVE,4HRSE )
C DATA ((DL(I),I=1,2)=4HCK I,4HNVER)
C DATA ((EL(I),I=1,2)=4HTRAN,4HS MT)
C DATA ((FL(I),I=1,2)=4HCK T,4HRANS)
C *****
C INPUT SECTION
C 999 CONTINUE
C CALL MOUTPT(A,3,3,3,3,AL)
C CALL MOUTPT(B,3,3,3,3,BL)
C *****
C SOLUTION FOR T IS T = B*A-INVERSE
C FORM INVERSE OF A
C CALCULATE MATRIX OF COFACTORS OF A IN D
C D(1,1) = A(2,2)*A(3,3)-A(2,3)*A(3,2)
C D(1,2) = -(A(2,1)*A(3,3)-A(2,3)*A(3,1))
C D(1,3) = A(2,1)*A(3,2)-A(2,2)*A(3,1)
C D(2,1) = -(A(1,2)*A(3,3)-A(1,3)*A(3,2))
C D(2,2) = A(1,1)*A(3,3)-A(1,3)*A(3,1)
C D(2,3) = -(A(1,1)*A(3,2)-A(1,2)*A(3,1))
C D(3,1) = A(1,2)*A(2,3)-A(1,3)*A(2,2)
C D(3,2) = -(A(1,1)*A(2,3)-A(1,3)*A(2,1))
C D(3,3) = A(1,1)*A(2,2)-A(1,2)*A(2,1)
C *****
C CALCULATE DETERMINANT OF A AND OUTPUT
C DET = A(1,1)*D(1,1)+A(1,2)*D(1,2)+A(1,3)*D(1,3)
C IF( ABS(DET).LT.1.0E-5) GO TO 5
C GO TO 6
C 5 PRINT 1002, DET
C 1002 FORMAT(//,24H MATRIX SINGULAR, DET = ,D15.5,//)
C STOP
C 6 CONTINUE
C PRINT 1000, DET
C 1000 FORMAT(//,7H DET = ,D15.5,//)
C *****
C FORM ELEMENTS OF INVERSE
C DO 1 I=1,3

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DO 1 J=1,3
1 C(I,J) = D(J,I)/DET
CALL MOUTPT(C,3,3,3,3,CL)
C *****
C CHECK INVERSE
DO 2 I=1,3
DO 2 J=1,3
D(I,J) = 0.
DO 2 K=1,3
2 D(I,J) = D(I,J)+A(I,K)*C(K,J)
CALL MOUTPT(D,3,3,3,3,DL)
C *****
C FORM TRANSFORMATION MATRIX
DO 3 I=1,3
DO 3 J=1,3
T(I,J) = C
DO 3 K=1,3
3 T(I,J) = T(I,J)+B(I,K)*C(K,J)
CALL MOUTPT(T,3,3,3,3,EL)
C *****
C CHECK TRANSFORMATION MATRIX
DO 4 I=1,3
DO 4 J = 1,3
E(I,J) = 0
DO 4 K=1,3
4 E(I,J) = F(I,J)+T(I,K)*A(K,J)
CALL MOUTPT(E,3,3,3,3,FL)
1111 CONTINUE
RETURN
END
SUBROUTINE MOUTPT(A,M,N,MDIM,NDIM,NAME)
C OUTPUT OF M X N MATRIX DIMENSIONED TO MDIM X NDIM
DIMENSION NAME(2)
DIMENSION A(MDIM,NDIM)
REAL NAME
PRINT 1000,NAME
1000 FORMAT (/,3X,2A4,/)
KITE = 0
20 LOW = KITE+1
KITE = KITE+14
KITE = MIN0(KITE,N)
PRINT 19,(I,I=LOW,KITE)
19 FORMAT( // .4X,14(6X,12),/)
DO 32 I=1,M
32 PRINT 18,I,(A(I,J),J=LOW,KITE)
18 FORMAT(I4,2X,14F10.4)
IF(N-KITE) 40,40,20
40 RETURN
END
SUBROUTINE UNZMAT(C,R,NN,AN,INTER)
C THIS ROUTINE ACCEPTS A COORDINATE SYSTEM, AND AN INTERATOMIC
C DISTANCE MATRIX, AND GENERATES BOND ANGLES AND DIHEDRAL ANGLES.

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C      IT THEN GENERATES AND TESTS INPUT TO ZMAT.
COMMON/IIII/LTEST
COMMON/BONDS/NNCIM(40,40), NCIM
COMMON/JIM/IJIM
COMMON/INFO/ORS
COMMON/JJJJ/BONDBL
INTEGER AN
DIMENSION EL(9)
DIMENSION R(60,60),RR(40,40)
DIMENSION LDU(40)
DIMENSION ORS(60,3)
DATA( (EL(I),I=1,9)=4H   H,4H  HE,4H  LI,4H  BE,4H  B,4H  C,
*4H  N,4H  O,4H  F)
INTEGER Z
DIMENSION T(40,40,40)
DIMENSION INTER(60)
DIMENSION AN(40),Z(60,4),BL(40),ALPHA(40),BETA(40)
DIMENSION C(60,3),RA(60,60),
*      A(3,3)
DATA(HOUS=4H HOUS)
LTEST=0
DO 8180 I=1,NN
DO 8180 J=1,NN
DO 8180 K=1,NN
RR(I,J) = 0.
T(I,J,K) = 0.
Z(I,4) = 0
Z(I,3) = 0
Z(I,2) = 0
Z(I,1) = 0
ALPHA(I) = 0.
BETA(I) = 0.
BL(I) = 0.
8180 CONTINUE
C      CALCULATE BOND ANGLES
DO 7777 JJ = 1,NN
DO 7777 KK = 1,NN
DO 7777 LL = 1,NN
IF(JJ .EQ. LL) GO TO 7777
IF(JJ .EQ. KK) GO TO 7777
IF(LL .EQ. KK) GO TO 7777
IF(JJ .LT. LL) GO TO 7777
IF(JJ .LT. KK) GO TO 7777
IF((NCIM.EQ.1).AND.(NNCIM(JJ, KK).EQ.1).AND.(NNCIM(KK, LL).EQ.1))GO
*TO 1001
IF((R(JJ, KK) .LT. BONDBL) .AND. (R(KK, LL) .LT. BONDBL)) GO TO
*1001
GO TO 7777
1001 CONTINUE
CT = C.0
DO 1130 I = 1,3
1130 CT = CT - (C(LL, I) - C(KK, I)) * (C(KK, I) - C(JJ, I))

```

```

A
A
A
A
A
CT = CT/(R(JJ, KK)*R(KK, LL))
XXXX = (1.0 - CT*CT)
IF (XXXX .LT. 0.0) GO TO 1200
GO TO 1201
1200 PRINT 1202
1202 FORMAT (/ , 3X, 11HXXXX IS NEG. /)
1201 CONTINUE
ST = SQRT ( ABS(1.0 - CT*CT) )
T(JJ, KK, LL) = (180./3.141592654) * .ATAN2(ST, CT)
PRINT 8, JJ, KK, LL, T(JJ, KK, LL), R(JJ, KK), R(KK, LL)
8 FORMAT (/ 3X, 6HANGLE(, I2, 1H, ., I2, 1H, ., I2, 2H)=, F10.5, 2CX, 2F10.5)
7777 CONTINUE
C*****CALCULATE DIHYDRAL ANGLES
DO 1949 JJ= 1, NN
DO 1949 KK= 1, NN
DO 1949 LL = 1, NN
IF( T(JJ, KK, LL) .EQ. 0) GO TO 1949
DO 1948 MM= 1, NN
IF (JJ, LL, MM) GO TO 1948
IF ((JJ, EQ, LL).OR.(JJ, EQ, KK).OR.(LL, EQ, KK).OR.(LL, EQ, MM)) GO TO
*1948
IF ((MM, EQ, KK) .OR. (MM, EQ, JJ)) GO TO 1948
IF ((NCIM, EQ, 1).AND.(NCCIM(LL, MM), EQ, 1)) GO TO 13
IF (R(LL, MM) .LT. BONDBL) GO TO 13
GO TO 14
13 CONTINUE
C AT THIS POINT JJ, KK, LL, MM ARE SEQUENTIALLY BONDED ATOMS, WHERE JJ
C IS GREATER THAN MM
CC=0.0
DO 1240 I = 1, 3
1240 CC = CC+(C(KK, I)-C(JJ, I))*(C(LL, I)-C(KK, I))
CC = CC/(R(JJ, KK)*R(KK, LL))
DO 1230 I = 1, 3
1230 A(1, I)=(C(LL, I)-C(KK, I))/R(KK, LL)
DO 1250 I = 1, 3
YYYY = (1.0 - CC*CC)
IF (YYYY .LT. 0.0) GO TO 1205
GO TO 1206
1205 PRINT 1202
1206 CONTINUE
1250 A(2, I)=(-(C(KK, I)-C(JJ, I))/R(JJ, KK)+CC*(C(LL, I)-C(KK, I))/R(KK, LL))
*/ SQRT( ABS(1.0 -CC*CC) )
A(3, 1)=A(1, 2)*A(2, 3)-A(1, 3)*A(2, 2)
A(3, 2)=A(2, 1)*A(1, 3)-A(1, 1)*A(2, 3)
A(3, 3)=A(1, 1)*A(2, 2)-A(2, 1)*A(1, 2)
ZO=0.0
YO=0.0
DO 1260 I=1, 3
ZO=ZO+A(3, I)*(C(MM, I)-C(KK, I))
1260 YO=YO+A(2, I)*(C(MM, I)-C(KK, I))
CT = YO
ST = ZO

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      TAU=( 180./3.141592654)          * ATAN2(IST,CT)
      IF(JJ .EQ. 4) BETA4 = TAU
      IF(MM .EQ. 5) PRINT 2712
2712  FORMAT(1X,6HMM = 5)
      PRINT 9, JJ, KK, LL, MM, TAU, R(JJ, KK), R(KK, LL), R(LL, MM)
9     FORMAT (/10X,4HTAU(, I2, 1H., I2, 1H., I2, 1H., I2, 2H)=, F10.5, 2CX, 3F10.5
*)
C     GENERATE ZMAT
      IF(Z(JJ,1) .NE. 0) GO TO 1949
      Z(JJ,1) = KK
      BL(JJ) = R(JJ, KK)
      Z(JJ,2) = LL
      ALPHA(JJ) = T(JJ, KK, LL)
      IF(INTER(JJ) .EQ. HOUS) GO TO 6238
      AAAA=C.
      DO 6139 LO=1, NN
      IF((LO .EQ. KK) .OR. (LO .EQ. JJ)) GO TO 6139
      IF(LO .EQ. LL) GO TO 6139
      IF(T(JJ, KK, LO) .NE. 0.) GO TO 6138
      GO TO 6139
6138  Z(JJ,3) = LO
      BETA(JJ) = T(JJ, KK, LO)
      Z(JJ,4) = 1
      AAAA = 1.
6139  CONTINUE
      IF(AAAA .EQ. 0.) GO TO 6238
      GO TO 1949
6238  BETA(JJ) = TAU
      Z(JJ,3) = MM
      Z(JJ,4) = 0
      14  CONTINUE
1948  CONTINUE
1949  CONTINUE
C     ZMAT FOR ATOM 2
      BL(2) = R(1,2)
      Z(2,1) = 1
C     ZMAT FOR ATOM 3
      IF(Z(3,1) .NE. 0) GO TO 7612
      DO 1297 I=1,2
      IF((NCCIM .EQ. 1) .AND. (NCCIM(3, I) .EQ. 1)) Z(3,1) = I
      IF(R(3, I) .LT. BONDBL) Z(3,1) = I
1297  CONTINUE
      KA = Z(3,1)
      BL(3) = R(3, KA)
      DO 1296 I=1,2
      KA = Z(3,1)
      IF(T(3, KA, .1) .NE. 0) Z(3,2) = I
1296  CONTINUE
      KA = Z(3,1)
      KB = Z(3,2)
      ALPHA(3) = T(3, KA, KB)
7612  CONTINUE

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C      ZMAT FOR ATOM 4
      IF(Z(4,1) .NE. 0) GO TO 7613
      DO 1295 I=1,3
      IF((NCIM(4,I).EQ.1).AND.(NNCIM(4,I).EQ.1)) Z(4,1) = I
      IF(R(4,1) .LT. BONDBL) Z(4,1) = I
1295  CONTINUE
      KC = Z(4,1)
      BL(4) = R(4,KC)
      NMN = 0
      IK=0
1909  CONTINUE
      DO 1294 I=1,3
      KC = Z(4,1)
      IF((NMN.EQ.0).AND.(T(4,KC   ,I).NE.0))GO TO 1336
      IF((NMN.EQ.1).AND.(T(4,KC   ,I).NE.0))GO TO 1337
      GO TO 1294
1336  IJ=I
      NMN = NMN+1
      GO TO 1909
1337  IK = I
1294  CONTINUE
C      IF(IK .EQ. 0.) ATOM 4 FORMS ONLY ONE BOND ANGLE AND THEREFORE MUST
C      BE DESIGNATED BY A DIHEDRAL
      IF(IK .EQ. 0) GO TO 1207
      GO TO 1208
1207  Z(4,2) = IJ
      KC = Z(4,1)
      KD = Z(4,2)
      ALPHA(4) = T(4,KC,KD)
      Z(4,3) = 16- (KC+KD)
      KE = Z(4,3)
      Z(4,4) = 0
      BETA(4) = BETA4
      GO TO 7613
1208  Z(4,2) = IK
      Z(4,3) = IJ
      Z(4,4) = 1
      KC = Z(4,1)
      KD = Z(4,2)
      ALPHA(4) = T(4,KC,KD)
      KE = Z(4,3)
      BETA(4) = T(4,KC,KE)
7613  CONTINUE
C      CHECK TO SEE IF ATOM 5 IS DESIGNATED PROPERLY.  IF IT IS POSSIBLE
C      TO DESIGNATE 5 BY A DIHEDRAL, THE ZMAT FOR ATOM 5 IS WRITTEN
C      PROPERLY.  IF NOT, NO ZMAT IS WRITTEN FOR 5.  UNZMAT MUST WRITE
C      IT NOW.
      IF(Z(5,1) .NE. 0) GO TO 9190
      DO 9180 I=1,NN
      IF((NCIM(5,I).EQ.1).AND.(NNCIM(5,I).EQ.1)) GO TO 9181
      IF(R(5,I) .LT. BONDBL) GO TO 9181
      GO TO 9180

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9181 7(5,1) = I
      BL(5) = R(5,1)
      GO TO 9185
9180 CONTINUE
9185 CONTINUE
      LORS = 0
      DO 9182 I=1,NN
      JJ=Z(5,1)
      IF((T(5,JJ,1) .NE. 0) .AND. (LORS .EQ.0)) GO TO 9183
      IF((T(5,JJ,1) .NE. 0) .AND. (LORS .NE.0)) GO TO 9184
      GO TO 9182
9183 KK=I
      LORS = LORS + 1
      GO TO 9186
9184 LL=I
      GO TO 9187
9186 CONTINUE
9182 CONTINUE
9187 CONTINUE
      ALPHA(5) = T(5,JJ,LL)
      Z(5,2) = LL
      BETA(5) = T(5,JJ,KK)
      Z(5,3) = KK
      Z(5,4) = 1
9190 CONTINUE
C     THIS CODE TESTS IF AN ATOM IS DESIGNATED BY A DIHYDRAL, AND
C     DETERMINES IF DESIGNATION BY MORE THAN ONE DIHYDRAL IS POSSIBLE.
C     IF THE LATTER CASE IS TRUE, AND THE POSSIBLE DIHYDRALS IN QUESTION
C     ARE TAU(J,K,L,M), THE DIHYDRAL WITH THE LARGER VALUE OF K
C     IS EMPLOYED. THIS FREQUENTLY IS OF VALUE IN GEARING RINGS.
      DO 8322 J=5,NN
      IF(Z(J,4) .NE. 0) GO TO 7015
      LWIN = 0
      DO 7010 K=1,NN
      DO 7016 L=1,NN
      IF(T(J,K,L) .EQ. 0) GO TO 7016
      DO 7018 M=1,NN
      IF(J .LT. M) GO TO 7018
      IF((J.LT.K).OR.(J.LT.L)) GO TO 7018
      IF((J .EQ. L) .OR. (J.EQ.K) .OR. (L.EQ.K).OR.(L.EQ.M)) GO TO 7018
      IF((M.EQ.K).OR.(M.EQ.J)) GO TO 7018
      IF((NOCIM.EQ.1).AND.(NOCIM(L,M).NE.1)) GO TO 7018
      IF((R(L,M) .GT. BONDRL)) GO TO 7018
      IF(LWIN .GT. 0) GO TO 7012
      GO TO 7099
7012 PRINT 7013, J
7013 FORMAT (///,3X,4HATOM,3X,14,3X,51HCAN BE DESIGNATED BY MORE THAN
      *ONE DIHYDRAL ANGLE.)
      CALL TAUFIX(BL,ALPHA,BETA,J,K,L,M,T,R,Z,C)
7099 CONTINUE
      LWIN = LWIN +1
7018 CONTINUE

```

```
7016 CONTINUE
7010 CONTINUE
7015 CONTINUE
8322 CONTINUE
C   WRITE OUT COMPLETED ZMAT
    PRINT 1997
1997 FORMAT(////)
C   PRINT 1998
1998 FORMAT (IX,9HZ MATRIX,/,42H NO AN  (1)  BL  (2)  ALPHA  (3)
*      .10HBETA  (4))
    DO 900 J = 1,NN
      INDI = AN(J)
C   PRINT 1999,(J,AN(J),Z(J,1),BL(J),Z(J,2),ALPHA(J),Z(J,3),BETA(J),
C   *Z(J,4))
    900 CONTINUE
1999 FORMAT (2I3,I4,F7.4,2(I4,F11.6),I4)
    DATA(HOVS=4HHOVS)
    DO 7196 IME = 4,NN
1325  FORMAT (IX,2HHI)
      IF((Z(IME,4) .EQ. 0) .OR. (Z(IME,4) .EQ. 2)) GO TO 7196
      CALL Z4FIX(C,Z,IME)
7196  CONTINUE
      CALL ZTEST (R,RR,AN,Z,BL,ALPHA,BETA,NN)
      IF(LTEST .EQ. 1) GO TO 1984
      NMNJ = 1
      DO 1979 I=1,NN
        IF(Z(I,4) .NE. 0) GO TO 1978
        GO TO 1979
1978  LUU(NMNJ) = I
        NMNJ = NMNJ+1
1979  CONTINUE
        NMNJ =NMNJ-1
        DO 4224 J=1,NMNJ
          I=LUU(J)
4224  Z(I,4) = 1
          CALL      ZTEST(R,RR,AN,Z,BL,ALPHA,BETA,NN)
          IF(LTEST .EQ.1) GO TO 1984
          IAOK = 0
          LOST = NMNJ + 1
          DO 7007 JKK=1,LOST
            LJKK = JKK-1
            IF(IAOK .EQ. 0) GO TO 7008
            LKK = LUU (LJKK)
            Z(LKK,4) = Z(LKK,4)*(-1)
7008  CONTINUE
            DO 7000 I=1,NMNJ
              DO 7001 J=1,NMNJ
                IF(J.EQ.1) GO TO 7002
                KM1=K
                Z(KM1,4) =Z(KM1,4)*(-1)
7002  K=LUU(J)
                Z(K,4) = Z(K,4)*(-1)
```

```

CALL      ZTEST(R,RR,AN,Z,BL,ALPHA,BETA,NN)
IF(LTEST .EQ.1) GO TO 1984
DO 7004 IK=1,NNNJ
II=LUU(IK)
Z(II,4) = Z(II,4)*(-1)
7004 CONTINUE
CALL ZTEST(R,RR,AN,Z,BL,ALPHA,BETA,NN)
IF(LTEST .EQ.1) GO TO 1984
DO 7005 IL=1,NNNJ
II=LUU(IL)
Z(II,4) = Z(II,4)*(-1)
7005 CONTINUE
7001 CONTINUE
K=LUU(I)
7000 Z(K,4) = Z(K,4)*(-1)
IF(IACK .EQ. 0) GO TO 7009
Z(LKK,4) = Z(LKK,4)*(-1)
7009 CONTINUE
- - IACK = IACK + 1
7007 CONTINUE
RETURN
SUBROUTINE Z4FIX (C,Z,IME)
C THIS ROUTINE THANKS TO CLINT COOK PROPERLY SETS Z(I,4) IN THE
C ZMAT WHICH IS GENERATED BY UNZMAT, IF THE ATOM I IS
C SPECIFIED BY TWO BOND ANGLES.
INTEGER Z
DIMENSION C(60,3),          Z(60,4), Q1(3),Q2(3),Q3(3),MY(4),
*QC(3),QD(3),QE(3),QL1(3),QL2(3),QL3(3),DIM1(3),DIM2(3)
MY(1)=Z(IME,2)
MY(2)=Z(IME,1)
MY(3)=Z(IME,3)
MY(4)=IME
1202 FORMAT (2HBO)
DO 14 I=1,3
IF(I.EQ.1) GO TO 5
GO TO 6
5 CONTINUE
MQS=MY(2)
MQR=MY(1)
6 CONTINUE
IF(I.EQ.2) GO TO 7
GO TO 8
7 CONTINUE
MQS=MY(3)
MQR=MY(2)
8 CONTINUE
IF(I.EQ.3) GO TO 9
GO TO 10
9 CONTINUE
MQS=MY(4)
MQR=MY(2)
10 CONTINUE

```

```

      DO 11 J=1,3
      QC(J)=C(MOS,J)-C(MOR,J)
11  CONTINUE
      IF(I.EQ.1) CALL UNIVVEC(QL1,QC)
      IF(I.EQ.2) CALL UNIVVEC(QL2,QC)
      IF(I.EQ.3) CALL UNIVVEC(QL3,QC)
14  CONTINUE
      CALL VECPRD(DIM1,QL1,QL2)
      CALL SCLPRD(DIM2,DIM1,QL3)
      ALPA=C.0
      DO 25 K=1,3
      ALPA=DIM2(K)+ALPA
25  CONTINUE
      IF(ALPA.GT.0.0) GO TO 100
      GO TO 101
100 CONTINUE
      Z(IME,4) = 1
      GO TO 103
101 CONTINUE
      Z(IME,4) =-1
103 CONTINUE
      RETURN
      END
      SUBROUTINE SCLPRD(VP,X,Y)
C*****VP IS THE VECTOR PRODUCT OF X DOT Y.
      DIMENSION VP(3),X(3),Y(3)
      DO 1 I=1,3
      VP(I) = X(I) * Y(I)
1  CONTINUE
      RETURN
      END
      SUBROUTINE REF(E,NN)
      DIMENSION E(60,3), A(1,3), R(60,60)
99  FORMAT (//,1X, 40HCARTESIAN COORDINATES SUBJECTED TO CLINT,/)
      DO 1 I=1,3
      A(1,I) = E(I,I)
1  CONTINUE
      DO 2 I=1,NN
      DO 2 J=1,3
      E(I,J) = E(I,J) - A(1,J)
2  CONTINUE
100 FORMAT (//,1X, 66HCARTESIAN COORDINATES SUBJECTED TO CLINT AND REFEC
      *RRED TO THE DRIGIN,/)
      RETURN
      END
      SUBROUTINE CFIX(C,APH,BET,GAM,NN)
      COMMON/TRANZ/ A(3,3)
      DIMENSION C(60,3)
      AAPH = APH * 3.141592654/180.
      ABET = BET * 3.141592654/180.
      AGAM = GAM * 3.141592654/180.
      ACON = 90. * 3.141592654/180.

```

```
SINA = SIN(AAPH - ACON)
COXA = COS(AAPH - ACON)
SINB = SIN(ABET - ACON)
COSB = COS(ABET - ACON)
SING = SIN (AGAM - ACON)
COSG = COS(AGAM - ACON)
IF((APH .EQ. 90.) .AND. (GAM .EQ. 90.)) GO TO 55
GO TO 66
55 CONTINUE
PRINT 98
98 FORMAT (//,1X,24HTHE SYSTEM IS MONOCLINIC,/)
GO TO 56
66 CONTINUE
IF((APH .EQ. 90.) .AND. (BET .EQ. 90.) .AND. (GAM .EQ. 120.)) GO
*TO 61
GO TO 62
61 CONTINUE
PRINT 99
99 FORMAT (//,1X,23HTHE SYSTEM IS HEXAGONAL,/)
GO TO 67
62 CONTINUE
IF((APH .NE. BET) .AND. (BET .NE. GAM) .AND. (GAM .NE. APH)) GO TO
*81
GO TO 82
81 CONTINUE
PRINT 100
100 FORMAT (//,2X,23HTHE SYSTEM IS TRICLINIC,/)
GO TO 83
82 CONTINUE
IF((APH .EQ. BET) .AND. (APH .EQ. GAM)) GO TO 91
GO TO 92
91 CONTINUE
IF((APH .LT. 120.)) GO TO 93
GO TO 94
93 CONTINUE
PRINT 101
101 FORMAT (//,2X,22HTHE SYSTEM IS TRIGONAL,/)
GO TO 95
94 CONTINUE
97 CONTINUE
PRINT 102
102 FORMAT (//,1X,77HTHE SYSTEM IS NOT ORTHORHOMBIC, MONOCLINIC, HEXAG
*ONAL, TRICLINIC OR TRIGONAL.,/)
GO TO 70
56 CONTINUE
D = COSB
A(1,1) = COSB/D
A(1,2) = 0.
A(1,3) = 0.
A(2,1) = 0.
A(2,2) = 1.
A(2,3) = 0.
```

```

      A(3,1) = SINB/D
      A(3,2) = C.
      A(3,3) = 1.0/D
      GO TO 70
67  CONTINUE
      D = COSG
      A(1,1) = COSG/D
      A(1,2) = 0.
      A(1,3) = 0.
      A(2,1) = SING/D
      A(2,2) = 1.0/D
      A(2,3) = 0.
      A(3,1) = 0.
      A(3,2) = 0.
      A(3,3) = 1.
      GO TO 70
83  CONTINUE
      GO TO 70
95  CONTINUE
      GO TO 70
70  CONTINUE
      RETURN
      END

```

C THIS ROUTINE ACCEPTS A SET OF CARTESIAN COORDINATES AND GENERATES
C THE INTERATOMIC DISTANCE MATRIX

```

      DIMENSION C(60,3), R(60,60)
      DO 1 I=1,NN
      DO 1 J=1,NN
      R(I,J) = SQRT((C(I,1)-C(J,1))**2 + (C(I,2)-C(J,2))**2
      *(C(I,3)- C(J,3))**2)
1  CONTINUE
      RETURN
      END

```

