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Douglas H. Reamer
Union College - Schenectady, NY

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Conformational Energy Calculations of the Pentapeptide PHE-DPHE-ASN-GLN-TYR of Tyrocidine

By

Douglas H. Reamer

* *

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in the Department of Chemistry

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ABSTRACT

REAMER, DOUGLAS The lowest energy conformation of tyrocidine: A peptide antibiotic which induces sporulation of a particular bacterial strain. Department of Chemistry, June 1990.

By virtue of employing a modified version of a popular program for the calculation of polypeptide conformational energies, the lowest energy conformation of the tyrocidine molecule is being sought. This antibiotic molecule, a cyclic decapeptide, invited study due to its role in the process of bacterial sporulation in the Bacillus Brevis ATCC 8185 strain. In the process of performing this investigation, lists of monopeptide lowest energy conformations, as determined by x-ray crystallographic studies, were combined to yield all possible combinations of half of the polypeptide chain. Beginning with a dipeptide, the conformations of lowest energy were calculated within a 'local-minimum' range; hereafter, a tripeptide was created from this dipeptide, as specified above, and similar calculations were performed. Finally, the tripeptide and a dipeptide calculated previously were then combined to yield the pentapeptide PHE-DPHE-ASN-GLN-TYR, which then underwent minimizing calculations to yield a set of 11 conformations, one of which possessed a probability of existence of 51.8%. The resulting lowest energy conformations of the pentapeptide will be joined with a pentapeptide from the lowest energy minima of gramicidin-S, PRO-DPHE-LEU-ORN-VAL, to yield the tyrocidine conformation.

Acknowledgment

I would like to take this opportunity to express my most sincere thanks to my research advisor, Professor Janet Anderson. The guidance and patience she has given to me over the course of this year has been greatly appreciated and will never be forgotten.

In addition, I would also like to thank my parents, June and Bill Reamer, for their love and support of my every endeavor, as well as for enabling me to pursue my education at Union.

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I. Introduction:

It is believed that all bacteria synthesize either small peptides or analogs of peptides immediately prior to undertaking the process of sporulation.[1] One such peptide antibiotic is tyrocidine, which has been shown to induce sporulation in the bacteria Bacillus Brevis ATCC 8185 in nitrogen-free environments. Further studies have also demonstrated that tyrocidine, and the properties peculiar to it, are, alone, responsible for the induction of sporulation under identical conditions, since neither analogs of tyrocidine nor its component amino acids could cause sporulation to occur.[2,3]

Tyrocidine has also been demonstrated to inhibit the synthesis of