```

SUBROUTINE RRED(AMAT,IROWS,TRANS)
  DIMENSION TRANS(3,3),AMAT(60,3)
  DIMENSION COPY(60,3)
  DO 1 I=1,IROWS
  DO 1 J=1,3
1  COPY(I,J)=AMAT(I,J)
  L=0
  DO 30 I=1,3
  IF (COPY(I,I)) 8,4,8
4  L=L+1
  IF (I+L-IROWS) 5,5,30
5  IF (COPY(I+L,I)) 6,4,6
6  CONTINUE
  DO 7 II=1,3
  M=I
  HOLD=COPY(II,M)
  COPY(II,M)=COPY(II+L,M)
7  COPY(II+L,M) = HOLD

```

```

      L = 0
8    CONTINUE
      DO 3 J=1,3
      3 COPY(I,J)=COPY(I,J)/COPY(I,1)
      DO 9 K=1,IRDWS
      IF (K+I-IRDWS) 10,10,30
10   CONTINUE
      DO 9 J=1,3
      9 COPY(I+K,J)=COPY(I+K,J) - COPY(I+K,1)*COPY(I,J)
30   CONTINUE
      DO 40 I=1,IRDWS
40   PRINT 50,(COPY(I,J),J=1,3)
50   FORMAT(3F20.10)
      DO 60 I=1,3
      DO 60 J=1,3
60   TRANS(I,J)=COPY(I,J)
      RETURN
      END
      SUBROUTINE ZTEST(R,RR,AN,Z,BL,ALPHA,BETA,NN)
C    THIS ROUTINE ACCEPTS AS INPUT THE ZMAT GENERATED BY UNZMAT, AND
C    USES SUBROUTINE ZMAT TO GENERATE THE INTERATOMIC DISTANCE MATRIX.
C    ZTEST THEN COMPARES THIS INTERATOMIC DISTANCE MATRIX TO THAT
C    GENERATED FROM THE CARTESIAN COORDINATES ACCEPTED AS INPUT TO XTAL
C    IF THE ZMAT WORKS, ZTEST SAYS SO, AND ALSO SETS LTEST = 1 SO THAT
C    UPON RETURN TO UNZMAT THE MACHINE EXITS TO XTAL.
      INTEGER Z
      COMMON/IIII/LTEST
      COMMON/JIM/IJIM
      COMMON/INFO/ORS
      DIMENSION ORS(60,3)
      DIMENSION RRRR(40,40)
      DIMENSION R(60,60),RR(40,40),AN(40),Z(60,4),BL(40),ALPHA(40),
      *BETA(40)
      IJIM = 0
      CALL ZMAT(AN,Z,BL,ALPHA,BETA,NN,RR)
      DO 2212 I=1,NN
      DO 2212 J=1,NN
2212  RRRR(I,J) = R(I,J) - RR(I,J)
      DO 2213 I=1,NN
      DO 2213 J=1,NN
      IF(ABS(RRRR(I,J)) .GT. .0001) GO TO 2214
      GO TO 2213
2214  GO TO 9999
2213  CONTINUE
      IJIM = IJIM + 1
      CALL ZMAT(AN,Z,BL,ALPHA,BETA,NN,RR)
      PRINT 99
99   FORMAT (///,3X,20HTHE ABOVE ZMAT WORKS,///)
      LTEST = 1
      DO 6969 I=1,NN
      PUNCH 1003, AN(I),Z(I,1),BL(I),Z(I,2),ALPHA(I),Z(I,3),BETA(I),
      *Z(I,4)

```

```

      A
      A
      A
      A
1003 FORMAT (I3,I4,F7.4,I4,F11.6,I4,F11.6,I4)
6969 CONTINUE
9999 RETURN
      END
      SUBROUTINE ZMAT(AN,Z,BL,ALPHA,BETA,NN,R)
C      *(INPUT,OUTPUT,TAPE5=INPUT,TAPE6=OUTPUT,PUNCH)
C      THIS PROGRAM ACCEPTS A DEFINITION OF A MOLECULE IN TERMS OF
C      ATOMIC NUMBERS, BOND LENGTHS, BOND ANGLES AND DIHEDRAL ANGLES
C      AND CALCULATES THE CARTESIAN COORDINATES IN ANGSTROMS
C      ADAPTED FROM MARK GORDON'S MELD SYSTEM BY D L BEVERIDGE
C      CODED IN CDC SCOPE 3.1 LEVEL FORTRAN FOR THE CIMS CDC 6600
      DIMENSION Z(60,4),BL(40),ALPHA(40),BETA(40)
      DIMENSION V1(3),V2(3),V3(3),VJ(3),VP(3),L1(3),L2(3),L3(3),L4(3),
*      A(80),B(80),D(80)
      TYPE REAL L1,L2,L3,L4
      COMMON/JIM/IJIM
      DIMENSIONC(60,3)
      DIMENSION BTB(60),ALB(60),BLB(60)
      DIMENSION AN(40)
      COMMON/INFO/C
      TYPE INTEGER AN,CHARGE,Z,PUNCH
      DIMENSION R(40,40)
      COMMON/IDENT/IDENT(10)
      COMMON/ELORB/EL(104),ORB(4,7)
      TYPE INTEGER ORB
      DATA((EL(I),I=1,36)=4H H,4H HE,4H LI,4H BE,4H B,4H C,
14H N,4H O,4H F,4H NE,4H NA,4H MG,4H AL,4H SI,4H P,
24H S,4H CL,4H AR,4H K,4H CA,4H SC,4H TI,4H V,4H CR,
34H MN,4H FE,4H CO,4H NI,4H CU,4H ZN,4H GA,4H GE,4H AS,
44H SE,4H BR,4H KR)
      DATA((EL(I),I=37,71)=4H RB,4H SR,4H Y,4H ZR,4H NB,4H MO,
14H TC,4H RV,4H RH,4H PD,4H AG,4H CD,4H IN,4H SN,4H SB,
24H TE,4H I,4H XE,4H CS,4H BA,4H LA,4H CE,4H PR,4H ND,
34H PH,4H SM,4H EU,4H GD,4H TB,4H DY,4H HO,4H ER,4H TM,
44H YB,4H LU)
      DATA((EL(I),I=72,102)=4H HF,4H TA,4H W,4H RE,4H OS,4H IR,
14H PT,4H AU,4H HG,4H TL,4H PB,4H BI,4H PO,4H AT,4H RN,
24H FR,4H RA,4H AC,4H TH,4H PA,4H U,4H NP,4H PU,4H AM,
34H CM,4H BK,4H CF,4H ES,4H FM,4H MD,4H NO)
      SINP(X)=SIN(X)
      COSP(X)=COS(X)
      ABSF(X)=ABS(X)
      SIGNF(X,Y)=SIGN(X,Y)
      SORTF(X) = SORT(X)
      ATANF(X)=ATAN(X)
C      *****
C      INPUT AND OUTPUT OF INPUT
      PUNCH = BHPUNCH
      M=NN
      NATOMS=NN
999 CONTINUE
C      READ 1000,(IDENT(I),I=1,10)

```

```

C      IF(EOF,5) 1,2
C      1 STOP
C      2 CONTINUE
C      PRINT 998
C      998 FORMAT(1H1)
C      PRINT 2006
C      2006 FORMAT(/,14H INPUT DATA..../)
C      PRINT 1000,(IDENT(I),I=1,10)
C      1000 FORMAT(10A8)
C      IF(IDENT(10).EQ.PUNCH)3,4
C      3 PRINT 2008
C      2008 FORMAT(/,16H PUNCH OPTION ON,/)
C      PUNCH 1000,(IDENT(I),I=1,10)
C      4 CONTINUE
C      READ 1001, NATOMS,CHARGE,MULTIP
C      1001 FORMAT(3I2)
C      PRINT1002, NATOMS,CHARGE,MULTIP
C      1002 FORMAT(//,10H NATOMS = ,I4,2X,10H CHARGE = ,I4,2X,10H MULTIP = ,I4,
C      *,I4,/)
C      IF(IDENT(10).EQ.5HPUNCH) 5,6
C      5 PUNCH 8,NATOMS,CHARGE,MULTIP
C      8 FORMAT(3I4)
C      6 CONTINUE
C      PRINT 1004
C      1004 FORMAT(//,9H Z MATRIX,/)
C      *****
C      CALCULATION OF COORDINATES
C      DO 6969 I=1,M
C      READ 1003, AN(I),Z(I,1),BL(I),Z(I,2),ALPHA(I),Z(I,3),BETA(I),
C      1Z(I,4)
C      1003 FORMAT(I3,I4,F7.4,I4,F11.6,I4,F11.6,I4,F10.5)
C6969 PRINT 1003, AN(I),Z(I,1),BL(I),Z(I,2),ALPHA(I),Z(I,3),BETA(I),
C      1Z(I,4)
C      6969 CONTINUE
C      DO 232 I=1,M
C      BTB(I) = BETA(I)
C      ALB(I) = ALPHA(I)
C      BLB(I) = BL(I)
C      232 CONTINUE
C      DO 502 J=1,M
C      502 ALPHA(J) = ALPHA(J)*3.141592654/180.
C      DO 503 J=1,M
C      503 BETA(J) = BETA(J)*3.141592654/180.
C      DO 504 J= 1,3
C      504 C(1,J)=0.0
C      C(2,1)=0.0
C      C(2,2)=0.0
C      C(2,3)=BL(2)
C      C(3,1)=BL(3)*SINF(ALPHA(3))
C      C(3,2)=0.0
C      *****
C      THE FOLLOWING IS AN ADDITION TO COORD FINDEP PROGRAM TO BE USED

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C     IF THE MOLECULE UNDER CONSIDERATION HAS ONLY ONE HEAVY ATOM OR FOR
C     A MOLECULE SUCH AS NEOPENTANE IN WHICH THE CENTRAL ATOM HAS NO
C     HYDROGENS BONDED TO IT
      IF(Z(3,1).EQ.1) 505,506
505  C(3,3) = BL(3)*COSF(ALPHA(3))
      GO TO 507
506  C(3,3) = C(2,3)-BL(3)*COSF(ALPHA(3))
507  I=3
      IF(ABSF(C(3,1)).LT..00001) 550,510
550  DO 509 I = 4,1000
      IF(I.LE.M.AND.ABSF(C(I-1,1)).LT..00001) 508,510
508  C(I,1) = BL(I)*SINF(ALPHA(I))
      C(I,2) = 0.0
      ITEMP = Z(I,1)
      JTEMP = Z(I,2)
      OC(I,3) = C(ITEMP,3)-BL(I)*COSF(ALPHA(I))*SIGNF(1.,C(ITEMP,3)-C(JTEMP,3))
509  CONTINUE
510  CONTINUE
      IF(I.EQ.3) 511,512
511  K=4
      GO TO 513
512  K=I
513  CONTINUE
      IF(K.GT.M) 601,600
600  CONTINUE
      DO 533 J = K,M
      IF(Z(J,4).EQ.0) 514,517
C     *****
C     THIS PART IS USED IF THE ATOM IS BEING DEFINED BY A DIHEDRAL ANGLE
514  CALL RELVEC(V1,Z(J,2),Z(J,3))
      CALL UNIVVEC(L1,V1)
C     V1 IS A VECTOR FROM ATOM Z(J,3) TO ATOM Z(J,2)
C     L1 IS A UNIT VECTOR OF V1.  BL(Z(J,2)) IS BONDLENGTH OF ATOM Z(J,2)
      CALL RELVEC(V2,Z(J,1),Z(J,2))
      CALL UNIVVEC(L2,V2)
C     V2 IS THE VECTOR FROM ATOM Z(J,2) TO ATOM Z(J,1)
C     L2 IS THE UNIT VECTOR OF V2.  BL(Z(J,1)) IS BONDLENGTH DEFINING
C     ATOM Z(J,1)
      CALL VECPRD(VP,L1,L2)
      DO 515 I = 1,3
515  L3(I) = VP(I)/SQRTF(1.-(L1(I)*L2(I)+L1(2)*L2(2)+L1(3)*L2(3))**2)
C     L3 IS THE UNIT VECTOR OF VP. ALPHA(Z(J,1)) IS THE ANGLE DEFINING
C     ATOM Z(J,1)
      CALL VECPRD(L4,L3,L2)
C     L4,L3,L2 ARE A NEW SET OF MUTUALLY ORTHOGONAL AXES. WE WILL NOW
C     OBTAIN COORD OF ATOM J IN TERMS OF THESE AXES RELATIVE TO ATOM Z(J,1)
      DO 516 I=1,3
      OVJ(I) = BL(J)*(-L2(I)*COSF(ALPHA(J))+L4(I)*SINF(ALPHA(J))*COSF(BETA(J))
      +L3(I)*SINF(ALPHA(J))*SINF(BETA(J)))
C     VJ IS THE VECTOR FROM ATOM Z(J,1) TO ATOM J
      ITEMP = Z(J,1)

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      C(J,I) = VJ(I) + C(ITEMP,I)
516 CONTINUE
      GO TO 533
517 IF(Z(J,4).EQ.1.OR.Z(J,4).EQ.-1) 549,528
C *****
C THIS PART IS USED IF ATOM IS DEFINED BY TWO BONDANGLES
549 CALL RELVEC(V1,Z(J,1),Z(J,3))
      CALL UNIVVEC(L1,V1)
      CALL RELVEC(V2,Z(J,2),Z(J,1))
      CALL UNIVVEC(L2,V2)
      ZETA = -(L1(1)*L2(1)+L1(2)*L2(2)+L1(3)*L2(3))
      A(J) = (-COSF(BETA(J))+ZETA*COSF(ALPHA(J)))/(1.-ZETA**2)
      B(J) = (COSF(ALPHA(J))-ZETA*COSF(BETA(J)))/(1.-ZETA**2)
      PI = 3.141592654
      IF(ZETA.LT.0) 518,519
518 TEMP = PI
      GO TO 520
519 TEMP = 0.0
520 CONTINUE
      IF(ZETA.EQ.0) 521,522
521 GAMMA = PI/2.
      GO TO 523
522 GAMMA = ATANF(SQRTF(1.-ZETA**2)/ZETA) +TEMP
523 CONTINUE
      IF (ABSF(GAMMA+ALPHA(J)+BETA(J)-2.*PI).LT..00000001) 524,525
524 D(J) = 0.0
      GO TO 526
525 D(J) = Z(J,4)*(SQRTF(1.+A(J)*COSF(BETA(J))-B(J)*COSF(ALPHA(J)))/S
      QRTF(1.-ZETA**2))
526 CONTINUE
      CALL VECPRD(V3,L1,L2)
      DO 527 I = 1,3
      L3(I) = A(J)*L1(I)+B(J)*L2(I)+D(J)*V3(I)
      VJ(I) = 8L(J)*L3(I)
      ITEMP = Z(J,1)
      C(J,I) = VJ(I)+C(ITEMP,I)
527 CONTINUE
      GO TO 533
C *****
C THIS PART IS USED IF ATOM IS DEFINED BY ONE BONDANGLE AND BY THE
C ANGLE WHICH BOND Z(J,1)-J MAKES WITH THE PLANE OF Z(J,1),Z(J,2)
C AND Z(J,3)
528 CALL RELVEC(V1,Z(J,1),Z(J,3))
      CALL UNIVVEC(L1,V1)
      CALL RELVEC(V2,Z(J,2),Z(J,1))
      CALL UNIVVEC(L2,V2)
      ZETA = -(L1(1)*L2(1)+L1(2)*L2(2)+L1(3)*L2(3))
      CALL VECPRD(V3,L1,L2)
C BETA(J) HERE REFERS TO 90-ANGLE WHICH BOND Z(J,1)-J MAKES WITH THE
C AFOREMENTIONED PLANE
      A(J) = COSF(BETA(J))/(1.-ZETA**2)
      IF(Z(J,4).EQ.2) 530,529

```

```

529 B(J) = -SQRTF((1.-COSF(ALPHA(J))**2-A(J)*COSF(BETA(J)))/(1.-ZETA**2
1))
GO TO 531
530 B(J) = SQRTF((1.-COSF(ALPHA(J))**2-A(J)*COSF(BETA(J)))/(1.-ZETA**2))
531 CONTINUE
D(J) = B(J)*ZETA+COSF(ALPHA(J))
DO 532 I=1,3
L3(I) = B(J)*L1(I)+D(J)*L2(I)+A(J)*V3(I)
VJ(I) = BL(J)*L3(I)
ITEMP = Z(J,1)
C(J,I) = VJ(I) + C(ITEMP,I)
532 CONTINUE
533 CONTINUE
601 CONTINUE
C *****
C OUTPUT SECTION
C PRINT 2007
IF(IJIM .EQ. 0) GO TO 11
PRINT 1998
1998 FORMAT (1X,8HZ MATRIX,/,42H NO AN (1) BL (2) ALPHA (3)
* ,20HBETA (4) EL ,8X,1HX,11X,1HY,12X,1HZ)
2007 FORMAT(/,15H OUTPUT DATA...,/)
C1998 FORMAT (/,20X,11HCOORDINATES,/,4X,10HNO OF ATOM,3X,6HSYMBOL,10X,
C 11HX,10X,1HY,10X,1HZ,/)
DO 900 J=1,M
IND1=AN(J)
900 PRINT 1999,J,AN(J),Z(J,1),BLB(J),Z(J,2),ALB(J),Z(J,3),BTB(J),
*Z(J,4),EL(IND1),1C(J,I),I=1,3)
1999 FORMAT (2I3,I4,F7.4,2(I4,F11.6),I4,6X,A4,4X,3F12.8)
C 900 PRINT 1999 ,J,EL(IND1),( C(J,I),I=1,3)
C1999 FORMAT(8X,12,5X,A4,4X,3F12.8)
C IF(IDENT(10).EQ.PUNCH) 7,11
C 7 PUNCH 9,(AN(I),(C(I,J),J=1,3),I=1,NATOMS)
9 FORMAT(14,3(3X,F12.7))
11 CONTINUE
DO 10I=1,NATOMS
DO 10J=1,NATOMS
10 K(I,J) = SQRT((C(I,1)-C(J,1))**2+(C(I,2)-C(J,2))**2+(C(I,3)-C(J,
*))**2)
C CALL MOUTP (R,NATOMS,NATOMS,40,40,10H DISTANCES)
DO 1502 J=1,M
ALPHA(J) = ALPHA(J) * 180./3.141592654
BETA(J) = BETA(J) * 180./3.141592654
1502 CONTINUE
RETURN
END
SUBROUTINE RELVEC(R,J,K)
COMMON/INFO/C
DIMENSIONC(60,3)
DIMENSION R(3)
TYPE REAL C,R
TYPE INTEGER J,K,I

```

```

      DO 1 I=1,3
1      R(I)=C(J,1)-C(K,1)
C      R IS THE RELATIVE VECTOR FROM ATOM K TO ATOM J
      RETURN
      END
      SUBROUTINE UNIVVEC(L,R)
      DIMENSION L(3),R(3)
      SORTF(X)=SORT(X)
      TYPE REAL L,R
      TYPE INTEGER I
      DO 2 I=1,3
2      L(I)=R(I)/SORTF(R(1)**2 + R(2)**2 + R(3)**2)
C      L IS THE UNITVECTOR OF R
      RETURN
      END
      SUBROUTINE VECPRD(VP,X,Y)
      DIMENSION VP(3),X(3),Y(3)
      TYPE REAL VP,X,Y
      VP(1)=X(2)*Y(3)-X(3)*Y(2)
      VP(2)=X(3)*Y(1)-X(1)*Y(3)
      VP(3)=X(1)*Y(2)-X(2)*Y(1)
C      VP IS THE VECTOR PRODUCT OF X CROSSED Y
      RETURN
      END
      SUBROUTINE MOUTP (A,M,N,MDIM,NDIM,NAME)
C      OUTPUT OF M X N MATRIX DIMENSIONED TO MDIM X NDIM
      DIMENSION A(MDIM,NDIM)
      XMINOF(I,J)=MINO(I,J)
      PRINT 1000,NAME
1000 FORMAT(//,A10)
      KITE = 0
      20 LOW = KITE+1
      KITE = KITE+14
      KITE = XMINOF(KITE,N)
      PRINT 19,(I,I=LOW,KITE)
19 FORMAT( //      .4X,14(6X,12),/)
      DO 32 I=1,M
32 PRINT 18,I,(A(I,J),J=LOW,KITE)
18 FORMAT(14,2X,14F8.4)
      IF(N-KITE) 40,40,20
40 RETURN
      END
      SUBROUTINE TAUFIX(BL,ALPHA,BETA,JJ,KK,LL,MM,T,R,Z,C)
C      THIS ROUTINE CALCULATES TAU(J,K,L,M) AND IS USED BY UNZMAT TO
C      GFAR RINGS.
      INTEGER Z
      DIMENSION A(3,3)
      DIMENSION C(60,3)
      DIMENSION BL(40),ALPHA(40),BETA(40),T(40,40,40),R(60,60)
      DIMENSION Z(60,4)
C      AT THIS POINT JJ,KK,LL,MM ARE SEQUENTIALLY BONDED ATOMS WHERE JJ
C      IS GREATER THAN MM

```

```

      CC=0.0
      DO 1240 I = 1,3
1240  CC = CC+(C(KK,I)-C(JJ,I))*(C(LL,I)-C(KK,I))
      CC = CC/(R(JJ,KK)*R(KK,LL))
      DO 1230 I = 1,3
1230  A(1,I)=(C(LL,I)-C(KK,I))/R(KK,LL)
      DO 1250 I = 1,3
      YYY = (1.0 - CC*CC)
      IF (YYY .LT. 0.0) GO TO 1205
      GO TO 1206
1205  PRINT 1202
1202  FORMAT(///,36HSORT HAS NEGATIVE ARGUMENT IN TAUFIX,///)
1206  CONTINUE
1250  A(2,I)=(-C(KK,I)-C(JJ,I))/R(JJ,KK)+CC*(C(LL,I)-C(KK,I))/R(KK,LL)
      */ SORT( ABS(1.0 -CC*CC)
      A(3,1)=A(1,2)*A(2,3)-A(1,3)*A(2,2)
      A(3,2)=A(2,1)*A(1,3)-A(1,1)*A(2,3)
      A(3,3)=A(1,1)*A(2,2)-A(2,1)*A(1,2)
      Z0=0.0
      Y0=0.0
      DO 1260 I=1,3
      Z0=Z0+A(3,I)*(C(MM,I)-C(KK,I))
1260  Y0=Y0+A(2,I)*(C(MM,I)-C(KK,I))
      CT = Y0
      ST = Z0
      TAU=( 180./3.141592654) * ATAN2(ST,CT)
      Z(JJ,1) = KK
      BL(JJ) = R(JJ,KK)
      Z(JJ,2) = LL
      ALPHA(JJ) = T(JJ,KK,LL)
      Z(JJ,3) = MM
      BETA(JJ) = TAU
      RETURN
      END

```

) NOT FOUND IN NM DIRECTORY. STOWED WITH TTR.

E WAS CCCCCC

Appendix B:

SZMAT accepts as input a description of a geometrical system of atoms in terms of bond lengths and angles, and four atom torsions, (model builder input to ZMAT of M. Gordon). It also accepts parameters for the systematic incrementing of up to two bond lengths, bond angles or four atom torsions. Having read the above input, SZMAT calculates an interatomic distance array for each of the configurations designated by the input. If any interatomic distance in any of the configurations goes below the arbitrarily set value of 3.0\AA , the atoms which did this are recorded in an array, KNOWL. Having the knowledge of which interatomic distances are sterically significant, SZMAT recalculates these distances and stores them on a peripheral disk. After all the distances are written on the disk, they are systematically examined to determine if they change as a function of conformation. If they do not, they cannot account for changes in conformational energy, and SZMAT makes note of this in an array LCIM. SZMAT then generates a summary steric grid (which for all interatomic distances which change as a function of conformation), writes for a conformation the following words based on the lowest interatomic distance:

BAD	under	$.7\text{\AA}$	$\overset{\circ}{\text{A}}$
FAIL	between	$.7\text{\AA}$	and 1.5\AA
CLOS	between	1.5\AA	and 2.0\AA

The symbol is printed if all changing interatomic distances are above 2.0\AA . The appearance of the steric grid is constructed for ease in visual scanning, and this relatively fast geometrical procedure can yield interesting information regarding steric intramolecular interactions.

RJR,LIST=ALL
100.NFW1=100

```

BLOCK DATA
  IMPLICIT REAL*8(A-H,O-Z)
COMMON/LIT/IBLANK,ITMAT,IBL,IALPHA,IBETA,ICLEAR,I11,I12
C   TEST INSERTION
C   COMMON/ARRAYS/ABC(19200)
C   COMMON/TAPF/RWTAPE,TPDSTN,ADDRSS(40)
C   COMMON/AUXINT/A(17),B(17)
C   COMMON/PERTBL/FL(18)
C   DIMENSION EL(18)
C   COMMON/ORB/ORB(9)
C   COMMON/I/XYZ(2000)
C   COMMON/INFO1/CZ(35),U(80),ULIM(35),LLIM(35),NELECS,OCCA,OCCB
C   COMMON/OPTION/OPTION,OPNCLO,HUCKEL,CNDO,INDO,CLOSED,OPEN,IONOFF
C   COMMON/ENGY/IC,BOE(3),ROE(3)
C   COMMON/SIMRUN/ID,I1,I2,II,III,BL(80),ANG1(80),ANG2(80),IE,DELTA,IS
C   A,ISS,PMIN
C   DATA EL(1),EL(2),EL(3),EL(4),EL(5),EL(6),EL(7),EL(8),EL(9) /'H',
C   *'HE','LI','BE','B','C','N','O','F'/
C   COMMON/NTMAT/LTMAT,NVAR,LID
C   INTEGER OPTION,OPNCLO,HUCKEL,CNDO,INDO,CLOSED,OPEN,IONOFF
C   INTEGER OFF
C   INTEGER ORB,EL,AN,CHARGE
C   COMMON/ZETA/FMU(18)
C   COMMON/GUESS/IGES,IGUESS
C   DIMENSION EGRID(1600)
C   14H DYZ,4HDX-Y,4H DXY)
C   DATA(INDO=4HINDO)
C   DATA(OPEN=6HOPEN )
C   DATA(CLOSED=6HCLOSED)
C   DATA IZMAT/'ZMAT'/
C   DATA (ITMAT = 4HZMAT)
C   DATA(OFF = 3HOFF)
C   DATA(IGUESS = 5HGUESS)
C   DATA(IOUT = 4HOUT)
COMMON/IPR/IOUT,LDUTT
DATA IOUT/'OUT'/
DATA I11/'I1'/
DATA I12/'I2'/
DATA IALPHA/'ALPH'/
DATA IBETA/'BETA'/
DATA IBLANK/'  '/
DATA ICLEAR/'  '/
DATA IBL/'BL  '/
DATA ITMAT/'TMAT'/
C   DATA(IBETA=5HBETA )
C   DATA(IBLANK=8H
C   DATA(ICLEAR=5H
C   DATA(IBL=5HBL )
C   DATA(I11=2HI1)
C   DATA ((LCAL(I),I=1,6)=4H      ,4H      ,4H      ,4H      ,4H      ,4H      )

```

```

C      DATA(I12=2HI2)
C      DATA (IALPHA=5HALPHA)
C      DATA(ITMAT=4HTMAT)
C      FND
C      IMPLICIT REAL*8(A-H,O-Z)
C      PROGRAM SZMAT
C      *(INPUT,OUTPUT,TAPE5=INPUT,TAPE6=OUTPUT,PUNCH,TAPE10,TAPE11)
C      INTEGER*2 LCIM,KNOW1,KNOW2
C      DIMENSION LCAL(6)
C      COMMON/LIT/IBLANK,ITMAT,IBL,IALPHA,IBETA,ICLEAR,I11,I12
C      COMMON/TPR/IOUT,LOUT
C      COMMON/LAB/I1STOR,I2STOR,TOP
C      COMMON/STR/JS1,JSS1,JS2,JSS2
C      COMMON/KNOW/KNOW1(600),KNOW2(600)
C      COMMON/CIM/JKJL,JKJLMN,LCIM
C      COMMON/COUNT/NOOO
C      INPUT IS READ IN THE FOLLOWING ORDER
C      (1) OPTION CARD WITH THE FOLLOWING INFORMATION
C      (A) OPTION (WAVEFUNCTION OPTION) IN COLUMNS 1 - 4. THE KEY
C          WORDS ARE          INDO          CNDO
C      (B) OPNCLO (OPEN OR CLOSED SHELL) IN COLUMNS 5 - 10. THE KEY
C          WORDS ARE          OPEN          CLOSED
C      (C) INPUT (TO READ IN THE MOLECULE IN TERMS OF BONDLENGTHS, BOND
C          ANGLFS, AND DIHEDRAL ANGLES. IN COLUMNS 11 - 14. THE KEY
C          WORD IS          ZMAT
C      (D) IONOFF (TO SUPPRESS MOST PRINTED OUTPUT) IN COLUMNS 15 - 17.
C          ANGLE(S), OR DIHEDRAL ANGLE(S) SPECIFIED IN LVAR1,ISS1, AND
C          ISS1 IS (OR ARE) TO BE VARIED BY THE AMOUNT DELTA1. I1 IS
C          SPECIFIED IN I3 FORMAT IN COLUMNS 27 - 29.
C      (H) LVAR1 (WHICH SPECIFIES WHAT IS TO BE VARIED) IN COLUMNS
C          30 - 34. THE KEY WORDS ARE
C
C              ALPHA          BETA          BL
C      (I - J) ISI AND ISS1 (THE SUBSCRIPT OF LVAR1) IN COLUMNS
C          35 - 38 AND 39 - 42 RESPECTIVELY (EACH) IN I4 FORMAT. EACH
C          MAY BE ANY POSITIVE INTEGER FROM 1 TO THE NUMBER OF ATOMS IN
C          THE MOLECULE. IF ONLY ONE IS BEING VARIED, LEAVE ISS1 BLANK
C      (K) DELTA1 (THE AMOUNT BY WHICH LVAR1(IS1) AND/OR LVAR1(ISS1) IS
C          OR ARE BEING VARIED) IN COLUMNS 43 - 53 (IN F11.6 FORMAT)
C      (L - P) G - K ARE REPEATED TO PERMIT A SECOND VARIABLE, LVAR2,
C          SUBSCRIPTED BY IS2 AND ISS2 TO BE VARIED BY DELTA2 SO THAT
C          A GRID SEARCH CAN BE CONDUCTED 12 TIMES.
C          I2 (IN I3 FORMAT) IS IN COLUMNS 54 - 56.
C          LVAR2 IS IN COLUMNS 57 - 61.
C          IS2 AND ISS2 ARE IN COLUMNS 62 - 65 AND 66 - 69
C      OF THE RUN.
C      (2) AN IDENTIFICATION CARD WHICH IS PRINTED AT THE BEGINNING
C          DELTA2 IS IN COLUMNS 70 - 80 (IN F11.6 FORMAT).
C          RESPECTIVELY (EACH IN I4 FORMAT).
C      (3) NATOMS, CHARGE, MULTIPLICITY          FORMAT (3I2)
C      (4) ATOMIC NUMBER, X COORDINATE, Y COORDINATE, Z COORDINATE ON
C          ONE CARD. FORMAT (I4,3(3X,F12.7))
C          DECIMAL POINTS IN COLUMNS 12, 27, AND 42

```

```

DATA IBCD/'IBCD'/
DATA IOK/'....'/
DATA IFAIL/'FAIL'/
DATA IBAD/'BAD'/
DATA ICLOS/'CLOS'/
  INTEGER AN, CHARGE
DIMENSION JGRD(36,36)
DIMENSION C(60,3),AN(60)
DIMENSION LCIM(60,60)
COMMON/INFO/C      ,NATOMS,CHARGE,MULTIP,AN      ,      N
DIMENSION FFEF(18,18), DOST(1000)
DIMENSION TOP(36), SIDE(36)
DIMENSION BOE(3), ROE(3),      BL(60),ANG1(60),ANG2(60)
COMMON/NTMAT/LTMAT,NVAR,LID
C COMMON/LIT/IBLANK,ITMAT,IBL,IALPHA,IBETA,ICLEAR,III,II2
COMMON/SIMRUN/BL,ANG1,ANG2,ID,I1,I2,II,III,IE,DELTA,IS
A,ISS,RMIN
COMMON/ENGY/      BOE,ROE      ,IC
SORTF(X) = DSORT(X)
996 CONTINUE
N000=0
KKK = 0
DO 9031 I = 1,60
DO 9031 J = 1,60
9031 LCIM(I,J)= 0
JKJLMN = 0
JKJL = 1
DO 4404 I=1,600
KNOW1(I) = 0
KNOW2(I) = 0
4404 CONTINUE
PRINT 9123
9123 FORMAT (IHL)
NSCR = 10
NDISK = 11
C DEFINE FILE 11(10,24000,U,JDUMP),10(1,400,U,JDUMP)
REWIND NDISK
REWIND NSCR
IC=0
JD = 1
JDD = 2
READ 4444, LFIN
4444 FORMAT (I4)
IF(LFIN .EQ. 1) GO TO 998
READ 40,
I1,LVAR1,IS1,ISS1,
XDELTA1,I2,LVAR2,IS2,ISS2,DELTA2
I1STOR = I1
I2STOR = I2
C IF(EOF(5)) 998,997
997 CONTINUE
JS1 = IS1
JSS1 = ISS1

```

```

      JS2 = IS2
      JSS2 = ISS2
      I1 = I1STOR
      I2 = I2STOR
      LID = I11
      ID=1
      JD=I1
      NVAR=LVAR1
      IS=IS1
      ISS=ISS1
      DELTA=DELTA1
      IF(IABS(I1).EQ.0) GO TO 999
992 CONTINUE
      DO 990 JD=1,I1
      LID = I11
      ID=JD
      GO TO 999
991 CONTINUE
      DO 993 JDD=2,I2
      LID = I12
      ID=JDD
999 CONTINUE
      IC=IC + 1
      IF=IC
      IF (IC.LT.3) GO TO 3470
3471 CONTINUE
C      IF (LTMAT.NE.ITMAT) GO TO3476
C3477 CALL TMAT
3476 IC=1
3470 CONTINUE
      IF(JKJLMN .NE.2) GO TO 51
      IF((LOUTT .NE. IOUT) .AND. (IE .EQ. 1)) GO TO 8015
      IF(LOUTT .NE. IOUT) GO TO 51
8015 CONTINUE
      IF(NOOO.NE.0) GO TO 51
      PRINT 41, I1,LVAR1,IS1,ISS1,
      ZDELTA1,I2,LVAR2,IS2,ISS2,DELTA2,ID,DELTA
C      CALL TIM
C      IF (INPUT.NE.IZMAT) GO TO 52
51 CALL ZMAT
      GO TO 53
52 CONTINUE
C      READ 20.(AN(I),I=1,10)
C      PRINT 30.(AN(I),I=1,10)
C      READ 50.NATOMS.CHARGE.MULTIP.IUNITS
C 50 FORMAT(4I4)
C      PRINT 60.NATOMS.CHARGE.MULTIP.IUNITS
C 60 FORMAT(/5X,I4,18H ATOMS CHARGE =,I4,18H MULTIPLICITY =,I4,12
C 1H IUNITS = ,I4,/)
C      DO 10 I = 1,NATOMS
C      READ 70,AN(I), C(I,1),C(I,2),C(I,3)
C      PRINT 70,AN(I), C(I,1),C(I,2),C(I,3)

```

```

C      CONVERSION OF COORDINATES FROM ANGSTROMS TO ATOMIC UNITS
C      IF(IUNITS.EQ.1) GO TO 10
C 11 CONTINUE
C      DO 9 J=1,3
C 9 C(I,J) = C(I,J)/.529167
C 10 CONTINUE
C 53 CONTINUE
C      IF (OPTION.NE.INDD) GO TO 6
1 DO 5 I=1,NATOMS
  IF (AN(I).LE.9) GO TO 4
2 PRINT 3
3 FORMAT(47H THIS PROGRAM DOES NOT DO INDD CALCULATIONS FOR,
1 51H MOLECULES CONTAINING ELEMENTS HIGHER THAN FLUORINE)
  STOP
4 CONTINUE
5 CONTINUE
6 CONTINUE
  IF(IJKJLMN .NE. 2) GO TO 96
  KGRD = IRCD
  DO 99 I=2,NATOMS
    IM1 = I-1
    DO 99 J=1,IM1
      IF(LCIM(I,J) .NE. 0) GO TO 99
      R=SQRT((C(I,1)-C(J,1))**2+(C(I,2)-C(J,2))**2+(C(I,3)-C(J,3))**2)
1 *0.529167
      IF(KGRD.EQ.IFAIL) GO TO 7173
      IF(R .LE. 1.5) KGRD = IBAD
      IF((R.GT.1.5).AND.(R.LT.2.).AND.(KGRD.NE.IBAD)) KGRD = ICLOS
7173 CONTINUE
      IF(IJKJLMN .NE. 2) GO TO 9009
      IF((LOUTT .NE. IOUT) .AND. (IE .EQ. 1)) GO TO 2093
      IF(LOUTT .NE. IOUT) GO TO 9009
2093 CONTINUE
      IF((R .LE. 1.5 ) .AND. (R .GT. .7)) PRINT 7093, I,J,R
9009 CONTINUE
7093 FORMAT ( 45H STERIC INTERACTION IS LIKELY SINCE . 3H R(,
  *I4,I4,4H) = ,F10.5)
      IF(R .GE. .7) GO TO 4445
      KGRD = IFAIL
      IF(IJKJLMN .NE.2) GO TO 99
      IF((LOUTT .NE. IOUT) .AND. (IE .EQ. 1)) GO TO 1387
      IF(LOUTT .NE. IOUT) GO TO 99
1387 CONTINUE
      IF(NQQQ .NE. 0) GO TO 99
98 PRINT 97,I,J,R
97 FORMAT( 45H NO CALCULATION OF THIS CONFORMATION BYPASSED,3H R(,
  *I4 ,I4,4H) = ,F10.5)
C      GO TO 96
4445 CONTINUE
99 CONTINUE
  IF(KGRD .EQ. IRCD) GO TO 1920
  GO TO 1921

```

```
1920 KGRD = IOK
1921 CONTINUE
      WRITE (NSCR) KGRD
C     CALL OVERLAY(6LCNINDO,1,0)
C     CALL OVERLAY(6LCNINDO,2,0)
C     KKK = KKK + 1
C     FGRID(KKK) = BOE(1)
C     CALL TIM
96    CONTINUE
7679 FORMAT (3X,3HI2=,I4,3X,4HLID=,A4,3HI1=,I4 )
      IF ((I2.GT.0).AND.(LID.EQ.I11)) GO TO 994
5432 FORMAT (3X,1HW)
      GO TO 993
994   CONTINUE
5433 FORMAT (3X,1HX)
      NVAR=LVAR2
      IS=IS2
      ISS=ISS2
      DELTA=DELTA2
      GO TO 991
993   CONTINUE
      LID = I11
      NVAR=LVAR1
      IS=IS1
      ISS=ISS1
      DELTA=DELTA1
      ID=JD
990   CONTINUE
C     IF ((IC.EQ.3).AND.(LTMAT.EQ.ITMAT)) 3570,3571
C3570 CALL TMAT
3571 CONTINUE
      IF(JKJLMN .NE. 2) GO TO 49
      IF(I1 .EQ. 0) GO TO 915
      GO TO 916
915   I1 = 1
916   CONTINUE
      IF(I2 .EQ. 0) GO TO 917
      GO TO 918
917   I2 = 1
918   CONTINUE
      DO 394 I = 1,I2
394   TOP(I) = (I-1)*DELTA2
      DO 395 I = 1,I1
395   SIDE(I) = (I-1)*DELTA1
      REWIND NSCR
      DO 331 = 1,I1
          DO 33J=1,I2
33   READ(NSCR) JGRD(I,J)
          IF(JKJLMN .NE. 2) GO TO 49
          PRINT 74
74   FORMAT (//,2X,38HGRID OF STERICALLY EXCLUDED CONFORMERS,/)
          PRINT 974
```

```

974  FORMAT (1X,5HKFY= ,3X,22HFMAIL - R LESS THAN 0.7,/,9X,43HBAD - R L
      *ESS THAN 1.5 AND GREATER THAN 0.7,/,9X,43HCLOS - F LESS THAN 2.0
      *ND GREATER THAN 1.5,/)
      KITE = 0
22   LOW = KITE + 1
      KITE = KITE + 14
      KITE = AMIN0(KITE,I2)
      PRINT 19, (TOP(I),I=LOW,KITE)
      PRINT 9124
9124  FORMAT(//)
      19  FORMAT (//,5X,14(2X,F6.2),/)
      DO 32 I = 1,I1
      32  PRINT 18, SIDE(I),(JGRD(I,J),J=LOW,KITE)
      18  FORMAT (1X,F6.2,14(2X,A4,2X))
      IF(I2-KITE) 49,49,22
      49  CONTINUE
      IF(JKJLMN .NE. 1) GO TO 1281
C     PRINT 9225, JKJL
9225  FORMAT(I10)
      CALL KFIX
      KOW = I1*I2
      DO 4231 MHO = 1,JKJL
      JHO = 1
      KHO = 1
      REWIND NDISK
      DO 4228 KEEP = 1,KOW
      DO 3225 IHO = 1,JKJL
      READ (NDISK) DOST(IHO)
3225  CONTINUE
      FEEEE(JHO,KHO) = DOST(MHO)
      IF(KHO .EQ. I2) GO TO 3227
      GO TO 3228
3227  CONTINUE
      JHO = JHO + 1
      KHO = 1
      GO TO 4227
3228  CONTINUE
      KHO = KHO + 1
4227  CONTINUE
4228  CONTINUE
      CALL MOUTPT(EEEE, I1, I2, 18, 18, LCAL)
      CALL ROUT(EEEE, MHO)
4231  CONTINUE
1281  CONTINUE
      JKJLMN = JKJLMN + 1
      IF((JKJLMN .EQ. 1) .OR. (JKJLMN .EQ. 2)) GO TO 9293
      GO TO 996
9293  CONTINUE
      NQQQ=0
      IC=0
      JD=1
      JGD = 2

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      GO TO 997
998 CONTINUE
C     PUNCH 888, (EGRID(I),I=1,KKK)
888  FORMAT (8F10.5)
      PRINT 80
20  FORMAT(10A8)
30  FORMAT( //,10A8)
40  FORMAT (2(I3,A4,1X,2I4,F11.6))
41  FORMAT (//////,6H I1 = ,I4.9H LV
CAR1 = ,A5.6H IS1 = ,1X,I4.5X,8H ISS1 = ,I4.5X,10H DELTA1 = ,F11.6, /
D/,6H I2 = ,I4.9H LVAR2 = ,A5.7H IS2 = ,I4.5X,8H ISS2 = ,I4.5X,10H
EDELTA2 = ,F11.6,////,14H CURRENT ID = ,I4.10X,17H CURRENT DELTA = ,
FF12.6)
70  FORMAT(I4,3(3X,F12.7))
80  FORMAT(16H END OF THIS RUN)
4443 CONTINUE
      END
      SUBROUTINE ZMAT
      IMPLICIT REAL*8(A-H,O-Z)
      INTEGER*2 LCIM,KNOW1,KNOW2
C     THIS PROGRAM ACCEPTS A DEFINITION OF A MOLECULE IN TERMS OF
C     ATOMIC NUMBERS, BOND LENGTHS, BOND ANGLES AND DIHEDRAL ANGLES
C     AND CALCULATES THE CARTESIAN COORDINATES IN ANGSTROMS
C     ADAPTED FROM MARK GORDON'S MBLD SYSTEM BY D L BEVERIDGE
C     CODED IN CDC SCOPE 3.1 LEVEL FORTRAN FOR THE CIMS CDC 6600
      DIMENSION Z(60,4),ALPHA(60),BETA(60)
      COMMON/TAU/ALPHA,BETA
      DATA JCIM/'JCIM'/
      DIMENSION V1(3),V2(3),V3(3),VJ(3),VP(3),L1(3),L2(3),L3(3),L4(3),
*  A(60),B(60),D(60)
      DIMENSION BOE(3), ROE(3),AN(60),C(60,3),BL(60),ANG1(60),ANG2(60)
      COMMON/COUNT/N000
      COMMON/INFO/C,M      .CHARGE,MULTIP,AN, N
      COMMON/IPR/IDUT,LOUT
      COMMON/CIM/JKJL,JKJLMN,LCIM
      DIMENSION LCIM(60,60)
      COMMON/STR/JS1,JSS1,JS2,JSS2
      COMMON/KNOW/KNOW1(600),KNOW2(600)
      INTEGER AN,CHARGE,Z,PUNCH
      EQUIVALENCE(M,NATOMS)
      REAL*8 L1,L2,L3,L4
      DIMENSION BLB(60),ALB(60),RTB(60)
      DIMENSION R(60,60)
      DIMENSION IDENT(20)
      DIMENSION EL(17),ORB(4,7)
      INTEGER ORB
      COMMON/ENGY/ BOE,ROE      ,IC
      COMMON/SIMRUN/BL,ANG1,ANG2,LD,I1,I2,II,III,IF,DELTA,IS
A,ISS,RMIN
      COMMON/LIT/IBLANK,ITMAT,IBL,IALPHA,IBETA,ICLEAR,III,II2
      COMMON/NTMAT/LTMAT,NVAR,LID
      INTEGER FL

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      INTEGER OPTION,OPNCLO,HUCKEL,CNDD,INDD,CLOSED,OPEN,IONOFF
      INTRGER OFF
C     COMMON/OPTION/OPTION,OPNCLO,HUCKEL,CNDD,INDD,CLOSED,OPEN,IONOFF
C     DATA (OFF = 3HOFF)
      DIMENSION NAL(6)
      DATA NAL(1),NAL(2),NAL(3),NAL(4),NAL(5),NAL(6) / 'INTE', 'PATO',
* 'MIC ', 'DIST', 'ANCE', 'S  ' /
      DATA EL(1),EL(2),EL(3),EL(4),EL(5),EL(6),EL(7),EL(8),EL(9) / 'H',
* 'HE', 'LI', 'BE', 'B', 'C', 'N', 'O', 'F' /
C     DATA((NAL(I),I=1,6)=4HINTE,4HRATO,4HMIC ,4HDIST,4HANCE,4HS  )
C     DATA ((EL(I),I=1,9)=4H  H,4H  HE,4H  LI,4H  BE,4H  B,4H  C,
C     *4H  N,4H  O,4H  F)
C     *****
C     FORTFAN II TO IV CONVERSION
      ABSF(X) =DABS(X)
      ATANF(X) =DATAN(X)
      COSF(X) =DCOS(X)
      SINF(X) =DSIN(X)
      SIGNF(X,Y) =DSIGN(X,Y)
      SQRTF(X) =DSORT(X)
C     INPUT AND OUTPUT OF INPUT
C     PUNCH = 3HPUNCH
      NBFN = 0
      IF (IE.EQ.1) GO TO 999
      GO TO 2919
999  CONTINUE
      IF(JKJLMN .NE. 0) GO TO 2
      READ 1000,(IDENT(I),I=1,20)
      GO TO 1324
C     IF(EOF(5)) 999,2
      2  CONTINUE
      DO 1325 IKL=1,NATOMS
      ALPHA(IKL) = ALPHA(IKL)*180./3.141592654
      BETA(IKL) = BETA(IKL)*180./3.141592654
1325  CONTINUE
1324  CONTINUE
2919  CONTINUE
      IF(NOOO .NE. 0) GO TO 4
      IF((JKJLMN .EQ. 0) .AND. (IE .EQ. 1)) GO TO 7091
      IF(JKJLMN .NE. 2) GO TO 4
      IF((LOUTT .NE. IOUT) .AND. (IE .EQ. 1)) GO TO 7091
      IF(LOUTT .NE. IOUT) GO TO 4
7091  CONTINUE
      PRINT 1111, (IDENT(I),I=1,20)
1000  FORMAT(20A4)
1111  FORMAT (//,20A4)
C     IF (IDENT(10).EQ.PUNCH)3,4
C     3  PRINT 2008
2008  FORMAT(/,16H PUNCH OPTION ON,/)
C     PUNCH 1000.(IDENT(I),I=1,10)
      4  CONTINUE
      IF (IE.EQ.1) GO TO 101

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      GO TO 102
101  CONTINUE
      IF(JKJLMN .NE. 0) GO TO 102
      READ 1001, NATOMS,CHARGE,MULTIP
1001  FORMAT(3I2)
102  CONTINUE
      IF(JKJLMN .NE. 2) GO TO 6
      IF((LOUTT .NE. IOUT) .AND. (IE .EQ. 1)) GO TO 6091
      IF(LOUTT .NE. IOUT) GO TO 6
6091  CONTINUE
      IF(N000 .NE. 0) GO TO 6
      PRINT1002, NATOMS,CHARGE,MULTIP
1002  FORMAT(//.1CH NATOMS = .I4,2X,1CH CHARGE = .I4,2X,1CH MULTIP = .I4
      *.I4,/)
C     IF(IDENT(10).EQ.5HPUNCH) 5,6
C     5 PUNCH 8,NATOMS,CHARGE,MULTIP
      8  FORMAT(3I4)
      6  CONTINUE
      - IF((JKJLMN .EQ. 0) .AND. (IE .EQ. 1)) READ 4919, LDENT ,LOUTT
4919  FORMAT (2A4)
C     *****
C     CALCULATION OF COORDINATES
      IF (IE.GT.1) GO TO 104
103  CONTINUE
      DO 6969 I=1,M
      IF(JKJLMN .NE. 0) GO TO 1193
      READ 1003, AN(I),Z(I,1),BL(I),Z(I,2),ALPHA(I),Z(I,3),BETA(I),Z(I,
      *4),(LCIM(I,IRO),IFQ=1,10)
1193  CONTINUE
1003  FORMAT (I3,I4,F7.4,I4,F11.6,I4,F11.6,I4,1X,10I3)
C     ANG1 AND ANG2 STORE THE ANGLES ALPHA AND BETA IN DEGREE FORM
C     ANG1 AND ANG2 STORE THE ANGLES ALPHA AND BETA IN DEGREE FORM
      ANG1(I)=ALPHA(I)
      ANG2(I)=BETA(I)
      IF(AN(I) .LE. 10) GO TO 361
      NBFN = NBFN + 9
      GO TO 371
361  IF(AN(I) .LT. 3) GO TO 362
      NBFN = NBFN + 4
      GO TO 371
362  NBFN = NBFN + 1
371  CONTINUE
6969  CONTINUE
      IF((JKJLMN .EQ. 0) .AND. (IE .EQ. 1) .AND. (LDENT .EQ. JCIM))
      * GO TO 4920
      GO TO 4921
4920  DO 4148 IT = 1,NATOMS
4148  READ 4149, (LCIM(IT,JT),JT=1,NATOMS)
4149  FORMAT (80I1)
4921  CONTINUE
      IF(IE .EQ. 1) GO TO 388
      GO TO 389

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388 CONTINUE
   IF(JKJLMN .NE. 0) GO TO 399
   AALPHA = ALPHA(JS1)
   ABETA = BETA(JS1)
   ABL = BL(JS1)
   BALPHA = ALPHA(JS2)
   BBETA = BETA(JS2)
   BBL = BL(JS2)
   GO TO 389
399 CONTINUE
   ALPHA(JS1) = AALPHA
   BETA(JS1) = ABETA
   BL(JS1) = ABL
   ALPHA(JS2) = BALPHA
   BETA(JS2) = BBETA
   BL(JS2) = BBL
   ANG2(JS1) = BETA(JS1)
   ANG2(JS2) = BETA(JS2)
   ANG1(JS1) = ALPHA(JS1)
   ANG1(JS2) = ALPHA(JS2)
389 CONTINUE
   IF(JKJLMN .NE. 2) GO TO 104
   IF((LOUTT .NE. IOUT) .AND. (IE .EQ. 1)) GO TO 5091
   IF(LOUTT .NE. IOUT) GO TO 6
5091 CONTINUE
   PRINT 374, NBFN, NATOMS
374 FORMAT (/, 3X, I4, 29H BASIS FUNCTIONS REQUIRED FOR, I3, 6H ATOMS, /)
104 CONTINUE
   DO 232 I = 1, M
   BTB(I) = BETA(I)
   ALB(I) = ALPHA(I)
   BLB(I) = BL(I)
232 CONTINUE
   IF ((NVAR.EQ.ICLEAR).OR.(ID.EQ.1)) GO TO 7000
7001 CONTINUE
   IF (NVAR.EQ.IBL) GO TO 7002
   GO TO 7003
7002 BL(IS)=BL(IS) + DELTA
   IF (ISS.EQ.0) GO TO 7000
   BL(ISS)=BL(ISS) + DELTA
   GO TO 7000
7003 CONTINUE
   IF (NVAR.EQ.IALPHA) GO TO 7004
   GO TO 7005
7004 ANG1(IS)=ANG1(IS) + DELTA
   IF (ISS.EQ.0) GO TO 7000
   ANG1(ISS)=ANG1(ISS) + DELTA
   GO TO 7000
7005 CONTINUE
   IF (NVAR.EQ.IBETA) GO TO 7006
   GO TO 7007
7006 ANG2(IS)=ANG2(IS) + DELTA
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      IF (ISS.EQ.0) GO TO 7000
      ANG2(ISS)=ANG2(ISS) + DELTA
      GO TO 7000
7007 CONTINUE
      PRINT 7008
7008 FORMAT (/////, 55H ERROR ON FIRST CARD IN COLUMNS 30 - 34 OR 57 -
C61, ///, 37H PROGRAM TERMINATED DUE TO THIS ERROR, ///, 60H CHECK PERM
DISSIBLE STATEMENTS FOR THESE COLUMNS AND RESUBMIT, ///)
      GO TO 1984
7009 CONTINUE
      IF (IE.EQ.1) GO TO 106
105 CONTINUE
      DO 109 I = 1, M
      ALB(I) = ANG1(I)
      BTB(I) = ANG2(I)
      BLB(I) = BL(I)
      ALPHA (I) = ANG1(I)
      BFTAB(I) = ANG2(I)
109 CONTINUE
106 CONTINUE
      IF ((NVAR.NE.ICLEAR).AND.(ID.EQ.I2).AND.(LID.EQ.II2)) GO TO 7201
      GO TO 7200
7201 DID=I2 - 1
      IF (NVAR.EQ.IBL) GO TO 7202
      GO TO 7203
7202 BL(IS)=BL(IS) - (DID * DELTA)
      IF (ISS.EQ.0) GO TO 7200
      BL(ISS)=BL(ISS) - (DID * DELTA)
      GO TO 7200
7203 CONTINUE
      IF (NVAR.EQ.IALPHA) GO TO 7204
      GO TO 7205
7204 ANG1(IS)=ANG1(IS) - (DID * DELTA)
      IF (ISS.EQ.0) GO TO 7200
      ANG1(ISS)=ANG1(ISS) - (DID * DELTA)
      GO TO 7200
7205 ANG2(IS)=ANG2(IS) - (DID * DELTA)
      IF (ISS.EQ.0) GO TO 7200
      ANG2(ISS)=ANG2(ISS) - (DID * DELTA)
7200 CONTINUE
      IF ((LTMAT.EQ.ITMAT).AND.(NVAR.NE.ICLEAR).AND.(IC.EQ.2)) GO TO 7401
      GO TO 7400
7401 CONTINUE
      IF (NVAR.EQ.IBL) GO TO 7402
      GO TO 7403
7402 ROE(2)=BL(IS)
      GO TO 7406
7403 CONTINUE
      IF (NVAR.EQ.IALPHA) GO TO 7404
      GO TO 7405
7404 ROE(2)=ANG1(IS)
      GO TO 7406
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7405 ROE(2)=ANG2(I5)
7406 ROE(1)= ROE(2) - DELTA
      ROE(3)= ROE(2) + DELTA
7400 CONTINUE
      DO 502 J=1,M
502  ALPHA(J) = ALPHA(J)*3.141592654/180.
      DO 503 J=1,M
503  BETA(J) = BETA(J)*3.141592654/180.
      DO 504 J= 1,3
504  C(1,J)=0.0
      IF(M .EQ. 1) GO TO 601
      C(2,1)=0.0
      C(2,2)=0.0
      C(2,3)=BL(2)
      IF(M .EQ. 2) GO TO 601
      C(3,1)=BL(3)*SINF(ALPHA(3))
      C(3,2)=0.0
C *****
C - THE FOLLOWING IS AN ADDITION TO COORD FINDER PROGRAM TO BE USED
C IF THE MOLECULE UNDER CONSIDERATION HAS ONLY ONE HEAVY ATOM OR FOR
C A MOLECULE SUCH AS NEOPENTANE IN WHICH THE CENTRAL ATOM HAS NO
C HYDROGENS BONDED TO IT
      IF(Z(3,1).EQ.1) GO TO 505
      GO TO 506
505  C(3,3) = BL(3)*COSF(ALPHA(3))
      GO TO 507
506  C(3,3) = C(2,3)-BL(3)*COSF(ALPHA(3))
507  I=3
      IF(ABSF(C(3,1)).LT..00001) GO TO 550
      GO TO 510
550  DO 509 I = 4,1000
      IF(I.LE.M.AND.ABSF(C(I-1,1)).LT..00001) GO TO 508
      GO TO 510
508  C(I,1) = BL(I)*SINF(ALPHA(I))
      C(I,2) = 0.0
      ITEMP = Z(I,1)
      JTEMP = Z(I,2)
      CC(I,3) = C(ITEMP,3)-BL(I)*COSF(ALPHA(I))*SIGNF(1.,C(ITEMP,3)-C(JTEMP,3))
509  CONTINUE
510  CONTINUE
      IF(I.EQ.3) GO TO 511
      GO TO 512
511  K=4
      GO TO 513
512  K=I
513  CONTINUE
      IF(K.GT.M) GO TO 601
600  CONTINUE
      DO 533 J = K,M
      IF(Z(J,4).EQ.0) GO TO 514
      GO TO 517
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C *****
C THIS PART IS USED IF THE ATOM IS BEING DEFINED BY A DIHEDRAL ANGLE
514 CALL RELVEC(V1,Z(J,2),Z(J,3))
    CALL UNIVVEC(L1,V1)
C V1 IS A VECTOR FROM ATOM Z(J,3) TO ATOM Z(J,2)
C L1 IS A UNIT VECTOR OF V1. BL(Z(J,2)) IS BONDLENGTH OF ATOM Z(J,2)
    CALL RELVEC(V2,Z(J,1),Z(J,2))
    CALL UNIVVEC(L2,V2)
C V2 IS THE VECTOR FROM ATOM Z(J,2) TO ATOM Z(J,1)
C L2 IS THE UNIT VECTOR OF V2. BL(Z(J,1)) IS BONDLENGTH DEFINING
C ATOM Z(J,1)
    CALL VECPRD(VP,L1,L2)
    XXX = 0.0
    XXX = (1.-(L1(1)*L2(1)+L1(2)*L2(2)+L1(3)*L2(3))**2)
    IF(XXX.LT.0.0) GO TO 1888
    GO TO 1889
1888 PRINT 1913,XXX
1913 FORMAT(3X,32HARGUMENT OF DSQRT IS LESS THAN 0.6H XXX =,F40.20)
1889 CONTINUE
    DO 515 I = 1,3
515 L3(I) = VP(I)/SQRTF(DABS(1.-(L1(1)*L2(1)+L1(2)*L2(2)+L1(3)*L2(3))
    ***2))
1985 FORMAT(3X,1HA)
C L3 IS THE UNIT VECTOR OF VP.ALPHA(Z(J,1)) IS THE ANGLE DEFINING
C ATOM Z(J,1)
    CALL VECPRD(L4,L3,L2)
C L4,L3,L2 ARE A NEW SET OF MUTUALLY ORTHOGONAL AXES. WE WILL NOW
C OBTAIN COORD OF ATOM J IN TERMS OF THESE AXES RELATIVE TO ATOM Z(J,1)
    DO 516 I=1,3
    OVJ(I) = BL(J)*(-L2(I)*COSF(ALPHA(J))+L4(I)*SINF(ALPHA(J))*COSF(BET
    1A(J))+L3(I)*SINF(ALPHA(J))*SINF(BETA(J)))
C VJ IS THE VECTOR FROM ATOM Z(J,1) TO ATOM J
    ITEMP = Z(J,1)
    C(J,I) = VJ(I) + C(ITEMP,I)
516 CONTINUE
    GO TO 533
517 IF(Z(J,4).EQ.1.OR.Z(J,4).EQ.-1) GO TO 549
    GO TO 528
C *****
C THIS PART IS USED IF ATOM IS DEFINED BY TWO BONDANGLES
549 CALL RELVEC(V1,Z(J,1),Z(J,3))
    CALL UNIVVEC(L1,V1)
    CALL RELVEC(V2,Z(J,2),Z(J,1))
    CALL UNIVVEC(L2,V2)
    ZETA = -(L1(1)*L2(1)+L1(2)*L2(2)+L1(3)*L2(3))
    A(J) = (-COSF(BETA(J))+ZETA*COSF(ALPHA(J)))/(1.-ZETA**2)
    B(J) = (COSF(ALPHA(J))-ZETA*COSF(BETA(J)))/(1.-ZETA**2)
    PI = 3.141592654
    IF(ZETA.LT.0) GO TO 518
    GO TO 519
518 TEMP = PI
    GO TO 520

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519 TEMP = 0.0
520 CONTINUE
    IF(ZETA.EQ.0) GO TO 521
    GO TO 522
521 GAMMA = PI/2.
    GO TO 523
522 GAMMA = ATANF(SQRTF(1.-ZETA**2)/ZETA) +TEMP
1986 FORMAT (3X,1HB)
523 CONTINUE
    IF (ABSF(GAMMA+ALPHA(J)+BETA(J)-2.*PI).LT..0000001) GO TO 524
    GO TO 525
524 D(J) = 0.0
    GO TO 526
525 CONTINUE
    VXY = (1.-ZETA**2)
    IF(ABSF(SQRTF(ABSF(VXY))) .GT. .0001) GO TO 1209
    PRINT 1210,VXY,J
1210 FORMAT (///,3X,4HVXY=,3X,F10.5,4HJ = ,I4,///)
1209 CONTINUE
    XYZ = (1.+A(J)*COSF(BETA(J))-B(J)*COSF(ALPHA(J)))
    IF(XYZ .GE.0.) GO TO 1204
    PRINT 1206
1206 FORMAT (///,3X,4HBUGS,///)
1204 CONTINUE
    IF(VXY .GE.0.) GO TO 1207
    PRINT 1208
1208 FORMAT(///,3X,5HBUGS2,///)
1207 CONTINUE
    D(J)=Z(J,4)*(SQRTF( ABSF(1.+A(J)*COSF(BETA(J))-B(J)*COSF(ALPHA(
    *J)))) )/SQRTF(ABSF(1.-ZETA**2))
1987 FORMAT (3X,1HC)
526 CONTINUE
    CALL VECPRD(V3,L1,L2)
    DO 527 I = 1,3
    L3(I) = A(J)*L1(I)+B(J)*L2(I)+D(J)*V3(I)
    VJ(I) = BL(J)*L3(I)
    ITEMP = Z(J,1)
    C(J,I) = VJ(I)+C(ITEMP,I)
527 CONTINUE
    GO TO 533
C *****
C THIS PART IS USED IF ATOM IS DEFINED BY ONE BONDANGLE AND BY THE
C ANGLE WHICH BOND Z(J,1)-J MAKES WITH THE PLANE OF Z(J,1),Z(J,2)
C AND Z(J,3)
528 CALL RELVEC(V1,Z(J,1),Z(J,3))
    CALL UNIVFC(L1,V1)
    CALL RELVEC(V2,Z(J,2),Z(J,1))
    CALL UNIVFC(L2,V2)
    ZETA = -(L1(1)*L2(1)+L1(2)*L2(2)+L1(3)*L2(3))
    CALL VECPRD(V3,L1,L2)
C BETA(J) HERE REFERS TO 90-ANGLE WHICH BOND Z(J,1)-J MAKES WITH THE
C AFOREMENTIONED PLANE

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      A(J) = COSF(BETA(J))/(1.-ZETA**2)
      IF(Z(J,4).EQ.2) GO TO 530
529  B(J) = -SQRTF((1.-COSF(ALPHA(J))**2-A(J)*COSF(BETA(J)))/(1.-ZETA**2)
1))
1988  FORMAT (3X,1HD)
      GO TO 531
530  B(J) = SQRTF((1.-COSF(ALPHA(J))**2-A(J)*COSF(BETA(J)))/(1.-ZETA**2))
1989  FORMAT (3X,1HE)
531  CONTINUE
      D(J) = B(J)*ZETA+COSF(ALPHA(J))
      DO 532 I=1,3
      L3(I) = R(J)*L1(I)+D(J)*L2(I)+A(J)*V3(I)
      VJ(I) = BL(J)*L3(I)
      ITEMP = Z(J,1)
      C(J,1) = VJ(I) + C(ITEMP,I)
532  CONTINUE
533  CONTINUE
601  CONTINUE
C - *****
C   OUTPUT SECTION
      IF(JKJLMN .NE. 2) GO TO 1994
      IF((LOUTT .NE. IOUT) .AND. (IE .EQ. 1)) GO TO 4093
      IF(LOUTT .NE. IOUT) GO TO 1994
4093  CONTINUE
      IF(NQQQ .NE. 0) GO TO 1994
      PRINT 1998
1998  FORMAT (1X,8HZ MATRIX,///,42H NO AN (1) BL (2) ALPHA (3)
* ,2CHBETA (4) EL ,8X,1HX,11X,1HY,12X,1HZ)
      DO 900 J = 1,M
      INDI = AN(J)
900  PRINT 1999,J,AN(J),Z(J,1),BLB(J),Z(J,2),ALB(J),Z(J,3),BTB(J),
* Z(J,4),EL(INDI),(C(J,I),I=1,3)
1999  FORMAT (2I3,I4,F7.4,2(I4,F11.6),I4,6X,A4,4X,3F12.8)
C   IF(IDENT(10).EQ.PUNCH) 7,11
C   7 PUNCH 9,(AN(I),(C(I,J),J=1,3),I=1,NATOMS)
9   FORMAT(I4,3(3X,F12.7))
11  CONTINUE
1994  CONTINUE
      DO 10I=1,NATOMS
      DO 10J=1,NATOMS
10  R(I,J) = SQRTF((C(I,1)-C(J,1))**2+(C(I,2)-C(J,2))**2+(C(I,3)-C(J,3)
*)**2)
      IF((JKJLMN .EQ. 0) .AND. (IE .EQ. 1)) PRINT 8081
8081  FORMAT (///,3X,68H STERICALLY AND/OR ELECTRONICALLY SIGNIFICANT INC
* TERATOMIC DISTANCES,///,3X,5HORDER,6X,1HI,8X,1HJ,6X,6HR(I,J),6X,
* 31H CONFORMATION FIRST ENCOUNTERED,/)
      IF(JKJLMN .EQ. 0) CALL RSEARC (R)
      IF((JKJLMN .EQ. 1) .AND. (IE .EQ. 1)) GO TO 8188
      GO TO 8199
8188  CONTINUE
      IF((JKJLMN .EQ. 1) .AND. (IE .EQ. 1)) JKJL = JKJL - 1
      DO 8210 IX = 1,JKJL

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```

C      PRINT 8211,KNOW1(IX),KNOW2(IX)
      8210 CONTINUE
      8211 FORMAT(2I8)
      8199 CONTINUE
            IF(JKJLMN .EQ. 1) CALL DOUT(R)
      2222 FORMAT(3X,2HNN)
            13 CONTINUE
            IF(JKJLMN .NE. 2) GO TO 1995
            IF((LOUTT .NE. IOUT) .AND. (IE .EQ. 1)) GO TO 3093
            IF(LOUTT .NE. IOUT) GO TO 1995
      3093 CONTINUE
            IF(NQQQ .NE. 0) GO TO 1995
            CALL MDOUTPT(R,NATOMS,NATOMS,60,60,NAL)
      1995 CONTINUE
            12 CONTINUE
C      CONVERT COORDINATES TO ATOMIC UNITS
      DO 90 I=1,NATOMS
      DO 90 J=1,3
            90 C(I,J) = C(I,J)/0.529167
      1984 CONTINUE
      RETURN
      END
      SUBROUTINE RELVEC(R,J,K)
      IMPLICIT REAL*8(A-H,O-Z)
      INTEGER CHARGE, AN
      COMMON/INFO/C(60,3),M      ,CHARGE,MULTIP,AN(60),N
      DIMENSION R(3)
      INTEGER J,K,I
      DO 1 I=1,3
            1 R(I)=C(J,I)-C(K,I)
C      R IS THE RELATIVE VECTOR FROM ATOM K TO ATOM J
      RETURN
      END
      SUBROUTINE UNIVVEC(L,R)
      IMPLICIT REAL*8(A-H,O-Z)
      DIMENSION L(3),R(3)
      REAL*8 L
      SQRTF(X) = DSORT(X)
      INTEGER I
      DO 2 I=1,3
            2 L(I)=R(I)/SQRTF(R(1)**2 + R(2)**2 + R(3)**2)
C      L IS THE UNITVECTOR OF R
      RETURN
      END
      SUBROUTINE VECPRD(VP,X,Y)
      IMPLICIT REAL*8(A-H,O-Z)
      DIMENSION VP(3),X(3),Y(3)
      VP(1)=X(2)*Y(3)-X(3)*Y(2)
      VP(2)=X(3)*Y(1)-X(1)*Y(3)
      VP(3)=X(1)*Y(2)-X(2)*Y(1)
C      VP IS THE VECTOR PRODUCT OF X CROSSED Y
      RETURN

```

```

END
SUBROUTINE MOUTPT(A,M,N,MDIM,NDIM,NAL)
IMPLICIT REAL*8(A-H,O-Z)
C OUTPUT OF M X N MATRIX DIMENSIONED TO MDIM X NDIM
DIMENSION NAL(6)
DIMENSION A(MDIM,NDIM)
PRINT 1000,NAL
1000 FORMAT (//,2X, 6A4)
KITE = 0
20 LOW = KITE+1
KITE = KITE+14
KITE = AMINO(KITE,N)
PRINT 19,(I,I=LOW,KITE)
19 FORMAT( //      ,4X,14(6X,I2),/)
DO 32 I=1,M
32 PRINT 18,I,(A(I,J),J=LOW,KITE)
18 FORMAT(I4,2X,14F8.4)
IF(N-KITE) 40,40,20
40 RETURN
END
SUBROUTINE RSEARC (R)
IMPLICIT REAL*8(A-H,O-Z)
INTEGER*2 LCIM,KNOW1,KNOW2
DIMENSION R(60,60)
COMMON/TAU/ALPHA(60),BETA(60)
COMMON/KNOW/KNOW1(600),KNOW2(600)
COMMON/STR/JS1,JSS1,JS2,JSS2
COMMON/CIM/JKJL,JKJLMN,LCIM
COMMON/INFO/C(60,3),NATOMS,CHARGE,MULTIP,AN(60),N
INTEGER AN, CHARGE
DIMENSION LCIM(60,60)
DO 9 I=1,NATOMS
ALPHA(I) = ALPHA(I)*180./3.141592654
BETA(I) = BETA(I)*180./3.141592654
9 CONTINUE
DO 1 I=2,NATOMS
IM1=I-1
DO 1 J=1,IM1
IF(LCIM(I,J) .NE. 0) GO TO 1
IF(R(I,J) .LT. 3.00) GO TO 2
GO TO 3
2 CONTINUE
DO 5 II=1,JKJL
IF((II .EQ. KNOW1(II)) .AND. (J .EQ. KNOW2(II))) GO TO 1
IF((J .EQ. KNOW1(II)) .AND. (I .EQ. KNOW2(II))) GO TO 1
5 CONTINUE
PRINT 7, JKJL,I,J,R(I,J),BETA(JS1),BETA(JS2)
7 FORMAT (3I8,3(3X,F10.5))
KNOW1(JKJL) = I
KNOW2(JKJL) = J
JKJL = JKJL + 1
3 CONTINUE

```

```

1 CONTINUE
DO 10 I=1,NATOMS
ALPHA(I) = ALPHA(I)*3.141592654/180.
BETA(I) = BETA(I)*3.141592654/180.
10 CONTINUE
RETURN
END
SUBROUTINE OUT(AGR )
IMPLICIT REAL*8(A-H,O-Z)
DIMENSION AGR(18,18)
COMMON/LAB/LROW,LCOL,A
DIMENSION A(36)
KITE = 0
20 LOW = KITE + 1
KITE = KITE + 12
KITE = AMINO(KITE,LCOL)
PRINT 19, (A(I),I=LOW,KITE)
19 FORMAT (//,6X,12F10.1,///)
PRINT 212
212 FORMAT (//)
DO 32 I =1,LROW
32 PRINT 18,A(I),(AGR (I,J),J=LOW,KITE)
18 FORMAT(2X,F5.1,2X,12F10.4)
IF(LCOL-KITE) 40,40,20
40 RETURN
END
SUBROUTINE DOUT(R)
IMPLICIT REAL*8(A-H,O-Z)
INTEGER*2 LCIM,KNOW1,KNOW2
COMMON/TAU/ALPHA(60),BETA(60)
COMMON/STR/JS1,JSS1,JS2,JSS2
COMMON/CIM/JKJL,JKJLMN,LCIM
COMMON/INFO/C(60,3),NATOMS,CHARGE,MULTIP,AN(60),N
DIMENSION LCIM(60,60)
INTEGER CHARGE,AN
COMMON/KNOW/KNOW1(600),KNOW2(600)
DIMENSION R(60,60)
DO 20 I=1,NATOMS
ALPHA(I) = ALPHA(I) * 180./3.141592654
BETA(I) = BETA(I)*180./3.141592654
20 CONTINUE
NDISK = 11
DO 1 I=1,NATOMS
IM1=I-1
DO 1 J=1,IM1
DO 1 K=1,JKJL
LL = KNOW1(K)
MM = KNOW2(K)
C IF((I .EQ. LL) .AND. (J .EQ. MM)) WRITE(NDISK) R(I,J)
C IF((I .EQ. MM) .AND. (J .EQ. LL)) WRITE(NDISK) R(I,J)
IF((I .EQ. LL) .AND. (J .EQ. MM)) GO TO 5
GO TO 6

```

```
5 CONTINUE
  WRITE(NDISK) R(I,J)
  PRINT 8,R(I,J),I,J,BETA(JS1),BETA(JS2)
8  FORMAT (3X,11HLL MM NDISK,3X,F10.5,2I3,2F10.5)
6  CONTINUE
  IF((I .EQ. MM) .AND. (J .EQ. LL)) GO TO 9
  GO TO 10
9  CONTINUE
  WRITE(NDISK) R(I,J)
  PRINT 11,R(I,J),I,J,BETA(JS1),BETA(JS2)
11  FORMAT (3X,11HMM LL NDISK,3X, F10.5,2I3,2F10.5)
10 CONTINUE
1  CONTINUE
  DO 30 I=1,NATOMS
  ALPHA(I) = ALPHA(I)*3.141592654/180.
  BETA(I) = BETA(I)*3.141592654/180.
30 CONTINUE
  RETURN
  END
  SUBROUTINE KFIX
  IMPLICIT REAL*8(A-H,O-Z)
  INTEGER*2 LCIM,KNOW1,KNOW2
  ABSF(X) = DABS(X)
  COMMON/KNOW/KNOW1(600),KNOW2(600)
  COMMON/CIM/JKJL,JKJLMN,LCIM
  DIMENSION LCIM(60,60)
  KKLL = JKJL - 1
2394 CONTINUE
  MOOSE = 0
  DO 2333 IH = 1, KKLL
  IF(KNOW1(IH) .EQ. KNOW1(IH+1)) GO TO 2395
  GO TO 2396
2395 CONTINUE
  IF(KNOW2(IH) .GT. KNOW2(IH+1)) GO TO 2397
  GO TO 2398
2397 CONTINUE
  MOOSE = MOOSE + 1
  IHOLD2 = KNOW2(IH)
  JHOLD2 = KNOW2(IH+1)
  KNOW2(IH) = JHOLD2
  KNOW2(IH+1) = IHOLD2
2398 CONTINUE
2396 CONTINUE
  IF(KNOW1(IH) .GT. KNOW1(IH+1)) GO TO 2387
  GO TO 2398
2387 CONTINUE
  MOOSE = MOOSE + 1
  IHOLD1 = KNOW1(IH)
  JHOLD1 = KNOW1(IH+1)
  IHOLD2 = KNOW2(IH)
  JHOLD2 = KNOW2(IH+1)
  KNOW1(IH) = JHOLD1
```

```
      KNOW2(IH) = JHOLD2
      KNOW1(IH+1) = IHOLD1
      KNOW2(IH+1) = IHOLD2
3398 CONTINUE
2333 CONTINUE
      IF(MOOSE .NE. 0) GO TO 2394
      RETURN
      END
      SUBROUTINE ROUT (EEEE,MHO)
      IMPLICIT REAL*8(A-H,O-Z)
      INTEGER*2 LCIM,KNOW1,KNOW2
      DIMENSION EEEEF(18,18)
      COMMON/KNOW/KNOW1(600),KNOW2(600)
      COMMON/CIM/JKJL,JKJLMN,LCIM
      COMMON/LAB/I1,I2,A
      DIMENSION A(36)
      ABSF(X) = DABS(X)
      DIMENSION LCIM(60,60)
      DO 1178 IQ = 1,I1
      DO 1178 JQ = 1,I2
      DO 1178 IR = 1,I1
      DO 1178 JR = 1,I2
      IF(ABSF (EEEE(IQ,JQ) - EEEEE(IR,JR)) .GT. .00001) GO TO 1179
1178 CONTINUE
      EDD = EEEEE(1,1)
      PRINT 1174, KNOW1(MHO), KNOW2(MHO) ,EDD
1174 FORMAT (3X,2HR(.I3,3H , .I3,5H ) = ,F10.5,3X,48H, AND IS CONSTANT
      * FOR THE ROTATIONS CONSIDERED.)
      IHEL = KNOW1(MHO)
      IHEV = KNOW2(MHO)
      LCIM(IHEV,IHEL) = 1
      LCIM(IHEL,IHEV) = 1
      GO TO 1864
1179 CONTINUE
      PRINT 1171,KNOW1(MHO), KNOW2(MHO)
1171 FORMAT (///,11H GRID OF R(.I3,3H , .I3, 3H ) ,31H AS A FUNCTION OF
      * CONFORMATION.,///)
      CALL OUT(EEEE)
1864 CONTINUE
      RETURN
      END
```

NOT FOUND IN NM DIRECTORY. STOWED WITH TTR.
WAS-00000000

Appendix C:

The following routine is a modification of the INDO routine of Pople, Beveridge and Dobosh which allows for a significant reduction in required computer central memory. Central to this modification is the EIGN subroutine of P. Dobosh which diagonalizes an array and outputs the resulting array within the same area of computer memory. Other changes in the routine were in SUBROUTINES INTGRL, HUCKCL, SCFCL and CPRINT. The central change in the SCFCL circuitry was the storage of the core hamiltonian on peripheral disk, and the reading of this disk file upon the entry to SCFCL. Thus one area of central memory at different times stores the overlap integral matrix (INTGRL), core hamiltonian (HUCKCL), Fock matrix (SCFCL) and density matrix (SCFCL). These changes were designed by Professor Beveridge, and coded by R.J.R.

=RJR,LIST=ALL
=ICD,REF=1=100

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C      IMPLICIT REAL*8(A-H,O-Z)
C      TO CHANGE THE SIZE OF THE ROUTINE AS A FUNCTION OF IAT AND IBF
C      CHANGE ALL DIMENSION STATEMENTS IN THE MAIN PROGRAM, AND ALSO
C      TEST INSERTION
C      TEST INSERTION
C      IN EIGN AND EIGOUT
C      ALSO RESET THE VALUES FOR IAT AND IBF IN THE MAIN PROGRAM.
C      DIMENSION PDIAG( 90),Q( 90),CZ(50),U( 90),ULIM(50),LLIM(50),
*XXX( 90),ASDA( 90, 90),GAMMA(50,50),Z(50,4),BL(50),ALPHA(50),
*BETA(50),NUM( 90),C(50,3),AN(50)
C      INTEGER*4 U,ULIM
C      INTEGER*4 CZ
C      COMMON/ENGY/RWF(3),RQE(3),FTOT,VOL,DP,IC
C      COMMON/INFG/N,NATOMS,CHARGE,MULTIP
C      COMMON/SIMRUN/DELTA,RMIN,ID,I1,I2,I1,I1,IE,IS,ISS
C      INTEGER*4 7
C      COMMON/JRCOV/IRCOV,IJC,IDISK,IRCCC,JDISK
C      IRCOV=TEST FOR CONVERGENCE
C      IJC=PLACE IN GRID
C      IDISK=SEQUENTIAL DISK ASSIGNMENT
C      IRCCC = TEST FOR INITIALLY CONVERGED CALCULATION
C      COMMON/MTMAT/LTMAT,MVAR,LID
C      INTEGER OFF
C      COMMON/PERTBL/FL( 9)
C      COMMON/DRB/GRB(9)
C      COMMON/OPTION/OPTION,OPNCLO,HUCKEL,CNDO,INDO,CLOSED,OPEN,IONOFF
C      COMMON/LIT/IBLANK,ITMAT,IBL,IALPHA,IBETA,ICLEAR,I11,I12
C      INTEGER OPTION,OPNCLO,HUCKEL,CNDO,INDO,CLOSED,OPEN,IONOFF
C      INTEGER GRB,FL,AN,CHARGE
C      DIMENSION EGRD(18,18),VGRD(18,18),DGRD(18,18)
C      COMMON/GRID/LROW,LCOL
C      DATA IZMAT/'ZMAT'/
C      DATA IBLK/'  '/
C      DATA OFF/'OFF'/
C      INPUT IS READ IN THE FOLLOWING ORDER
C      (1) OPTION CARD WITH THE FOLLOWING INFORMATION
C      (A) OPTION (WAVEFUNCTION OPTION) IN COLUMNS 1 - 4. THE KEY
C      WORDS ARE          INDO          CNDO
C      (B) OPNCLO (OPEN OR CLOSED SHELL) IN COLUMNS 5 - 10. THE KEY
C      WORDS ARE          OPEN          CLOSED
C      WORDS ARE          OPEN          CLSD
C      (C) INPUT (TO READ IN THE MOLECULE IN TERMS OF BONDLENGTHS, BOND
C      ANGLES, AND DIHEDRAL ANGLES. IN COLUMNS 11 - 14. THE KEY
C      WORD IS          ZMAT
C      (D) IONOFF (TO SUPPRESS MOST PRINTED OUTPUT) IN COLUMNS 15 - 17.
C      THE KEY WORD IS          OFF
C      (E) IGES IN COLUMNS 18 - 22. THE KEY WORD IS          GUESS
C      (F) LTMAT (TO FIT THE ENERGIES OF THREE CONSECUTIVE OUTPUT SETS
C      TO A PARABOLA IN ORDER TO FIND THE MINIMUM ENERGY
C      CONFIGURATION) IN COLUMNS 23 - 26. THE KEY WORD IS

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C          TMAP .
C          (G) I1 (THE NUMBER OF TIMES THAT THE BONDLENGTH(S), BOND
C          ANGLE(S), OR DIHEDRAL ANGLE(S) SPECIFIED IN LVAR1, IS1, AND
C          ISS1 IS (OR ARE) TO BE VARIED BY THE AMOUNT DELTA1. I1 IS
C          SPECIFIED IN I3 FORMAT IN COLUMNS 27 - 29.
C          (H) LVAR1 (WHICH SPECIFIES WHAT IS TO BE VARIED) IN COLUMNS
C          30 - 34. THE KEY WORDS ARE
C          ALPHA          BETA          BL
C          (I - J) IS1 AND ISS1 (THE SUBSCRIPT OF LVAR1) IN COLUMNS
C          35 - 38 AND 39 - 42 RESPECTIVELY (EACH) IN I4 FORMAT. EACH
C          MAY BE ANY POSITIVE INTEGER FROM 1 TO THE NUMBER OF ATOMS IN
C          THE MOLECULE. IF ONLY ONE IS BEING VARIED, LEAVE ISS1 BLANK
3128 CONTINUE
C          (K) DELTA1 (THE AMOUNT BY WHICH LVAR1(IS1) AND/OR LVAR1(ISS1) IS
C          OR ARE BEING VARIED) IN COLUMNS 43 - 53 (IN F11.6 FORMAT)
C          SUBSCRIPTED BY IS2 AND ISS2 TO BE VARIED BY DELTA2 SO THAT
C          (L - P) G - K ARE REPEATED TO PERMIT A SECOND VARIABLE, LVAR2,
C          A GRID SEARCH CAN BE CONDUCTED I2 TIMES.
C          I2 (IN I3 FORMAT) IS IN COLUMNS 54 - 56.
C          LVAR2 IS IN COLUMNS 57 - 61.
C          IS2 AND ISS2 ARE IN COLUMNS 62 - 65 AND 66 - 69
C          RESPECTIVELY (EACH IN I4 FORMAT).
C          DELTA2 IS IN COLUMNS 70 - 80 (IN F11.6 FORMAT).
C          (2) AN IDENTIFICATION CARD WHICH IS PRINTED AT THE BEGINNING
C          OF THE RUN.
C          (3) NATOMS, CHARGE, MULTIPLICITY          FORMAT (3I2)
C          (4) ATOMIC NUMBER, X COORDINATE, Y COORDINATE, Z COORDINATE ON
C          ONE CARD. FORMAT (I4,3(3X,F12.7))
C          DECIMAL POINTS IN COLUMNS 12, 27, AND 42
996 CONTINUE
IAT=50
IBF=90
IJC = 0
K1 = 1
K2 = 1
JDISK = 10
IDISK = 11
IRCCC=0
IC=0
JD=1
JDD=2
READ 40, OPTION,OPNCLO,INPUT,IONOFF,IGES,LTMAP,I1,LVAR1,IS1,ISS1,
XDELTA1,I2,LVAR2,IS2,ISS2,DELTA2
IF(OPTION.EQ.IBLK) GO TO 998
997 CONTINUE
LID = I11
ID=1
JD=11
NVAR=LVAR1
IS=IS1
ISS=ISS1
DELTA=DELTA1

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          IF(IARS(I1) .EQ. 0) GO TO 999
992 CONTINUE
C LOOP OVER VARIABLE ZMAT ELEMENTS
      DO 990 JD=1,I1
          LID = I11
          ID=JD
          GO TO 999
991 CONTINUE
      DO 993 JDD=2,I2
          LID = I12
          ID=JDD
999 CONTINUE
          IC=IC + 1
          IF=IC
          IF (IC .GT. 3) GO TO 3471
          GO TO 3470
3471 CONTINUE
          IF (LTMAT .EQ. ITMAT) GO TO 3477
          GO TO 3476
3477 CONTINUE
          CALL TMAT
3476 IC=1
3470 CONTINUE
          PRINT 41, OPTION,OPNCLO,INPUT,IONOFF,IGES,LTMAT,I1,LVAR1,IS1,ISS1,
          *DELTA1,I2,LVAR2,IS2,ISS2,DELTA2
          CALL TIM
          IF (INPUT .EQ. IZMAT) GO TO 51
          GO TO 52
51 CONTINUE
          CALL ZMAT(ALPHA,BETA,C,BL,ALPHA,BETA,GAMMA,AN,IAT,IBF,7)
          CALL MINERT(C,AN,IBF,IAT)
          DO 90 I=1,NATOMS
          DO 90 J=1,3
90 C(I,J)=C(I,J)/C.52916700
6178 FORMAT(2I10)
          IJC = IJC + 1
          GO TO 53
52 CONTINUE
          READ 20,(AN(I),I=1,10)
          PRINT 30,(AN(I),I=1,10)
          READ 50,NATOMS,CHARGE,MULTIP,IUNITS
50 FORMAT(4I4)
          PRINT 60,NATOMS,CHARGE,MULTIP,IUNITS
60 FORMAT(/5X,I4,18H ATOMS   CHARGE  =,I4,18H   MULTIPLICITY  =,I4,1200
1H   IUNITS  = ,I4,/)
          DO 10 I = 1,NATOMS
          PEAD 70,AN(I), C(I,1),C(I,2),C(I,3)
          PRINT 70,AN(I), C(I,1),C(I,2),C(I,3)
C      CONVERSION OF COORDINATES FROM ANGSTROMS TO ATOMIC UNITS
          IF(IUNITS .EQ. 1)GO TO 10
          GO TO 11
11 CONTINUE

```

```

C
C
DO 9 J=1,3
9 C(I,J)=C(I,J)/0.52916700
10 CONTINUE
53 CONTINUE
IF(OPTION.EQ.INDO) GO TO 1
GO TO 6
1 DO 5 I=1,NATOMS
IF(AN(I).GT.9) GO TO 2
GO TO 4
2 PRINT 3
3 FORMAT(47H THIS PROGRAM DOES NOT DO INDO CALCULATIONS FOR,
1 51H MOLECULES CONTAINING ELEMENTS HIGHER THAN FLUORINE)
STOP
4 CONTINUE
5 CONTINUE
6 CONTINUE
C
C   DEFAULT IF ANY ATOMS ARE TOO CLOSE TOGETHER
   KKK = KKK+1
   DO 99 I=2,NATOMS
     IM1 = I-1
     DO 99 J=1,IM1
C     CHECK FOR BONDED ATOMS
C     ELSE CHECK FOR CLOSEST APPROACH
     R=DSQRT((C(I,1)-C(J,1))**2+(C(I,2)-C(J,2))**2+(C(I,3)-C(J,3))**2)
1 *0.52916700
     IF(R.GE.0.5)GO TO 99
C     SET DEFAULT VALUES
     ETOT=999.9900
     VOL=0.000
     DP=99.9900
98 PRINT 97,I,J,R
97 FORMAT(//,45H NO CALCULATION OF THIS CONFORMATION BYPASSED,3H R(,
*14.1H,14.4H) = ,F10.5,/)
GO TO 96
99 CONTINUE
   CALL INTGRL(ASDA,C,GAMMA,CZ,U,ULIM,LLIM,AN,IBF,IAT)
   CALL HUCKCL(PDIAG,Q,GAMMA,GAMMA,ASDA,C,AN,IAT,IBF,CZ,U,ULIM,LLIM,XXX
*XX,NUM)
   CALL SCFCL(GAMMA,GAMMA,ASDA,C,AN,IAT,IBF,PDIAG,Q,CZ,U,ULIM,LLIM,XXX
*XX,NUM)
   CALL CPRINT(GAMMA,ASDA,C,AN,IBF,IAT,XXX,CZ,U,ULIM,LLIM,PDIAG,XXX
*.NUM)
96 CONTINUE
   IF(I1.EQ.0.AND.I2.EQ.0) GO TO 1750
C   TUCK AWAY CURRENT VALUES OF RESULTS
   EGRD(K1,K2) = ETOT
   VGRD(K1,K2) = VOL
   DGRD(K1,K2) = DP
   IF(K2.LT.I2) GO TO 1748
   GO TO 1749
1748 CONTINUE
   K2 = K2 + 1

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GO TO 1750
1749 CONTINUE
    K2 = 1
    K1 = K1 + 1
1750 CONTINUE
    CALL TIM
    IF ((I2.GT.0).AND.(LID.EQ.II1)) GO TO 994
    GO TO 993
994 CONTINUE
    NVAR=LVAR2
    IS=IS2
    ISS=ISS2
    DELTA=DELTA2
    GO TO 991
993 CONTINUE
    LID = II1
    NVAR=LVAR1
    IS=IS1
    ISS=ISS1
    DELTA=DELTA1
    ID=JD
990 CONTINUE
C   END OF LOOP OVER VARIABLE ZMAT ELEMENTS
    IF(I1.EQ.0.AND.I2.EQ.0) GO TO 996
C   FILL GRDVERT ARRAYS
    KKK=0
    LROW = I1
    LCOL = I2
    DELT = DELTA1
    CALL GROVER (EGRD,VGRD,DGRD,DELT)
    GO TO 9999
3569 CONTINUE
    IF ((IC.EQ.3).AND.(LTMAT.EQ.ITMAT)) GO TO 3570
    GO TO 3571
3570 CONTINUE
    CALL TMAT
3571 CONTINUE
9999 CONTINUE
    GO TO 996
998 CONTINUE
    PRINT 80
20 FORMAT(10A8)
30 FORMAT( //,10A8)
40 FORMAT (A4,A6,A4,A3,A5,A4,2(I3,A5,2I4,F11.6))
41 FORMAT(/,1X,A4,3X,A6,3X,A4,3X,A3,3X,A5,3X,A4,/,6H I1 = ,I4, 9H LVOC
CAR1 = ,A5,6H IS1 = ,1X,I4,5X,8H ISS1 = ,I4,5X,10H DELTA1 = ,F11.6,/OC
D/,6H I2 = ,I4,9H LVAR2 = ,A5,7H IS2 = ,I4,5X,8H ISS2 = ,I4,5X,10H OC
*DELTA2 = ,F11.6)
70 FORMAT(I4,3(3X,F12.7))
80 FORMAT(16H END OF THIS RUN)
    END
    BLOCK DATA

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```

COMMON/PF=TRL/EL(9)
COMMON/DRB/DRH(9)
COMMON/OPTION/OPTION,OPNCLO,HUCKEL,CNDD,INDO,CLOSED,OPEN,IONOFF
COMMON/LIT/IBLANK,ITMAT,IBL,IALPHA,IBETA,ICLEAR,I11,I12
INTEGER OPTION,OPNCLO,HUCKEL,CNDD,INDO,CLOSED,OPEN,IONOFF
INTEGER OFR,EL,AN,CHARGE
DATA EL(1),EL(2),EL(3),EL(4),EL(5),EL(6),EL(7),EL(8),EL(9) /'H',
*'H', 'LIT', 'OFR', 'B', 'C', 'N', 'O', 'F' /
DATA DRB(1),DRB(2),DRB(3),DRB(4),DRB(5),DRB(6),DRB(7),DRB(8),
*DRB(9) /' S', ' PX', ' PY', ' PZ', ' DZ2', ' DX2', ' DYZ', ' DX-Y',
*' DXY' /
DATA CNDD/'CNDD' /
DATA INDO/'INDO' /
DATA OPEN/'OPEN' /
DATA CLOSED/'CLOSED' /
DATA I11/'I1' /
DATA I12/'I2' /
DATA ITMAT/'ITMAT' /
DATA IBLANK/' /
DATA ICLEAR/' /
DATA IRL/'RL' /
DATA IALPHA/'ALPHA' /
DATA IBETA/'BETA' /
END
SUBROUTINE MOUTPT(A,M,N,MDIM,NDIM,NAL)
OUTPUT OF M X N MATRIX DIMENSIONED TO MDIM X NDIM
IMPLICIT REAL*8(A-H,O-Z)
DIMENSION NAL(6)
DIMENSION A(MDIM,NDIM)
PRINT 1000,NAL
1000 FGRMAT (//,2X, 6A4)
KITE = 0
20 LOW = KITE+1
KITE = KITE+14
KITE = AMINO(KITE,N)
PRINT 19,(I,I=LOW,KITE)
19 FORMAT(// ,4X,14(6X,I2),/)
DO 32 I=1,M
32 PRINT 18,I,(A(I,J),J=LOW,KITE)
18 FORMAT(14,2X,14F8.4)
IF(N-KITE) 40,40,20
40 RETURN
END
SUBROUTINE TMAT
IMPLICIT REAL*8(A-H,O-Z)
TO SOLVE MATRIX EQ B = T#A FOR T GIVEN A AND B
COMMON/ENGY/B(3),R(3),ETOT,VOL,DP,IC
COMMON/SIMRUN/DELTA,RMIN,ID,11,12,11,11,11,1E,IS,ISS
COMMON/LIT/IBLANK,ITMAT,IBL,IALPHA,IBETA,ICLEAR,I11,I12
COMMON/NTMAT/LTMAT,NVAR,LID
DIMENSION A(3,3),C(3,3),O(3,3),T(3)
*****

```

C

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00

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C      INPUT SECTION
      DO 9 J=1,3
      A(1,J)=1.000
      A(2,J)=R(J)
9     A(3,J)=R(J)*R(J)
      CALL MOUTPT(A,3,3,3,3,9H MATRIX A)
      CALL MOUTPT(B,1,3,1,3,9H MATRIX B)
C      *****
C      SOLUTION FOR T IS T = B*A-INVERSE
C      FORM INVERSE OF A
C      CALCULATE MATRIX OF COFACTORS OF A IN D
      D(1,1)=A(2,2)*A(3,3)-A(2,3)*A(3,2)
      D(1,2)=- (A(2,1)*A(3,3)-A(2,3)*A(3,1))
      D(1,3)=A(2,1)*A(3,2)-A(2,2)*A(3,1)
      D(2,1)=- (A(1,2)*A(3,3)-A(1,3)*A(3,2))
      D(2,2)=A(1,1)*A(3,3)-A(1,3)*A(3,1)
      D(2,3)=- (A(1,1)*A(3,2)-A(1,2)*A(3,1))
      D(3,1)=A(1,2)*A(2,3)-A(1,3)*A(2,2)
      D(3,2)=- (A(1,1)*A(2,3)-A(1,3)*A(2,1))
      D(3,3)=A(1,1)*A(2,2)-A(1,2)*A(2,1)
C      *****
C      CALCULATE DETERMINANT OF A AND OUTPUT
      DET=A(1,1)*D(1,1)+A(1,2)*D(1,2)+A(1,3)*D(1,3)
      IF (DABS(DET).LT.1.0D-18) GO TO 5
      GO TO 6
5     PRINT 1002, DET
1002  FORMAT(//,24H MATRIX SINGULAR, DET = ,E15.5,/)
      STOP
6     CONTINUE
      PRINT 1000, DET
1000  FORMAT(//,7H DET = ,E15.5,/)
C      *****
C      FORM ELEMENTS OF INVERSE
      DO 1 I=1,3
      DO 1 J=1,3
1     C(I,J)=D(J,I)/DET
      CALL MOUTPT(C,3,3,3,3,8H INVERSE)
C      *****
C      CHECK INVERSE
      DO 2 I=1,3
      DO 2 J=1,3
      D(I,J)=0.0D0
      DO 2 K=1,3
2     D(I,J)=D(I,J)+A(I,K)*C(K,J)
      CALL MOUTPT(D,3,3,3,3,7H CK INV)
C      *****
C      FORM TRANSFORMATION MATRIX
      DO 3 J=1,3
      T(J)=0.0D0
      DO 3 K=1,3
3     T(J)=T(J)+B(K)*C(K,J)
      CALL MOUTPT(T,1,3,1,3,10H TRANS MAT)

```

```

RMIN=-T(2)/(2.000*T(3))
PRINT 750, RMIN
750 FORMAT (//.8H RMIN = .F20.16)
RETURN
END
SUBROUTINE TIM
IMPLICIT REAL*8(A-H,O-Z)
C CALL S19V1(TIME)
C PRINT 1111, TIME
C1111 FORMAT(1X,A8)
RETURN
END
SUBROUTINE DMAT(PDIAG,XXX,B,C,N,OCCA,IBF,AN,IAT,CZ,U,ULIM,LLIM,NUM
*M)
IMPLICIT REAL*8(A-H,O-Z)
DIMENSION CZ(IAT),U(IBF),ULIM(IAT),LLIM(IAT)
DIMENSION NUM(IBF)
INTEGER*4 CZ
INTEGER *4 U,ULIM
DIMENSION C(IAT,3), AN(IAT)
DIMENSION XXX(IBF)
DIMENSION PDIAG(IBF)
C THIS ROUTINE ACCEPTS THE COEFFICIENTS OR EIGENVECTORS IN B
C AND GENERATES THE DENSITY MATRIX ALSO IN B
INTEGER OCCA
DIMENSION B(IBF,IBF)
COMMON/OPTION/OPTION,OPNCLO,HUCKEL,CNDO,INDO,CLOSED,OPEN,IONOFF
INTEGER OPTION,OPNCLO,HUCKEL,CNDO,CLOSED,OPEN
INTEGER OFF
DATA OFF/'OFF'/
IF(IONOFF .EQ. OFF) GO TO 2222
PRINT 1111
1111 FORMAT(13H COEFFICIENTS)
CALL SCFOUT(C,AN,B,CZ,U,ULIM,LLIM,NUM,0,1,IBF,IAT)
2222 CONTINUE
DO 140 I=1,N
DO 120 J=1,N
XXX(J) = 0.00
DO 110 K=1,OCCA
110 XXX(J) = XXX(J) + 2.00*B(I,K)*B(J,K)
120 CONTINUE
DO 130 J=1,N
130 B(I,J) = XXX(J)
140 CONTINUE
DO 150 I=1,N
DO 150 J=1,N
PDIAG(I) = B(I,I)
150 B(J,I) = B(I,J)
C WRITE THE DIAGONAL OF THE NEWLY GENERATED DENSITY MATRIX ON DISK
C KDISK = 11
C IKDISK=12
C REWIND IKDISK

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C      RFWIND KDISK                                000
C      DO 2222 IY=1,N                              000
C      DO 2222 JY=1,N                              000
C      IF(IY .NE. JY) GO TO 2222                   000
C      WRITE (KDISK) B(IY,JY)                     000
C      WRITE (IKDISK) B(IY,JY)                    000
C2222 CONTINUE                                     000
      IF(IDNOFF .EQ. OFF) GO TO 4444               000
      PRINT 3333                                    000
3333  FORMAT (15H DENSITY MATRIX)                  000
      CALL SCFOUT(C,AN,B,CZ,U,ULIM,LLIM,NUM,0.1,IBF,IAT) 000
4444  CONTINUE                                     000
      RETURN                                        000
      END                                           000
      SUBROUTINE EIGN(NN,RHO,IBF,A)                 000
      IMPLICIT REAL*8(A-H,O-Z)                     000
C      ONE MATRIX VERSION                          000
C      RHO= UPPER LIMIT FOR OFF-DIAGONAL ELEMENT  000
C      NN= SIZE OF MATRIX                          000
C      A = F MATRIX (ONLY LOWER TRIANGLE IS USED + THIS IS DESTROYED) 000
C      EIG = RETURNED EIGENVALUES IN ALGEBRAIC ASCENDING ORDER 000
C      VEC = RETURNED EIGENVECTORS IN COLUMNS    000
      DIMENSION A(1BF,1BF)                         000
      DIMENSION W( 90),GAMMA( 90),BETA( 90),BETASQ( 90),IPOSV( 90),IVPOS( 90),
*      *( 90),IORD( 90)                             000
      COMMON/8YE/EIG( 90)                           000
C      THE FOLLOWING DIMENSIONED VARIABLES ARE EQUIVALENCED 000
C      DIMENSION VEC(1BF,1BF)                       000
C      EQUIVALENCE (A(1),VEC(1))                     000
C      EQUIVALENCE (VFC,A)                           000
      DIMENSION P(50),Q(50)                          000
      EQUIVALENCE (P(1),BETA(1)),(Q(1),BETA(1))      000
      EQUIVALENCE (IPOSV(1),GAMMA(1)),(IVPOS(1),BETA(1)),
1      1(IORD(1),BETASQ(1))                           000
      ABSF(X) =DABS(X)                               000
      SQRTF(X) =DSQRT(X)                             000
C      PRINT 1917                                    000
1917  FORMAT( 8H IN EIGN)                            000
      RHOSQ=RHO*RHO                                  000
      N=NN                                           000
      IF(N .EQ. 0) GO TO 560                          000
1      N1=N-1                                        000
      N2=N-2                                        000
      GAMMA(1)=A(1,1)                                000
      IF(N2) 280,270,120                             000
120  DO 260 NR=1,N2                                  000
      B=A(NR+1,NR)                                    000
      S=0.00                                          000
      DO 130 I=NR,N2                                  000
130  S=S+A(I+2,NR)**2                                000
C      PREPARE FOR POSSIBLE BYPASS OF TRANSFORMATION 000
      A(NR+1,NR)=0.00                                000

```

C
C
C

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140 IF (S) 250,250,140
140 S=S+0*B
    SGN=+1.00
    IF (B) 150,160,160
150 SGN=-1.00
160 SORTS=SQRTF(S)
    TSQR = SORTS +SQRTS
    PRINT 1111,TSQR
C 1111 FORMAT (F80.60)
    D=SGN/(SORTS+SQRTS)
    TEMP=SQRTF(.500+B*D)
    W(NR)=TEMP
    A(NR+1,NR)=TEMP
C PRINT 1111,TEMP
    D=D/TFMP
    R=-SGN*SQRTS
C D IS FACTOR OF PROPORTIONALITY. NOW COMPUTE AND SAVE W VECTOR.
C EXTRA SINGLY SUBSCRIPTED W VECTOR USED FOR SPEED.
    DO 170 I=NR,N2
    TEMP=D*A(I+2,NR)
    W(I+1)=TEMP
170 A(I+2,NR)=TEMP
C PREMULTIPLY VECTOR W BY MATRIX A TO OBTAIN P VECTOR.
C SIMULTANEOUSLY ACCUMULATE DOT PRODUCT WP.(THE SCALAR K)
    WTAW=C.00
    DO 220 I=NR,N1
    SUM=C.00
    DO 180 J=NR,I
    SUM=SUM+A(I+1,J+1)*W(J)
180 I=I+1
    IF(N1-I) 210,190,190
190 DO 200 J=I,N1
200 SUM=SUM+A(J+1,I+1)*W(J)
210 P(I)=SUM
220 WTAW=WTAW+SUM*W(I)
C P VECTOR AND SCALAR K NOW STORED. NEXT COMPUTE Q VECTOR
    DO 230 I=NR,N1
230 Q(I)=P(I)-WTAW*W(I)
C NOW FORM PAP MATRIX. REQUIRED PART
    DO 240 J=NR,N1
    QJ=Q(J)
    WJ=W(J)
    DO 240 I=J,N1
240 A(I+1,J+1)=A(I+1,J+1)-2.00*(W(I)*QJ+WJ*Q(I))
250 BFTA(NR)=B
    BETASQ(NR)=B*B
260 GAMMA(NR+1)=A(NR+1,NR+1)
270 B=A(N,N-1)
    BETA(N-1)=B
    BETASQ(N-1)=B*B
    GAMMA(N)=A(N,N)
280 BETASQ(N)=0.00

```

```

00 800 I=1,M
00 810 J=I,N
00 A(I,J)=0,DO
00 800 A(I,I)=1,DO
00 FORM PRODUCT P1*P2*...*PN-2
00 K=N
00 540 KP=K
00 K=K-1
00 KM=K-1
00 DO 550 J=KP,N
00 DO 580 I=K,N
00 SUM=C,DO
00 DO 600 L=K,N
00 SUM=SUM+A(L,KM)*A(L,J)
00 SUM=SUM+SUM
00 580 W(I)=A(I,J)-SUM*A(I,KM)
00 DO 620 I=K,N
00 A(I,J)=W(I)
00 550 CONTINUE
00 DO 640 I=KP,N
00 A(I,K)=-2,DO*A(I,KM)*A(K,KM)
00 A(K,K)=1,DO-2,DO*A(K,KM)*A(K,KM)
00 IF(K.GE.3) GO TO 540
00 660 CONTINUE
00 DO 900 I=2,N
00 A(I,1)=0,DO
00 M=N
00 SUM=0,DO
00 GO TO 400
00 310 SUM=SUM+SHIFT
00 COSA=1,DO
00 G=GAMMA(1)-SHIFT
00 PP=G
00 PPBS=PP*PP+RETASQ(I)
00 PPBR=SORTF(PPBS)
00 DO 370 J=1,M
00 COSAP=COSA
00 IF(PPBR.NE.C,DO) GO TO 320
00 311 SINA=0,DO
00 SINA2=C,DO
00 COSA=1,DO
00 GO TO 350
00 320 SINA=BETA(J)/PPBR
00 PRINT 1111,PPBR
00 PRINT 1111,PPBS
00 SINA2=BFTASQ(J)/PPBS
00 COSA=PP/PPBR
00 POSTMULTIPLY P1*...*PN-2 BY ROTATION MATRIX (P-TRANPOSE)
00 330 DO 340 I=1,N
00 TEMP=COSA*VEC(I,J)+SINA*VEC(I,J+1)
00 TEMP=COSA* A(I,J)+SINA* A(I,J+1)
00 VEC(I,J+1)=-SINA*VEC(I,J)+COSA*VEC(I,J+1)

```

C
C
C

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C 340 A(I,J+1)=-SINA* A(I,J)+COSA* A(I,J+1) 00
C 340 VEC(I,J)=TEMP 00
C 340 A(I,J)=TEMP 00
C 350 DIA=GAMMA(J+1)-SHIFT 00
C 350 U=SINA2*(G+DIA) 00
C 350 GAMMA(J)=G+U 00
C 350 G=DIA-U 00
C 350 PP=DIA*COSA-SINA*COSAP*BETA(J) 00
C 351 IF(J.NE.M) GO TO 360 00
C 351 BETA(J)=SINA*PP 00
C 351 BETA(J)=SINA2*PP*PP 00
C 360 GO TO 380 00
C 360 PPRS=PP*PP+BETASQ(J+1) 00
C 360 PPBR=SORTF(PPRS) 00
C 370 BETA(J)=SINA*PPBR 00
C 380 BETASQ(J)=SINA2*PPBR 00
C 380 GAMMA(M+1)=G 00
C 390 TEST FOR CONVERGENCE OF LAST DIAGONAL ELEMENT 00
C 390 IF(BETASQ(M).GT.RHOSO) GO TO 410 00
C 400 EIG(M+1)=GAMMA(M+1)+SUM 00
C 400 BETA(M)=O.DO 00
C 400 BETASQ(M)=O.DO 00
C 400 M=M-1 00
C 401 IF(M.EQ.O) GO TO 430 00
C 401 TAKE ROOT OF CORNER 2 BY 2 NEAREST TO LOWER DIAGONAL IN VALUE 00
C 410 AS ESTIMATE OF EIGENVALUE TO USE FOR SHIFT 00
C 410 A2=GAMMA(M+1) 00
C 410 R2=.5DC*A2 00
C 410 R1=.5DC*GAMMA(M) 00
C 410 R12=R1+R2 00
C 410 DIF=R1-R2 00
C 410 TEMP=SORTF(DIF*DIF+BETASQ(M)) 00
C 410 R1=R12+TEMP 00
C 410 R2=R12-TEMP 00
C 410 DIF=ABSF(A2-R1)-ABSF(A2-R2) 00
C 410 IF(DIF.LT.O.DO) GO TO 420 00
C 411 SHIFT=R2 00
C 411 GO TO 310 00
C 420 SHIFT=R1 00
C 420 GO TO 310 00
C 430 FIG(1)=GAMMA(1)+SUM 00
C 430 INITIALIZE AUXILIARY TABLES REQUIRED FOR REARRANGING THE VECTORS 00
C 440 J=1.N 00
C 440 IPOSV(J)=J 00
C 440 IVPOS(J)=J 00
C 440 IORD(J)=J 00
C 440 USE A TRANSPOSITION SORT TO ORDER THE EIGENVALUES 00
C 440 M=N 00
C 450 GO TO 470 00
C 450 DD 460 J=1.M 00
C 450 IF (EIG(J) .LE. FIG(J+1)) GO TO 460 00

```



```

000 DIMENSION NUM(1BF)
001 INTEGER*4 DP,AN,ANII,CZ,U,ORB,ULIM,EL
002 DO 10 I = 1,N
003   10 NUM(I) = I
004   DO 120 M=1,N,11
005     K=M+10
006     IF(K.GT.N) GO TO 20
007     GO TO 30
008   20 K=N
009   30 CONTINUE
010   PRINT 100
011   IF(GP.EQ.1) GO TO 40
012   GO TO 50
013   40 CONTINUE
014   50 CONTINUE
015   PRINT 60,(NUM(I),I=M,K)
016   60 FORMAT(13X,11I9)
017   DO 110 I=1,N
018     II=U(I)
019     ANII=AN(II)
020     L=I-LLIM(II)+1
021     70 PRINT 80,I,II,EL(ANII),ORB(L),(A(I,J),J=M,K)
022     80 FORMAT(1X,12,13,A4,1X,A4,11F9.4)
023     IF(I.EQ.ULIM(II)) GO TO 90
024     GO TO 110
025     90 PRINT 100
026     100 FORMAT(1X)
027     110 CONTINUE
028     120 CONTINUE
029     PRINT 100
030     PRINT 100
031     RETURN
032   END
033   SUBROUTINE ZMAT(ALPHA,BETA,C,BL,ANG1,ANG2,R,AN,IAT,IBF,Z)
034   IMPLICIT REAL*8(A-H,O-Z)
035   REAL*8 L1,L2,L3,L4
036   DIMENSION ALPHA(IAT),BETA(IAT),Z(IAT,4),C(IAT,3),AN(IAT),BL(IAT),
037   *ANG1(IAT),ANG2(IAT)
038   COMMON/INFO/N,NATOMS,CHARGE,MULTIP
039   THIS PROGRAM ACCEPTS A DEFINITION OF A MOLECULE IN TERMS OF
040   C ATOMIC NUMBERS, BOND LENGTHS, BOND ANGLES AND DIHEDRAL ANGLES
041   C AND CALCULATES THE CARTESIAN COORDINATES IN ANGSTROMS
042   C ADAPTED FROM MARK GORDON'S MBLD SYSTEM BY D L BEVERIDGE
043   C CODED IN CDC SCOPE 3.1 LEVEL FORTRAN FOR THE CIMS CDC 6600
044   DIMENSION VI(3),V2(3),V3(3),VJ(3),VP(3),L1(3),L2(3),L3(3),L4(3)
045   COMMON/JDENT/IDENT
046   INTEGER AN,CHARGE,Z,PUNCH
047   DIMENSION R(IAT,IAT)
048   DIMENSION IDENT(20)
049   DIMENSION FL(9)
050   COMMON/ENGY/BOE(3),RDE(3),FTOT,VOL,DP,IC
051   COMMON/SIMRUN/DELTA,RMIN,ID,11,12,11,11,IE,IS,ISS

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1003 FORMAT (I3,I4,F7.4,I4,F11.6,I4,F11.6,I4) 00
C   ANG1 AND ANG2 STORE THE ANGLES ALPHA AND BETA IN DEGREE FORM 00
   ANG1(I)=ALPHA(I) 00
   ANG2(I)=BETA(I) 00
   IF(AN(I) .LE. 10) GO TO 361 00
   NBFN = NBFN + 9 00
   GO TO 371 00
361 IF(AN(I) .LT. 3) GO TO 362 00
   NBFN = NBFN + 4 00
   GO TO 371 00
362 NBFN = NBFN + 1 00
371 CONTINUE 00
6969 CONTINUE 00
   PRINT 374, NBFN,NATOMS 00
374 FORMAT (/,3X,I4, 29H BASIS FUNCTIONS REQUIRED FOR,I3,6H ATOMS,/) 00
104 CONTINUE 00
C   DO 1124 I=1,NATOMS 00
C   PRINT 1125,AN(I),Z(I,1),BL(I),Z(I,2),ALPHA(I),Z(I,3),BETA(I), 00
C   *Z(I,4) 00
C1124 CONTINUE 00
C1125 FORMAT(I3,I4,F7.4,I4,F11.6,I4,F11.6,I4) 00
   IF ((NVAR.EQ.ICLEAR).OR.(ID.EQ.1)) GO TO 7000 00
7001 CONTINUE 00
   IF (NVAR.EQ.IBL) GO TO 7002 00
   GO TO 7003 00
7002 BL(IS)=BL(IS) + DELTA 00
   IF (ISS.EQ.0) GO TO 7000 00
   BL(ISS)=BL(ISS) + DELTA 00
   GO TO 7000 00
7003 CONTINUE 00
   IF (NVAR.EQ.IALPHA) GO TO 7004 00
   GO TO 7005 00
7004 ANG1(IS)=ANG1(IS) + DELTA 00
   IF (ISS.EQ.0) GO TO 7000 00
   ANG1(ISS)=ANG1(ISS) + DELTA 00
   GO TO 7000 00
7005 CONTINUE 00
   IF (NVAR.EQ.IBETA) GO TO 7006 00
   GO TO 7007 00
7006 ANG2(IS)=ANG2(IS) + DELTA 00
   IF (ISS.EQ.0) GO TO 7000 00
   ANG2(ISS)=ANG2(ISS) + DELTA 00
   GO TO 7000 00
7007 CONTINUE 00
   PRINT 7008 00
7008 FORMAT (/////, 55H ERROR ON FIRST CARD IN COLUMNS 30 - 34 OR 57 - 00
C61.///,37H PROGRAM TERMINATED DUE TO THIS ERROR,///,60H CHECK PERMCCC
   DISSIBLE STATEMENTS FOR THESE COLUMNS AND RESUBMIT,///) 00
   GO TO 1984 00
7000 CONTINUE 00
C   DO 1127 I=1,NATOMS 00
C   PRINT 1125,AN(I),Z(I,1),BL(I),Z(I,2),ALPHA(I),Z(I,3),BETA(I), 00

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C      *Z(I,4)
C1127 CONTINUE
C      CONVERT TO RADIANS
      DO 502 J=1,M
502  ALPHA(J)=ALPHA(J)*3.141592654D0/180.0D0
      DO 503 J=1,M
503  BETA(J)=BETA(J)*3.141592654D0/180.0D0
      DO 504 J= 1,3
504  C(1,J)=C.0D0
      IF(M.EQ. 1) GO TO 601
      C(2,1)=C.0D0
      C(2,3)=BL(2)
      C(2,2)=C.0D0
      IF(M.EQ. 2) GO TO 601
      C(3,1)=BL(3)*SINF(ALPHA(3))
      C(3,2)=C.0D0
      *****
C      IF THE MOLECULE UNDER CONSIDERATION HAS ONLY ONE HEAVY ATOM OF FOR
C      THE FOLLOWING IS AN ADDITION TO COORD FINDER PROGRAM TO BE USED
C      A MOLECULE SUCH AS NEOPENTANE IN WHICH THE CENTRAL ATOM HAS NO
C      HYDROGENS BONDED TO IT
      IF(Z(3,1).EQ.1) GO TO 505
      GO TO 506
505  C(3,3) = BL(3)*COSF(ALPHA(3))
      GO TO 507
506  C(3,3) = C(2,3)-BL(3)*COSF(ALPHA(3))
507  I=3
      IF(ABSF(C(3,1))-LT.0.00001D0) GO TO 550
      GO TO 510
550  DO 509 I = 4,1000
      IF(I.LE.M.AND.ABSF(C(I-1,1))-LT.0.00001D0) GO TO 508
      GO TO 510
508  C(I,1) = BL(I)*SINF(ALPHA(I))
      C(I,2)=C.0D0
      ITEMP = Z(I,1)
      JTEMP = Z(I,2)
      C(I,3)=C(ITEMP,3)-BL(I)*COSF(ALPHA(I))*SIGNF(1.0D0,C(ITEMP,3))-
      1C(JTEMP,3))
509  CONTINUE
510  CONTINUE
      IF(I.EQ.3) GO TO 511
      GO TO 512
511  K=4
      GO TO 513
512  K=1
513  CONTINUE
      IF(K.GT.M) GO TO 601
600  CONTINUE
      DO 533 J = K,M
      IF(Z(J,4).EQ.0) GO TO 514
      GO TO 517
      *****
C

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C
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C

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C THIS PART IS USED IF THE ATOM IS BEING DEFINED BY A DIHEDRAL ANGLE
514 CONTINUE
CALL RELVEC(V1,Z(J,2),Z(J,3),IAT,IBF,C)
CALL UNIVEC(L1,V1)
C V1 IS A VECTOR FROM ATOM Z(J,3) TO ATOM Z(J,2)
C L1 IS A UNIT VECTOR OF V1. BL(Z(J,2)) IS BONDLENGTH OF ATOM Z(J,2)
CALL RELVEC(V2,Z(J,1),Z(J,2),IAT,IBF,C)
CALL UNIVEC(L2,V2)
C V2 IS THE VECTOR FROM ATOM Z(J,2) TO ATOM Z(J,1)
C L2 IS THE UNIT VECTOR OF V2. BL(Z(J,1)) IS BONDLENGTH DEFINING
C ATOM Z(J,1)
CALL VECPRD(VP,L1,L2)
XXX=C.000
XXX=(1.000-(L1(1)*L2(1)+L1(2)*L2(2)+L1(3)*L2(3))*2)
IF(XXX.LT.0.000) GO TO 1888
GO TO 1889
1888 PRINT 1913, XXX
1913 FORMAT (3X,32HARGUMENT OF DSORT IS LESS THAN 0.6H XXX =,F40.2C)
1889 CONTINUE
DO 515 I = 1,3
515 L3(I)=VP(I)/SQRTF(DARS(1.000-(L1(1)*L2(1)+L1(2)*L2(2)+
L1(3)*L2(3))*2))
1985 FORMAT(3X,1HA)
C L3 IS THE UNIT VECTOR OF VP.ALPHA(Z(J,1)) IS THE ANGLE DEFINING
C ATOM Z(J,1)
CALL VECPRD(L4,L3,L2)
C L4,L3,L2 ARE A NEW SET OF MUTUALLY ORTHOGONAL AXES. WE WILL NOW
C OBTAIN COORD OF ATOM J IN TERMS OF THESE AXES RELATIVE TO ATOM Z(J,1)
DO 516 I=1,3
OVJ(I) = BL(J)*(-L2(I)*COSF(ALPHA(J))+L4(I)*SINF(ALPHA(J))*COSF(BETA(J))
+L3(I)*SINF(ALPHA(J))*SINF(BETA(J)))
C VJ IS THE VECTOR FROM ATOM Z(J,1) TO ATOM J
ITEMP = Z(J,1)
C(J,I) = VJ(I) + C(ITEMP,I)
516 CONTINUE
GO TO 533
517 IF(Z(J,4).EQ.1.OR.Z(J,4).EQ.-1) GO TO 549
GO TO 528
*****
C THIS PART IS USED IF ATOM IS DEFINED BY TWO BONDANGLES
549 CONTINUE
CALL RELVEC(V1,Z(J,1),Z(J,3),IAT,IBF,C)
CALL UNIVEC(L1,V1)
CALL RFLVFC(V2,Z(J,2),Z(J,1),IAT,IBF,C)
CALL UNIVEC(L2,V2)
ZFTA = -(L1(1)*L2(1)+L1(2)*L2(2)+L1(3)*L2(3))
A=(-COSF(BETA(J))+ZETA*COSF(ALPHA(J)))/(1.000-ZETA**2)
B=(COSF(ALPHA(J))-ZETA*COSF(BETA(J)))/(1.000-ZETA**2)
PI=3.14159265400
IF(ZETA.LT.0.000) GO TO 518
GO TO 519.
518 TFP = PI

```

```

000 GO TO 520
000 TFMP=C.0DC
000 520 CONTINUE
000 IF(ZETA.EQ.0.000) GO TO 521
000 GO TO 522
000 521 GAMMA=PI/2.0D0
000 GO TO 523
000 522 GAMMA=ATANF(SQRTF(1.0D0-ZETA**2)/ZETA)+TEMP
000 1986 FFORMAT (3X,1HB)
000 523 CONTINUE
000 IF(ABSF(GAMMA+ALPHA(J)+RETA(J)-2.0D0*PI).LT.0.0000001D0)
000 160 TO 524
000 GO TO 525
000 524 D = 0.0D0
000 GO TO 526
000 525 D=Z(J,4)*(SQRTF(1.0D0+A*COSF(BETA(J))-8*COSF(ALPHA(J))))
000 1/SQRTF(1.0D0-ZETA**2)
000 1987 FFORMAT (3X,1HC)
000 526 CONTINUE
000 *CALL VECPRD(V3,L1,L2)
000 DO 527 I = 1,3
000 L3(I) = A*L1(I)+R*L2(I)+D*V3(I)
000 VJ(I) = RL(J)*L3(I)
000 ITEMP = Z(J,1)
000 C(J,I) = VJ(I)+C(ITMP,I)
000 527 CONTINUE
000 GO TO 533
000 *****
000 C THIS PART IS USED IF ATOM IS DEFINED BY ONE BOND ANGLE AND BY THE
000 C ANGLE WHICH BOND Z(J,1)-J MAKES WITH THE PLANE OF Z(J,1),Z(J,2)
000 C AND Z(J,3)
000 528 CONTINUE
000 CALL RELVEC(V1,Z(J,1),Z(J,3),IAT,IBF,C)
000 CALL UNIVEC(L1,V1)
000 CALL RELVEC(V2,Z(J,2),Z(J,1),IAT,IBF,C)
000 CALL UNIVEC(L2,V2)
000 ZETA = -(L1(I)*L2(1)+L1(2)*L2(2)+L1(3)*L2(3))
000 CALL VECPRD(V3,L1,L2)
000 RETA(J) HERE REFERS TO 90-ANGLE WHICH BOND Z(J,1)-J MAKES WITH THEO
000 C AFOREMENTIONED PLANE
000 C A=COSF(BETA(J))/(1.0D0-ZETA**2)
000 IF(7(J,4).EQ.2) GO TO 530
000 529 B=-SQRTF((1.0D0-COSF(ALPHA(J))**2-A*COSF(BETA(J))))/
000 1(1.0D0-ZETA**2))
000 1988 FFORMAT (3X,1HD)
000 GO TO 531
000 530 B=SQRTF((1.0D0-COSF(ALPHA(J))**2-A*COSF(BETA(J)))/
000 1(1.0D0-ZETA**2))
000 1989 FFORMAT (3X,1HE)
000 531 CONTINUE
000 D = B*7ETA+COSF(ALPHA(J))
000 DO 532 I=1,3

```



```

C *****
C CALCULATION OF ELEMENTS OF MOMENT OF INERTIA TENSOR
  DO 10 I=1,3
  DO 10 J=1,3
  A(I,J)=0.0D0
  DO 10 K=1,NATOMS
  IAN = AN(K)
  IF(I.EQ.J) GO TO 11
  GO TO 12
C   ROUTE FOR DIAGONAL ELEMENTS
  11 RKSO = C(K,1)**2+C(K,2)**2+C(K,3)**2
  A(I,J)=A(I,J)+AW(IAN)*(RKSO-C(K,I)*C(K,J))*1.67D0
  GO TO 10
C   ROUTE FOR OFF DIAGONAL ELEMENTS
  12 A(I,J)=A(I,J)-AW(IAN)*C(K,I)*C(K,J)*1.67D0
  10 CONTINUE
C *****
C DIAGONALIZATION OF MOMENT OF INERTIA TENSOR AND OUTPUT
  CALL TPAT(A,B,E)
  DRIENT COORDINATE SYSTEM ALONG PRINCIPAL AXES
  DO 20 K=1,NATOMS
  DO 21 I=1,3
  A(I,I)=0.0D0
  DO 21 J=1,3
  21 A(I,I) = A(I,I)+B(J,I)*C(K,J)
  DO 20 J=1,3
  20 C(K,J) = A(J,J)
  IF(I.ONOFF .NE. OFF) PRINT 720
  720 FORMAT(15H LEAVING MINERT)
  RETURN
  END
C SUBROUTINE TPAT(A,S,ANGLE)
  IMPLICIT REAL*8(A-H,O-Z)
  PRINCIPLE AXIS TRANSFORMATION
  DIMENSION A(3,3),S(3,3),ANGLE(3,3)
  INTEGER N,I,J,P,Q,IND,LL,UL,K,NSMALL
  REAL*8 RHO,THR,MU,OMEGA,SINT,COST,INT1,V1,V2,V3,A,S,SMALL
  SORTF(X) =DSORT(X)
  ARSF(X) =DARS(X)
  ATANF(X) =DATAN(X)
  SIGMF(X,Y)=DSIGN(X,Y)
  FLOATF(I)=DFLOAT(I)
  RHO = 1.0D-6
  N = 3
  DO 30 I=1,N
  DO 20 J=1,N
  20 S(I,J)=0.0D0
  30 S(I,I)=1.0D0
  INT1=0.0D0
  DO 40 I=2,N
  UL = I-1
  DO 40 J=1,UL

```



```

MC(3)=-1
MC(4)=C
MC(5)=0
MC(6)=1
MC(7)=-1
MC(8)=?
MC(9)=-2
C STEP THRU PAIRS OF ATOMS
DO 320 K=1,NATOMS
DO 320 L=K,NATOMS
DO 100 I=1,3
C(I,I) = C(K,I)
100 C2(I) = C(L,I)
C CALCULATE UNIT VECTOR ALONG INTERATOM AXIS,E
CALL RLVFC(R,E,C1,C2)
LK = LLIM(K)
LL = LLIM(L)
ULK = ULIM(K)
ULL = ULIM(L)
NDRBK=ULK-LLK+1
NDRBL=ULL-LLL+1
ANK=ANIK)
ANL=AN(L)
C LOOP THRU PAIRS OF BASIS FUNCTIONS, ONE ON EACH ATOM
DO 200 I=1,NDRBK
DO 200 J=1,NDRBL
IF(K.FO.L) GO TO 160
IF(L.FO.L) GO TO 150
120 IF(MC(I).LT.C) GO TO 140
130 CONTINUE
PAIRS(I,J)=SORTF((MU(ANK)*P)**(2*NC(ANK)+1))*(MU(ANL)*R)**(2*NC(ANL)
11) + ((FACT(2*NC(ANK))*FACT(2*NC(ANL))))*(-1.DO)**(LC(J)+MC(J))
2*SS(NC(ANK),LC(I),MC(I),NC(ANL),LC(J),MU(ANK)*R,MU(ANL)*R)
GO TO 190
140 PAIRS(I,J)=PAIRS(I-1,J-1)
GO TO 190
150 PAIRS(I,J)=0.DO
GO TO 190
160 IF(I.FO.J) GO TO 170
GO TO 180
170 PAIRS(I,J)=1.DO
GO TO 190
180 PAIRS(I,J)=0.CPD
190 CONTINUE
200 CONTINUE
LCULK=LC(NDRBK)
LCULL=LC(NDRBL)
MAXL = XMAXOF(LCULK,LCULL)
IF(R.GT.0.000001DO) GO TO 220
210 GO TO 250
C ROTATE INTEGRALS FROM DIATOMIC BASIS TO MOLECULAR BASIS
220 CALL HARMTR(T,MAXL,E)

```

```

DO 230 I=1,NORBK
DO 230 J=1,NORPL
TEMP(I,J) = 0.00
DO 230 KK=1,NORBL
TEMP(I,J) = TEMP(I,J)+T(J,KK)*PAIRS(I,KK)
230 CONTINUE
DO 240 I=1,NORBK
DO 240 J=1,NORPL
PAIRS(I,J) = 0.00
DO 240 KK=1,NORBK
PAIRS(I,J) = PAIRS(I,J)+T(I,KK)*TEMP(KK,J)
240 CONTINUE
C FILL S MATRIX
250 CONTINUE
DO 260 I=1,NORBK
DO 260 J=1,NORBL
260 S(LLL+I-1,LLL+J-1) = PAIRS(I,J)
C COMPUTATION OF 1-CENTER COULOMB INTEGRALS OVER SLATER S FUNCTIONS
N1=NC(ANK)
N2=NC(ANL)
K1=MU(ANK)
K2=MU(ANL)
IF(K.NF.L) GO TO 290
270 TERM1 = FACT(2*N1-1)/((2.00C*K2)**(2*N1))
TERM2 = 0.00
LIM = 2*N1
DO 280 J=1,LIM
NUM =DFLOAT(J)*(2.00C*K1)**(2*N1-J)*FACT(4*N1-J-1)
DEN = FACT(2*N1-J)*2.00C*DFLOAT(N1)*(2.00C*(K1+K2))**(4*N1-J)
TERM2 = TERM2 + NUM/DEN
280 CONTINUE
GO TO 310
C COMPUTATION OF 2-CENTER COULOMB INTEGRALS OVER SLATER S FUNCTIONS
290 TERM1=(R/2.00C)**(2*N2)*SS(0,0,0,2*N2-1,0,0.00,2.00C*K2*R)
TERM2 = 0.00
LIM = 2*N1
DO 300 J=1,LIM
300 TERM2 = TERM2+(DFLOAT(J)*(2.00C*K1)**(2*N1-J)*(R/2.00C)**(2*
IN1-J+2*N2))/ (FACT(2*N1-J)*2.00C*DFLOAT(N1))*SS(2*N1-J,0,0,2*N2-1,0,0
2,2.00C*K1*R,2.00C*K2*R)
310 GAMMA(K,L) = ((2.00C*K2)**(2*N2+1)/FACT(2*N2))*(TERM1-TERM2)
320 CONTINUE
C SYMMETRIZATION OF OVERLAP AND COULOMB INTEGRAL MATRICES
DO 330 I=1,N
DO 330 J=1,N
330 S(J,I) = S(I,J)
DO 340 I=1,NATOMS
DO 340 J=1,NATOMS
340 GAMMA(J,I) = GAMMA(I,J)
IF(IGNOFF.F0.OFF) GO TO 12
13 CONTINUE
PRINT 350

```

```

350 FORMAT(24H OVERLAP INTEGRAL MATRIX)
    CALL MATOUT(GAMMA,N,1,IBF,S,IAT)
    PRINT 370
370 FORMAT(24H COULOMB INTEGRAL MATRIX)
    CALL MATOUT(GAMMA,NATOMS,2,IBF,S,IAT)
12 CONTINUE
    RETURN
    END
    SUBROUTINE HARMTR(T,MAXL,E)
    IMPLICIT REAL*8(A-H,O-Z)
    DIMENSION T(9,9),F(3)
    COST = E(3)
301 FORMAT (10H IN HARMTR)
    IF((1.000-COST**2).GT.0.0000000100) GO TO 20
10 SINT = 0.00
    GO TO 30
20 SINT=DSQRT(1.00-COST**2)
30 CONTINUE
    IF(SINT.GT.0.000000100) GO TO 50
40 COSP = 1.00
    SINP = 0.00
    GO TO 70
50 COSP = F(1)/SINT
60 SINP = F(2)/SINT
70 CONTINUE
    DO 80 I=1,9
    DO 80 J=1,9
80 T(I,J) = 0.00
    T(1,1) =1.00
    IF (MAXL.GT.1) GO TO 100
90 IF (MAXL.GT.0) GO TO 110
    GO TO 120
100 COS2T = COST**2-SINT**2
    SIN2T = 2.00*SINT*COST
    COS2P = COSP**2-SINP**2
    SIN2P = 2.00*SINP*COSP
C
    TRANSFORMATION MATRIX ELEMENTS FOR D FUNCTIONS
    SQR3=DSQRT(3.00)
    T(5,5) = (3.00*COST**2-1.00)/2.00
    T(5,6) = -SQR3 *SIN2T/2.00
    T(5,8) = SQR3 *SINT**2/2.00
    T(6,5) = SQR3 *SIN2T*COSP/2.00
    T(6,6) = COS2T*COSP
    T(6,7) = -COST*SINP
    T(6,8) =-T(6,5)/SQR3
    T(6,9) = SINT*SINP
    T(7,5) = SQR3 *SIN2T*SINP/2.00
    T(7,6) = COS2T*SINP
    T(7,7) = COST*COSP
    T(7,8) = -T(7,5)/SQR3
    T(7,9) = -SINT*COSP
    T(8,5) = SQR3 *SINT**2*COS2P/2.00

```

```

T(4,6) = SIN2T*COS2P/2.00
T(3,7) = -SINT*SIN2P
T(8,8) = (1.00+COST**2)*COS2P/2.00
T(3,9) = -COST*SIN2P
T(9,5) = SORT3 *SINT**2*SIN2P/2.00
T(9,6) = SIN2T*SIN2P/2.00
T(9,7) = SINT*COS2P
T(9,8) = (1.00+COST**2)*SIN2P/2.00
T(9,9) = COST*COS2P

```

110 CONTINUE

C TRANSFORMATION MATRIX ELEMENTS FOR P FUNCTIONS

```

T(2,2) = COST*COSP
T(2,3) = -SIMP
T(2,4) = SINT*COSP
T(3,2) = COST*SINP
T(3,3) = COSP
T(3,4) = SINT*SINP
T(4,2) = -SINT
T(4,4) = COST

```

120 CONTINUE

* -RETURN

END

FUNCTION SS(NN1,LL1,MM,NN2,LL2,ALPHA,BETA)

IMPLICIT REAL*8(A-H,O-Z)

PROCEDURE FOR CALCULATING REDUCED OVERLAP INTEGRALS

DIMENSION A(17), B(17)

INTEGFR*4 ULIM

SORTF(X)=DSORT(X)

XARSF(I) = IABS(I)

XMODF(I,J) = MOD(I,J)

C 100 PRINT 99

99 FORMAT (6H IN SS)

N1=NN1

L1=LL1

M=MM

N2=NN2

L2=LL2

PT=(ALPHA-BETA)/2.000

P=(ALPHA+BETA)/2.000

X=0.00

M=XARSF(M)

REVERSE QUANTUM NUMBERS IF NECESSARY

IF((L2.LT.L1).OR.((L2.E0.L1).AND.(N2.LT.N1))) GO TO 20

10 GO TO 30

20 K = N1

N1= N2

N2= K

K= L1

L1= L2

L2= K

PT=-PT

30 CONTINUE

DATA JZ2(19)/224/	00
DATA JZ2(20)/225/	00
DATA JZ2(21)/226/	00
DATA JZ2(22)/227/	00
DATA JZ2(23)/228/	00
DATA JZ2(24)/229/	00
DATA JZ2(25)/230/	00
DATA JZ2(26)/231/	00
DATA JZ2(27)/307/	00
DATA JZ2(28)/308/	00
DATA JZ2(29)/309/	00
DATA JZ2(30)/310/	00
DATA JZ2(31)/312/	00
DATA JZ2(32)/313/	00
DATA JZ2(33)/314/	00
DATA JZ2(34)/315/	00
DATA JZ2(35)/409/	00
DATA JZ2(36)/410/	00
DATA JZ2(37)/411/	00
DATA JZ2(38)/412/	00
DATA JZ2(39)/413/	00
DATA JZ2(40)/414/	00
DATA JZ2(41)/415/	00
DATA JZ2(42)/416/	00
DATA JZ2(43)/528/	00
DATA JZ2(44)/529/	00
DATA JZ2(45)/530/	00
DATA JZ2(46)/532/	00
DATA JZ2(47)/533/	00
DATA JZ2(48)/534/	00
DATA JZ2(49)/562/	00
DATA JZ2(50)/563/	00
DATA JZ2(51)/565/	00
DATA JZ2(52)/566/	00
DATA JZ2(53)/732/	00
DATA JZ2(54)/733/	00
DATA JZ2(55)/545/	00
DATA JZ2(56)/546/	00
DATA JZ2(57)/547/	00
DATA JZ2(58)/548/	00
DATA JZ2(59)/549/	00
DATA JZ2(60)/550/	00
DATA JZ2(61)/579/	00
DATA JZ2(62)/580/	00
DATA JZ2(63)/581/	00
DATA JZ2(64)/582/	00
DATA JZ2(65)/596/	00
DATA JZ2(66)/598/	00
DATA JZ2(67)/443/	00
DATA JZ2(68)/444/	00
DATA JZ2(69)/445/	00
DATA JZ2(70)/446/	00

DATA YY(140)/16.D0/	00
DATA YY(141)/16.D0/	00
DATA YY(142)/-16.D0/	00
DATA YY(143)/16.D0/	00
DATA YY(144)/-16.D0/	00
DATA YY(145)/-16.D0/	00
DATA YY(146)/16.D0/	00
DATA YY(147)/-16.D0/	00
DATA YY(148)/16.D0/	00
DATA YY(149)/16.D0/	00
DATA YY(150)/-16.D0/	00
DATA YY(151)/64.D0/	00
DATA YY(152)/-64.D0/	00
DATA YY(153)/-128.D0/	00
DATA YY(154)/128.D0/	00
DATA YY(155)/64.D0/	00
DATA YY(156)/-64.D0/	00
DATA YY(157)/64.D0/	00
DATA YY(158)/-64.D0/	00
DATA YY(159)/-64.D0/	00
DATA YY(160)/-64.D0/	00
DATA YY(161)/64.D0/	00
DATA YY(162)/64.D0/	00
DATA YY(163)/64.D0/	00
DATA YY(164)/-64.D0/	00
DATA YY(165)/-96.D0/	00
DATA YY(166)/32.D0/	00
DATA YY(167)/-96.D0/	00
DATA YY(168)/160.D0/	00
DATA YY(169)/96.D0/	00
DATA YY(170)/128.D0/	00
DATA YY(171)/-96.D0/	00
DATA YY(172)/96.D0/	00
DATA YY(173)/-128.D0/	00
DATA YY(174)/-96.D0/	00
DATA YY(175)/-160.D0/	00
DATA YY(176)/96.D0/	00
DATA YY(177)/-32.D0/	00
DATA YY(178)/96.D0/	00
DATA YY(179)/-96.D0/	00
DATA YY(180)/32.D0/	00
DATA YY(181)/32.D0/	00
DATA YY(182)/32.D0/	00
DATA YY(183)/96.D0/	00
DATA YY(184)/32.D0/	00
DATA YY(185)/-32.D0/	00
DATA YY(186)/-96.D0/	00
DATA YY(187)/-32.D0/	00
DATA YY(188)/-32.D0/	00
DATA YY(189)/-32.D0/	00
DATA YY(190)/96.D0/	00
DATA YY(191)/48.D0/	00

DATA YY(1923)/-48.D0/ 00
 DATA YY(1933)/-48.D0/ 00
 DATA YY(1943)/48.D0/ 00
 DATA YY(1953)/-48.D0/ 00
 DATA YY(1963)/48.D0/ 00
 DATA YY(1973)/48.D0/ 00
 DATA YY(1983)/-48.D0/ 00
 DATA YY(1993)/48.D0/ 00
 DATA YY(2003)/-48.D0/ 00
 DATA YY(2013)/-48.D0/ 00
 DATA YY(2023)/48.D0/ 00
 DATA YY(2033)/-64.D0/ 00
 DATA YY(2043)/64.D0/ 00
 DATA YY(2053)/64.D0/ 00
 DATA YY(2063)/-64.D0/ 00
 DATA YY(2073)/-64.D0/ 00
 DATA YY(2083)/-64.D0/ 00
 DATA YY(2093)/64.D0/ 00
 DATA YY(2103)/64.D0/ 00
 DATA YY(2113)/64.D0/ 00
 DATA YY(2123)/64.D0/ 00
 DATA YY(2133)/-64.D0/ 00
 DATA YY(2143)/-64.D0/ 00
 DATA YY(2153)/16.D0/ 00
 DATA YY(2163)/-16.D0/ 00
 DATA YY(2173)/-16.D0/ 00
 DATA YY(2183)/16.D0/ 00
 DATA YY(2193)/16.D0/ 00
 DATA YY(2203)/-16.D0/ 00
 DATA YY(2213)/-64.D0/ 00
 DATA YY(2223)/64.D0/ 00
 DATA YY(2233)/54.D0/ 00
 DATA YY(2243)/-64.D0/ 00
 DATA JYY(11)/7039/ 00
 DATA JYY(12)/7040/ 00
 DATA JYY(13)/7049/ 00
 DATA JYY(14)/7032/ 00
 DATA JYY(15)/7041/ 00
 DATA JYY(16)/7033/ 00
 DATA JYY(17)/7042/ 00
 DATA JYY(18)/7025/ 00
 DATA JYY(19)/7034/ 00
 DATA JYY(101)/7026/ 00
 DATA JYY(111)/7035/ 00
 DATA JYY(121)/7027/ 00
 DATA JYY(131)/6904/ 00
 DATA JYY(141)/6913/ 00
 DATA JYY(151)/6896/ 00
 DATA JYY(161)/6905/ 00
 DATA JYY(171)/6906/ 00
 DATA JYY(181)/6915/ 00
 DATA JYY(191)/6889/ 00

DATA JYY(20)/6907/	00
DATA JYY(21)/6890/	00
DATA JYY(22)/6899/	00
DATA JYY(23)/6891/	00
DATA JYY(24)/6900/	00
DATA JYY(25)/6892/	00
DATA JYY(26)/6901/	00
DATA JYY(27)/2954/	00
DATA JYY(28)/2663/	00
DATA JYY(29)/2847/	00
DATA JYY(30)/2856/	00
DATA JYY(31)/2865/	00
DATA JYY(32)/2840/	00
DATA JYY(33)/2849/	00
DATA JYY(34)/2858/	00
DATA JYY(35)/2842/	00
DATA JYY(36)/2851/	00
DATA JYY(37)/2710/	00
DATA JYY(38)/2719/	00
DATA JYY(39)/2711/	00
DATA JYY(40)/2720/	00
DATA JYY(41)/2729/	00
DATA JYY(42)/2703/	00
DATA JYY(43)/2712/	00
DATA JYY(44)/2721/	00
DATA JYY(45)/2704/	00
DATA JYY(46)/2713/	00
DATA JYY(47)/2722/	00
DATA JYY(48)/2731/	00
DATA JYY(49)/2705/	00
DATA JYY(50)/2714/	00
DATA JYY(51)/2723/	00
DATA JYY(52)/2706/	00
DATA JYY(53)/2715/	00
DATA JYY(54)/2724/	00
DATA JYY(55)/2707/	00
DATA JYY(56)/2716/	00
DATA JYY(57)/5329/	00
DATA JYY(58)/5322/	00
DATA JYY(59)/5340/	00
DATA JYY(60)/5315/	00
DATA JYY(61)/5333/	00
DATA JYY(62)/5326/	00
DATA JYY(63)/5185/	00
DATA JYY(64)/5194/	00
DATA JYY(65)/5186/	00
DATA JYY(66)/5195/	00
DATA JYY(67)/5204/	00
DATA JYY(68)/5178/	00
DATA JYY(69)/5187/	00
DATA JYY(70)/5196/	00
DATA JYY(71)/5179/	00

DATA JYY(72)/5188/	00
DATA JYY(73)/5197/	00
DATA JYY(74)/5206/	00
DATA JYY(75)/5180/	00
DATA JYY(76)/5189/	00
DATA JYY(77)/5198/	00
DATA JYY(78)/5181/	00
DATA JYY(79)/5190/	00
DATA JYY(80)/5199/	00
DATA JYY(81)/5182/	00
DATA JYY(82)/5191/	00
DATA JYY(83)/4375/	00
DATA JYY(84)/4384/	00
DATA JYY(85)/4393/	00
DATA JYY(86)/4368/	00
DATA JYY(87)/4386/	00
DATA JYY(88)/4395/	00
DATA JYY(89)/4370/	00
DATA JYY(90)/4379/	00
DATA JYY(91)/4397/	00
DATA JYY(92)/4372/	00
DATA JYY(93)/4381/	00
DATA JYY(94)/4390/	00
DATA JYY(95)/1900/	00
DATA JYY(96)/1909/	00
DATA JYY(97)/1893/	00
DATA JYY(98)/1920/	00
DATA JYY(99)/1895/	00
DATA JYY(100)/1922/	00
DATA JYY(101)/1906/	00
DATA JYY(102)/1915/	00
DATA JYY(103)/955/	00
DATA JYY(104)/964/	00
DATA JYY(105)/973/	00
DATA JYY(106)/948/	00
DATA JYY(107)/966/	00
DATA JYY(108)/975/	00
DATA JYY(109)/950/	00
DATA JYY(110)/959/	00
DATA JYY(111)/977/	00
DATA JYY(112)/952/	00
DATA JYY(113)/961/	00
DATA JYY(114)/970/	00
DATA JYY(115)/8155/	00
DATA JYY(116)/8156/	00
DATA JYY(117)/8165/	00
DATA JYY(118)/8148/	00
DATA JYY(119)/8157/	00
DATA JYY(120)/8149/	00
DATA JYY(121)/8158/	00
DATA JYY(122)/8150/	00
DATA JYY(123)/8020/	00

DATA JYY(124)/8029/ 002
DATA JYY(125)/8021/ 002
DATA JYY(126)/8013/ 002
DATA JYY(127)/8031/ 002
DATA JYY(128)/8014/ 002
DATA JYY(129)/8015/ 002
DATA JYY(130)/8024/ 002
DATA JYY(131)/7084/ 002
DATA JYY(132)/7076/ 002
DATA JYY(133)/7095/ 002
DATA JYY(134)/7086/ 002
DATA JYY(135)/7069/ 002
DATA JYY(136)/7070/ 002
DATA JYY(137)/7079/ 002
DATA JYY(138)/7071/ 002
DATA JYY(139)/3205/ 002
DATA JYY(140)/3214/ 002
DATA JYY(141)/3206/ 002
DATA JYY(142)/3215/ 002
DATA JYY(143)/3198/ 002
DATA JYY(144)/3216/ 002
DATA JYY(145)/3199/ 002
DATA JYY(146)/3217/ 002
DATA JYY(147)/3200/ 002
DATA JYY(148)/3209/ 002
DATA JYY(149)/3201/ 002
DATA JYY(150)/3210/ 002
DATA JYY(151)/7579/ 002
DATA JYY(152)/7580/ 002
DATA JYY(153)/7572/ 002
DATA JYY(154)/7573/ 002
DATA JYY(155)/7565/ 002
DATA JYY(156)/7566/ 002
DATA JYY(157)/5680/ 002
DATA JYY(158)/5681/ 002
DATA JYY(159)/5673/ 002
DATA JYY(160)/5691/ 002
DATA JYY(161)/5674/ 002
DATA JYY(162)/5692/ 002
DATA JYY(163)/5684/ 002
DATA JYY(164)/5685/ 002
DATA JYY(165)/7435/ 002
DATA JYY(166)/7444/ 002
DATA JYY(167)/7436/ 002
DATA JYY(168)/7445/ 002
DATA JYY(169)/7428/ 002
DATA JYY(170)/7437/ 002
DATA JYY(171)/7446/ 002
DATA JYY(172)/7429/ 002
DATA JYY(173)/7438/ 002
DATA JYY(174)/7447/ 002
DATA JYY(175)/7430/ 002

DATA JYY(1174)/7439/ 002
 DATA JYY(1177)/7431/ 002
 DATA JYY(1178)/7440/ 002
 DATA JYY(1179)/5545/ 002
 DATA JYY(1180)/5554/ 002
 DATA JYY(1181)/5546/ 002
 DATA JYY(1182)/5555/ 002
 DATA JYY(1183)/5538/ 002
 DATA JYY(1184)/5556/ 002
 DATA JYY(1185)/5539/ 002
 DATA JYY(1186)/5557/ 002
 DATA JYY(1187)/5540/ 002
 DATA JYY(1189)/5549/ 002
 DATA JYY(1189)/5541/ 002
 DATA JYY(1190)/5550/ 002
 DATA JYY(1191)/3070/ 002
 DATA JYY(1192)/3079/ 002
 DATA JYY(1193)/3071/ 002
 DATA JYY(1194)/3080/ 002
 DATA JYY(1195)/3063/ 002
 DATA JYY(1196)/3081/ 002
 DATA JYY(1197)/3064/ 002
 DATA JYY(1198)/3082/ 002
 DATA JYY(1199)/3065/ 002
 DATA JYY(1200)/3074/ 002
 DATA JYY(1201)/3066/ 002
 DATA JYY(1202)/3075/ 002
 DATA JYY(1203)/8200/ 002
 DATA JYY(1204)/8201/ 002
 DATA JYY(1205)/8193/ 002
 DATA JYY(1206)/8194/ 002
 DATA JYY(1207)/7615/ 002
 DATA JYY(1208)/7616/ 002
 DATA JYY(1209)/7625/ 002
 DATA JYY(1210)/7608/ 002
 DATA JYY(1211)/7617/ 002
 DATA JYY(1212)/7609/ 002
 DATA JYY(1213)/7618/ 002
 DATA JYY(1214)/7610/ 002
 DATA JYY(1215)/3250/ 002
 DATA JYY(1216)/3259/ 002
 DATA JYY(1217)/3243/ 002
 DATA JYY(1218)/3261/ 002
 DATA JYY(1219)/3245/ 002
 DATA JYY(1220)/3254/ 002
 DATA JYY(1221)/5725/ 002
 DATA JYY(1222)/5718/ 002
 DATA JYY(1223)/5736/ 002
 DATA JYY(1224)/5729/ 002
 IO = ((LHI-1)*45) + (9*(KHI-1)) + JHI 00
 IF((IO.LT. 948) .OR. (IO.GT. 8201)) GO TO 61 00
 DO 87 I=1,224 00

```

00 IF(IQ.EQ.JYY(I)) GO TO 81
00 GO TO 87
00 CONTINUE
00 YII = YY(I)
00 GOTQ 90
00 CONTINUE
00 61 CONTINUE
00 YII = 0.00
00 CONTINUE
00 RETURN
00 END
00 FUNCTION FACT(N)
00 IMPLICIT REAL*8(A-H,O-Z)
00 INTEGER*4 N,I,PRODT
00 FLOATF(I)=DFLOAT(I)
00
00 C 100 PRINT 99
00 99 FORMAT ( 8H IN FACT)
00 PRODT = 1
00 IF(N.FQ.0) GO TO 10
00 GO TO 20
00 10 GO TO 40
00 20 DO 30 I=1,N
00 30 PRODT = PRODT*I
00 40 FACT=FLOATF(PRODT)
00 RETURN
00 END
00 SUBROUTINE BINTGS(X,K,A,B)
00 IMPLICIT REAL*8(A-H,O-Z)
00 C FILLS ARRAY OF B-INTEGRALS. NOTE THAT B(I) IS B(I-1) IN THE
00 C USUAL NOTATION
00 C FOR X.GT.3
00 C FOR 2.LT.X.LE.3 AND K.LE.10 EXPONENTIAL FORMULA IS USED
00 C FOR 2.LT.X.LE.3 AND K.GT.10 EXPONENTIAL FORMULA IS USED
00 C FOR 1.LT.X.LE.2 AND K.LE.7 15 TERM SERIES IS USED
00 C FOR 1.LT.X.LE.2 AND K.GT.7 EXPONENTIAL FORMULA IS USED
00 C FOR .5.LT.X.LE.1 AND K.LE.5 12 TERM SERIES IS USED
00 C FOR .5.LT.X.LE.1 AND K.GT.5 EXPONENTIAL FORMULA IS USED
00 C FOR X.LE..5 7 TERM SERIES IS USED
00 C 6 TERM SERIES IS USED
00 C *****
00 DIMENSION A(17), B(17)
00 ABSF(X)=DABS(X)
00 EXPF(X)=DEXP(X)
00
00 C1234 PRINT 99
00 99 FORMAT (10H IN BINTGS)
00 IO=0
00 ABSX=ARSF(X)
00 IF(ABSX.GT.3.000) GO TO 120
00 10 IF(ABSX.GT.2.000) GO TO 20
00 GO TO 40
00 20 IF(K.LE.10) GO TO 120
00 30 LAST=15
00 GO TO 140

```



```

CC  K=U(I)
CC  L=AN(K)
CC  UL=I-1
CC  DD 90 J=1,UL
CC  KK=U(J)
CC  LL=AN(KK)
CC  IF((L.GT.9).OR.(LL.GT.9)) GO TO 7C
CC  GO TO 8C
CC  70 A(I,J)=C.75D0*A(I,J)*(BETA0(L)+BETA0(LL))/54.42D0
CC  A(J,I)=A(I,J)
CC  GO TO 9C
CC  80 A(I,J)=A(I,J)*(BETA0(L)+BETA0(LL))/54.42D0
CC  A(J,I)=A(I,J)
CC  90 CONTINUE
CC  DD 10C I=1,N
CC  100 O(I)=A(I,I)
CC  DD 9998 IO=1,N
CC  DD 9998 JO=1,N
CC  A(IO,JO) = A(JO,IO)
CC  9998 CONTINUE
CC  C WRITE LOWER TRIANGLE OF CORE HAMILTONIAN ON DISK FILE 10
CC  C WITH THE DIAGONAL ELEMENTS
CC  REWIND JDISK
CC  WRITE (JDISK) ((A(IERT,KERT),KERT=1,IERT),IERT=1,N)
CC  3334 FORMAT(1X,F10.5)
CC  IF((IJC.FQ.1).OR.(IRCCC.EQ.0)) GO TO 98
CC  REWIND IDISK
CC  READ(IDISK) ((A(IJO,JJO),IJO=1,N),JJO=1,N)
CC  PRINT 8013
CC  GO TO 96
CC  98 CONTINUE
CC  8013 FORMAT(33H READING DENSITY MATRIX FROM DISK)
CC  CALL EIGN(N,O,COCCO1D0,IBF,A)
CC  EIGENVECTORS (IN B) ARE CONVERTED INTO DENSITY MATRIX (IN B)
CC  CALL DMAT(PDIAG,XXX,A,C,N,OCCEA,IBF,AN,IAT,CZ,U,ULIM,LLIM,NUM)
CC  C ADD V(AB) TO HCORE--CNDO
CC  96 CONTINUE
CC  DD 17C I=1,N
CC  J=U(I)
CC  Q(I)=Q(I) +0.5D0*G(J,J)
CC  DD 16C K=1,NATOMS
CC  16C Q(I)=Q(I)-DFLOAT(CZ(K))*G(J,K)
CC  17C CONTINUE
CC  C EXIT SEGMENT IF ONLY CNDO APPROXIMATIONS ARE DESIRED
CC  IF(OPTION.EQ.INDO) GO TO 18C
CC  GO TO 29C
CC  C INDO MODIFICATION (CORRECTION TO U(I,I) )
CC  18C DD 28C I=1,NATOMS
CC  K=AN(I)
CC  J=LLIM(I)
CC  IF((K.GT.1).AND.(K.LT.10)) GO TO 19C
CC  GO TO 28C

```



```

00 41 J=LL,N
00 JJ=U(J)
00 A(J,I)=A(J,I)-B(J,I)*G(II,JJ)*0.5
00 A(J,I) = A(J,I) - A(I,J)*G(II,JJ)*0.5D0
00 41 CONTINUE
00 40 CONTINUE
00 INDO MODIFICATION
00 IF (OPTION.EQ.INDO) GO TO 50
00 GO TO 90
00 50 DO 80 II=1,NATOMS
00 K=AN(II)
00 I=LLIM(II)
00 IF (K.EQ.1) GO TO 80
00 GO TO 60
00 60 PAA=PDIAG(I)+PDIAG(I+1)+PDIAG(I+2)+PDIAG(I+3)
00 A(I,I) = A(I,I)-(PAA-PDIAG(I))*G1(K)/6.D0
00 DO 70 J=1,3
00 A(I+J,I+J)=A(I+J,I+J)-PDIAG(I)*G1(K)/6.D0-(PAA-PDIAG(I))*7.D0*F2(K)
00 *)/50.D0 + PDIAG(I+J)*11.D0*F2(K)/50.D0
00 A(I+J,I)=A(I+J,I)+A(I,I+J)*G1(K)/2.D0
00 JJ=J-1
00 IF (JJ.EQ.0) GO TO 70
00 GO TO 71
00 71 CONTINUE
00 DO 72 L=1,JJ
00 A(I+J,I+L) = A(I+J,I+L)+A(I+L,I+J)*11.D0*F2(K)/50.D0
00 72 CONTINUE
00 70 CONTINUE
00 80 CONTINUE
00 90 CONTINUE
00 CALL ECALC(2,ENERGY,N,IBF,A,PDIAG,0)
00 IF (IONOFF .NE. OFF) PRINT 9999, ENERGY
9999 FORMAT(1X,F20.10)
00 IF (IONOFF .EQ. OFF) GO TO 9123
00 PRINT 2137
2137 FORMAT(79H LOWER TRIANGLE AND DIAGONAL HAS FOCK MATRIX, UPPER TRIA
*NGLE HAS DENSITY MATRIX)
200 FORMAT(27H HARTREE-FOCK ENERGY MATRIX)
00 CALL SCFOU1(C,AN,A,CZ,U,ULIM,LLIM,NUM,0,1,IBF,IAT)
9123 CONTINUE
00 CALL EIGN1(N,,000001D0,IBF,A)
00 EDIFF = ENERGY-7LDENG
00 IF (EDIFF.LT.0.0D0) GO TO 401
400 PRINT 402,Z
402 FORMAT(/,30H ENERGY DIVERGING AT ITERATION, I4,/)
00 GO TO 405
401 CONTINUE
00 IF (ABS(ENERGY-OLDENG).LT..000001D0) GO TO 120
00 GO TO 150
120 CONTINUE
00 PRINT 1115, Z
00

```

```

1115 FORMAT(1X,15,11H ITERATIONS) 00
      Z=100 00
      IRCCC = 1 00
      IPCOV = 1 00
130 PRINT 140 00
140 FORMAT(/,17H ENERGY SATISFIED) 00
      GO TO 170 00
150 CONTINUE 00
160 OLDENG=ENFRGY 00
170 CONTINUE 00
      IF (Z.GT.IT)GO TO 220 00
      GO TO 240 00
220 CONTINUE 00
      IF(IONOFF.EQ.OFF) GO TO 14 00
15 CONTINUE 00
      PRINT 230 00
230 FORMAT(28HEIGENVALUES AND EIGENVECTORS) 00
      CALL SCFOU1(C,AN,A,CZ,U,ULIM,LLIM,NUM,1,1,IBF,IAT) 00
240 CONTINUE 00
14 CONTINUE 00
C EIGENVECTORS (IN B) ARE CONVERTED INTO DENSITY MATRIX (IN B) 00
      CALL DMA1(PDIAG,XXX,A,C,N,OCCA,IBF,AN,IAT,CZ,U,ULIM,LLIM,NUM) 00
      IF (Z.GT.IT) GO TO 300 00
      GO TO 10 00
300 CONTINUE 00
      IF(IRCOV.NE.1) GO TO 9133 00
      REWIND IDISK 00
      WRITE(IDISK) ((A(IJQ,JJQ),IJQ=1,N),JJQ=1,N) 00
      PRINT 8012 00
9133 CONTINUE 00
8012 FORMAT (31H WRITING DENSITY MATRIX ON DISK) 00
405 CONTINUE 00
      RETURN 00
      END 00
      SUBROUTINE ECALC(JOINT,ESUM,N,IBF,A,PDIAG,Q) 00
      IMPLICIT REAL*8(A-H,O-Z) 00
      DIMENSION PDIAG(1BF), Q(1BF) 00
      DIMENSION A(1BF,1BF) 00
      IF(JOINT .EQ. 1) ESUM=0.DO 00
      DO 3130 IBC=1,N 00
      DO 3130 JBC=1,N 00
      IF(JRC .LE. IBC) GO TO 3130 00
      ESUM = (A(IBC,JBC)*A(JBC,IBC)) + ESUM 00
3130 CONTINUE 00
      IF(JOINT .EQ. 2) GO TO 3333 00
      DO 3131 IBC=1,N 00
      ESUM = ESUM + ((PDIAG(IBC)*Q(IBC))/2.DO) 00
3131 CONTINUE 00
      GO TO 4444 00
3333 CONTINUE 00
      DO 1234 III=1,N 00
      ESUM = ESUM + ((PDIAG(III)*A(III,III))/2.DO) 00

```

```

1234 CONTINUE                                C
4444 CONTINUE                                C
RETURN                                        C
END
SUBROUTINE CPRINT(G,B,C,AN,IBF,IAT,XXX,CZ,U,ULIM,LLIM,PDIAG,0,NUM)
*)
IMPLICIT REAL*8(A-H,O-Z)
DIMENSION G(IAT,IAT)
DIMENSION XXX(1BF)
DIMENSION NUM(1BF)
DIMENSION C(IAT,3), AN(IAT)
CNDG=INDO SCF CLOSED SHELL- PRINTOUT SEGMENT
COMMON/HELLO/ENERGY
DIMENSION PDIAG(1BF), Q(1BF)
DIMENSION A(1BF,1BF)
COMMON/INFO/M,N,NATOMS,CHARGE,MULTIP
COMMON/INF01/NFLECS,OCCA,OCB8
DIMENSION CZ(IAT),U(1BF),ULIM(IAT),LLIM(IAT)
COMMON/PERTAL/EL(9)
COMMON/OPTION/OPTION,OPNCLO,HUCKEL,CNDD,INDO,CLOSED,OPEN,IONDFF
COMMON/ENGY/BAE(3),ROE(3),FTOT,MOLVOL,DP,IC
INTEGER*4 OPTION,OPNCLO,HUCKEL,CNDD,INDO,CLOSED,OPEN,IONDFF
INTEGER*4 CHARGE,AN,U,ULIM,EL,OCCA,OCB8,UL,CZ,ANI
DIMENSION DPM(3),DM(3),DMS(3),DMPD(3)
DIMENSION ATENG(18)
DIMENSION RCH(3),DMP(3)
REAL*8 MAXX,MINX,MAXY,MINY,MAXZ,MINZ,MDLVOL
INTEGER*4 OFF
DATA OFF/'OFF'/'
FLOATF(1)=DFLOAT(1)
SORTF(X)=DSORT(X)
PRINT 9898
C
9898 FDRMAT(10H IN CPRINT)
IF(ENERGY.NE.999.99DD) GO TO 400
SET DEFAULT VALUES
ETOT=999.99DD
MOLVOL=999.99DD
DP=999.99DD
GO TO 401
400 CONTINUE
IF(OPTION.EQ.INDO) GO TO 10
GO TO 20
10 CONTINUE
ATENG(1)=-0.6387302462 DO
ATENG(4)=0.0DD
ATENG(3)=0.0DD
ATENG(5)=0.0DD
ATENG(6)=-5.9349548261 DO
ATENG(7)=-10.6731741251 DO
ATENG(8)=-17.2920850650 DO
ATENG(9)=-26.2574377875 DO
GO TO 30

```

```

20 CONTINUE
  ATENG(1)=-C.6387302462  DO
  ATENG(3)=C.000
  ATENG(4)=0.000
  ATENG(5)=0.000
  ATENG(6)=-6.1649935261  DO
  ATENG(7)=-11.0763746252  DO
  ATENG(8)=-18.3819458651  DO
  ATENG(9)=-27.5491302860  DO
  ATENG(11)=-.1977009568  DO
  ATENG(12)=-.8671913833  DO
  ATENG(13)=-2.0364557744  DO
  ATENG(14)=-3.8979034686  DO
  ATENG(15)=-6.7966009163  DO
  ATENG(16)=-10.7658174341DO
  ATENG(17)=-16.0467017940DO
30 CONTINUE
  K=NATOMS-1
13 CONTINUE
  IF(IONOFF.EQ.OFF) GO TO 12
  PRINT 40
40 FORMAT(15H DENSITY MATRIX/)
  IF(IONOFF.NE.OFF)CALL SCFDU2(C,AN,B,CZ,U,ULIM,LLIM,NUM,0.1,IBF,IATOC
*)
12 CONTINUE
  DO 50 I=1,K
  L=I+1
  DO 50 J=L,NATOMS
  RAD=SQRTF((C(I,1)-C(J,1))**2+(C(I,2)-C(J,2))**2
  +(C(I,3)-C(J,3))**2)
  50 ENERGY=ENERGY+(FLOATF(CZ(I))*FLOATF(CZ(J)))/RAD
  BWE(IC)=ENERGY
  PRINT 60,ENERGY
  60 FORMAT(/ /16H TOTAL ENERGY = F16.10)
  ETOT = ENERGY
  IF(IONOFF.EQ.OFF) GO TO 81
  DO 70 I=1,NATOMS
  IAN = AN(I)
  70 ENERGY = ENERGY-ATENG(IAN)
  PRINT 80,ENERGY
  80 FORMAT(/ /16HRINDING ENERGY= ,F16.10,5H A.U.)
  81 CONTINUE
  PRINT 82
  82 FORMAT(/,17H CHARGE DENSITIES,/)
  DO 110 I=1,NATOMS
  FCHG=C.000
  TCHG=C.000
  LL=LLIM(I)
  UL=ULIM(I)
  DO 90 J=LL,UL
  FCHG = C.DO
  90 TCHG = TCHG+B(J,J)

```

```

ANI=AN(I)
DCHG=DFLOAT(CZ(I))-TCHG
PRINT 100,I,EL(ANI),TCHG,DCHG,FCHG
100 FORMAT(13,A4,FX,3F7.4)
XX(I)=TCHG
110 CONTINUE
C
CALCULATE MOLECULAR VOLUME
MINX = C(1,1)
MAXX = C(1,1)
MINY = C(1,2)
MAXY = C(1,2)
MINZ = C(1,3)
MAXZ = C(1,3)
DO 310 IA=2,NATOMS
MINX=DMINI(C(IA,1),MINX)
MAXX=DMAXI(C(IA,1),MAXX)
MINY=DMINI(C(IA,2),MINY)
MAXY=DMAXI(C(IA,2),MAXY)
MINZ=DMINI(C(IA,3),MINZ)
MAXZ=DMAXI(C(IA,3),MAXZ)
310 CONTINUE
MOLVOL=(MAXX-MINX+1.000)*(MAXY-MINY+1.000)*(MAXZ-MINZ+1.000)*0.52900
116800
PRINT 311,MOLVOL
311 FORMAT(/,2GH MOLECULAR VOLUME = ,F10.5,5H A**3,/)
C
COMPUTE VECTOR COMPONENTS OF CENTER OF POSITIVE CHARGE
DO 300 I=1,3
FNUM=C.000
FDEN=C.000
DO 301 IA=1,NATOMS
FNUM = FNUM+FLOAT(CZ(IA))*C(IA,I)
FDEN = FDEN+FLOAT(CZ(IA))
301 CONTINUE
RCH(I) = FNUM/FDEN
REFER CARTESIAN COORDINATES TO CENTER OF POSITIVE CHARGE
DO 300 IA=1,NATOMS
C(IA,I) = C(IA,I)-RCH(I)
DO 120 I=1,3
DM(I)=0.000
DMSP(I)=C.000
DMPD(I)=C.000
DO 200 J=1,NATOMS
IF(AN(J).LT.3) GO TO 180
130 IF(AN(J).LT.11) GO TO 140
GO TO 160
140 INDEX=ILIM(J)
DO 150 K=1,3
150 DMSP(K)=DMSP(K)-B(INDEX,INDEX+K)*7.3369700/
1 (.32500*DFLOAT(AN(J)-1))
GO TO 180
160 SLTR1=(.6500*DFLOAT(AN(J))-4.9500)/3.00
FACTOR=2.541600*7.00/(DSORT(5.00)*SLTR1)

```


C
C
C

```

C IKDISK=12
C REWIND IKDISK
C REWIND KDISK
C DO 2222 IY=1,N
C DO 2222 JY=1,N
C IF(IY.NE.JY) GO TO 2222
C WRITE (KDISK) B(IY,JY)
C WRITE (IKDISK) B(IY,JY)
C2222 CONTINUE
      IF(IDNOFF.EQ.OFF) GO TO 4444
      PRINT 3333
3333 FORMAT (15H DENSITY MATRIX)
      CALL SCFOUL(C,AN,B,CZ,U,ULIM,LLIM,NUM,C,1,IBF,IAT)
4444 CONTINUE
      RETURN
      END
      SUBROUTINE MOUTP1(A,M,N,MDIM,NDIM,NAL)
      OUTPUT OF M X N MATRIX DIMENSIONED TO MDIM X NDIM
      IMPLICIT REAL*8(A-H,O-Z)
      DIMENSION NAL(6)
      DIMENSION A(MDIM,NDIM)
      PRINT 1000,NAL
1000 FORMAT (//,2X,6A4)
      KITE = 0
      20 LOW = KITE+1
      KITE = KITE+14
      KITE = AMIN0(KITE,N)
      PRINT 19,(I,I=LOW,KITE)
19 FORMAT(//,4X,14(6X,I2),/)
      DO 32 I=1,M
      32 PRINT 18,I,(A(I,J),J=LOW,KITE)
      18 FORMAT(14,2X,14F8.4)
      IF(N-KITE) 40,40,20
      40 RETURN
      END
      SUBROUTINE SCFOUL(C,AN,A,CZ,U,ULIM,LLIM,NUM,OP,MOP,IBF,IAT)
      IMPLICIT REAL*8(A-H,O-Z)
      THIS ROUTINE PRINTS THE ARRAY IN COMMON/ARRAYS/ WHICH IS DESIGNATED
      MOP. IF OP = 1 THE EIGENVALUES CONTAINED IN COMMON/1/ ARE ALSO
      PRINTED. IF OP= C THE EIGENVALUES ARE NOT PRINTED
      DIMENSION C(IAT,3), AN(IAT)
      DIMENSION A(1BF,IBF)
      COMMON/INFO/N,NATOMS,CHARGE,MULTIP
      INTEGER*4 CHARGE,OCCA,OCCB,UL,ANI
      COMMON/ORB/ORB(9)
      COMMON/INFO1/NELECS,OCCA,OCCB
      DIMENSION CZ(IAT),U(1RF),ULIM(IAT),LLIM(IAT)
      COMMON/PERTBL/FL(9)
      DIMENSION NUM(1BF)
      INTEGER*4 OP,AN,ANI,CZ,U,ORB,ULIM,EL
      DO 10 I = 1,N
      10 NUM(I) = I

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10 NUM(I) = I

DO 10 I = 1,N

DIMENSION NUM(1BF)

COMMON/PERTBL/FL(9)

DIMENSION CZ(IAT),U(1RF),ULIM(IAT),LLIM(IAT)

COMMON/INFO1/NELECS,OCCA,OCCB

COMMON/ORB/ORB(9)

INTEGER*4 CHARGE,OCCA,OCCB,UL,ANI

COMMON/INFO/N,NATOMS,CHARGE,MULTIP

DIMENSION A(1BF,IBF)

DIMENSION C(IAT,3), AN(IAT)

PRINTED. IF OP= C THE EIGENVALUES ARE NOT PRINTED

MOP. IF OP = 1 THE EIGENVALUES CONTAINED IN COMMON/1/ ARE ALSO

THIS ROUTINE PRINTS THE ARRAY IN COMMON/ARRAYS/ WHICH IS DESIGNATED

SUBROUTINE SCFOUL(C,AN,A,CZ,U,ULIM,LLIM,NUM,OP,MOP,IBF,IAT)

END

40 RETURN

IF(N-KITE) 40,40,20

DO 32 I=1,M

32 PRINT 18,I,(A(I,J),J=LOW,KITE)

18 FORMAT(14,2X,14F8.4)

KITE = AMIN0(KITE,N)

KITE = KITE+14

20 LOW = KITE+1

KITE = 0

1000 FORMAT (//,2X,6A4)

DIMENSION A(MDIM,NDIM)

DIMENSION NAL(6)

IMPLICIT REAL*8(A-H,O-Z)

OUTPUT OF M X N MATRIX DIMENSIONED TO MDIM X NDIM

SUBROUTINE MOUTP1(A,M,N,MDIM,NDIM,NAL)

END

RETURN

CONTINUE

CONTINUE

WRITE (IKDISK) B(IY,JY)

WRITE (KDISK) B(IY,JY)

IF(IY.NE.JY) GO TO 2222

DO 2222 JY=1,N

DO 2222 IY=1,N

REWIND KDISK

REWIND IKDISK

IKDISK=12

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001 00 120 M=1,N,11
002 K=M+10
003 IF(K.GT.N) GO TO 20
004 GO TO 30
005 20 K=N
006 30 CONTINUE
007 PRINT 100
008 IF(OP.EQ.1) GO TO 40
009 GO TO 50
010 40 CALL FIGOUT(M,K)
011 CONTINUE
012 PRINT 60,(NUM(I),I=M,K)
013 FORMAT(13X,1119)
014 DO 110 I=1,N
015 11=U(I)
016 ANTI=AN(11)
017 L=-LLIM(I1)+1
018 PRINT 80,I,11,EL(ANTI),ORR(L),(A(I,J),J=M,K)
019 FORMAT(1X,12,13,A4,1X,A4,11F9.4)
020 JF(1.EQ.ULIM(I1)) GO TO 90
021 GO TO 110
022 90 PRINT 100
023 100 FORMAT(1X)
024 110 CONTINUE
025 120 CONTINUE
026 PRINT 100
027 PRINT 100
028 RETURN
029 END
030 SUBROUTINE SCFNU2(C,AN,A,CZ,U,ULIM,LLIM,NUM,OP,MDP,IBF,IAT)
031 IMPLICIT REAL*8(A-H,O-Z)
032 THIS ROUTINE PRINTS THE ARRAY IN COMMON/ARRAYS/ WHICH IS DESIGNATED
033 MDP. IF OP = 1 THE EIGENVALUES CONTAINED IN COMMON/1/ ARE ALSO
034 PRINTED. IF OP= C THE EIGENVALUES ARE NOT PRINTED
035 DIMENSION C(IAT,3), AN(IAT)
036 DIMENSION A(1BF,1BF)
037 COMMON/INFD/N,NATOMS,CHARGE,MULTIP
038 INTEGER*4 CHARGE,DCCA,DCCR,UL,ANI
039 COMMON/ORR/ORR(9)
040 COMMON/INF01/NELECS,DCCA,DCCR
041 DIMENSION CZ(IAT),U(1BF),ULIM(IAT),LLIM(IAT)
042 COMMON/PERTBL/EL(9)
043 DIMENSION NUM(1BF)
044 INTEGER*4 OP,AN,ANTI,CZ,U,ORR,ULIM,EL
045 DO 10 I = 1,N
046 10 NUM(I) = I
047 DO 120 M=1,N,11
048 K=M+10
049 IF(K.GT.N) GO TO 20
050 GO TO 30
051 20 K=N
052 30 CONTINUE
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      GAMMA(1)=A(1,1)
      IF(N2) 280,270,120
120  DO 260 NR=1,N2
      B=A(NR+1,NR)
      S=0.00
      DO 130 I=NR,N2
130  S=S+A(I+2,NR)**2
C    PREPARE FOR POSSIBLE BYPASS OF TRANSFORMATION
      A(NR+1,NR)=0.00
      IF (S) 250,250,140
140  S=S+B*B
      SGN=+1.00
      IF (B) 150,160,160
150  SGN=-1.00
160  SORTS=SQRTF(S)
      TSQR = SORTS +SORTS
C    PRINT 1111,TSQR
1111 FORMAT (F80.60)
      D=SGN/(SORTS+SORTS)
      TEMP=SQRTF(.500+B*D)
      W(NR)=TEMP
      A(NR+1,NR)=TEMP
C    PRINT 1111,TEMP
      D=D/TEMP
      B=-SGN*SORTS
C    D IS FACTOR OF PROPORTIONALITY. NOW COMPUTE AND SAVE W VECTOR.
C    EXTRA SINGLY SUBSCRIBED W VECTOR USED FOR SPEED.
      DO 170 I=NR,N2
      TEMP=D*A(I+2,NR)
      W(I+1)=TEMP
170  A(I+2,NR)=TEMP
C    PREMULIPLY VECTOR W BY MATRIX A TO OBTAIN P VECTOR.
C    SIMULTANEOUSLY ACCUMULATE DOT PRODUCT WP,(THE SCALAR K)
      WTAW=0.00
      DO 220 I=NR,N1
      SUM=0.00
      DO 180 J=NR,I
180  SUM=SUM+A(I+1,J+1)*W(J)
      I1=I+1
      IF(N1-I1) 210,190,190
190  DO 200 J=I1,N1
200  SUM=SUM+A(J+1,I+1)*W(J)
210  P(I)=SUM
220  WTAW=WTAW+SUM*W(I)
C    P VECTOR AND SCALAR K NOW STORED. NEXT COMPUTE Q VECTOR
      DO 230 I=NR,N1
230  Q(I)=P(I)-WTAW*W(I)
C    NOW FORM PAP MATRIX. REQUIRED PART
      DO 240 J=NR,N1
      QJ=Q(J)
      WJ=W(J)
      DO 240 I=J,N1

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C  PRINT 1111, PPAR                      00
C  PRINT 1111, PPBS                      00
C  SINAZ=BETASQ(J)/PPBS                  00
C  COSA=PP/PPBR                          00
C  POSTMULTIPLY P1*...*PN-2 BY ROTATION MATRIX (P-TRANSPOSE) 00
C 330 DO 340 I=1,N                       00
C  TEMP=COSA*VEC(I,J)+SINA*VEC(I,J+1)    00
C  TEMP=COSA* A(I,J)+SINA* A(I,J+1)      00
C  VEC(I,J+1)=-SINA*VEC(I,J)+COSA*VEC(I,J+1) 00
C  A(I,J+1)=-SINA* A(I,J)+COSA* A(I,J+1) 00
C 340 VEC(I,J)=TEMP                      00
C 34G A(I,J)=TEMP                         00
C 350 DIA=GAMMA(J+1)--SHIFT              00
C  U=SINAZ*(G+DIA)                       00
C  GAMMA(J)=G+U                          00
C  G=DIA-U                                00
C  PP=DIA*COSA-SINA*COSAP*BETA(J)        00
C  IF(J.NE.M) GO TO 360                  00
C 351 BETA(J)=SINA*PP                    00
C  BETASQ(J)=SINAZ*PP*PP                 00
C  GO TO 380                             00
C 360 PPBS=PP*PP+BETASQ(J+1)             00
C  PPBR=SORTF(PPBS)                     00
C  BFTA(J)=SINA*PPBR                     00
C 370 BETASQ(J)=SINAZ*PPBS               00
C 380 GAMMA(M+1)=G                       00
C  TEST FOR CONVERGENCE OF LAST DIAGONAL ELEMENT 00
C  IF(BETASQ(M).GT.RHOSO) GO TO 410      00
C 390 EIG(M+1)=GAMMA(M+1)+SUM            00
C 400 BETA(M)=0.DO                       00
C  BETASQ(M)=0.DO                       00
C  M=M-1                                  00
C  IF(M.EQ.0) GO TO 430                  00
C 401 IF(BETASQ(M).LE.RHOSO) GO TO 390   00
C  TAKE ROOT OF CORNER 2 BY 2 NEAREST TO LOWER DIAGONAL IN VALUE 00
C  AS ESTIMATE OF EIGENVALUE TO USE FOR SHIFT 00
C 410 A2=GAMMA(M+1)                      00
C  R2=.500*A2                            00
C  R1=.500*GAMMA(M)                     00
C  R12=R1+R2                             00
C  DIF=R1-R2                              00
C  TFMP=SORTF(DIF*DIF+BETASQ(M))         00
C  R1=R12+TFMP                            00
C  R2=R12-TFMP                            00
C  DIF=ABSF(A2-R1)-ARSF(A2-R2)           00
C  IF(DIF.LT.0.DO) GO TO 420            00
C 411 SHIFT=R2                          00
C  GO TO 310                             00
C 420 SHIFT=R1                          00
C  GO TO 310                             00
C 430 EIG(1)=GAMMA(1)+SUM                00
C  INITIALIZE AUXILIARY TABLES REQUIRED FOR REARRANGING THE VECTORS 00

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      DO 440 J=1,N
      IPOSV(J)=J
      IVPOS(J)=J
440   IORD(J)=J
C     USE A TRANSPOSITION SORT TO ORDER THE EIGENVALUES
      M=N
      GO TO 470
450   DO 460 J=1,M
      IF (EIG(J) .LE. EIG(J+1)) GO TO 460
451   TEMP=EIG(J)
      EIG(J)=EIG(J+1)
      EIG(J+1)=TEMP
      ITEMP=IORD(J)
      IORD(J)=IORD(J+1)
      IORD(J+1)=ITEMP
460   CONTINUE
470   M=M-1
      IF(M .NE. 0) GO TO 450
471   IF(N1 .EQ. 0) GO TO 500
472   DO 490 L=1,N1
      NV=IORD(L)
      NP=IPOSV(NV)
      IF(NP .EQ. L) GO TO 490
473   LV=IVPOS(L)
      IVPOS(NP)=LV
      IPOSV(LV)=NP
      DO 480 I=1,N
C     TEMP=VEC(I,L)
      TEMP= A(I,L)
C     VEC(I,L)=VEC(I,NP)
      A(I,L)= A(I,NP)
C 480   VEC(I,NP)=TEMP
480   A(I,NP)=TEMP
490   CONTINUE
500   CONTINUE
560   CONTINUE
C     PRINT 1919
1919  FORMAT(13H LEAVING EIGN)
      RETURN
      END
      FUNCTION FAC1(N)
      IMPLICIT REAL*8(A-H,O-Z)
      INTEGER*4 N,I,PRODT
      FLOATF(I)=DFLOAT(I)
      PRODT = 1
      IF(N.EQ.0) GO TO 10
      GO TO 20
10   GO TO 40
20   DO 30 I=1,N
30   PRODT = PRODT*I
40   FAC1=FLOATF(PRODT)
      RETURN

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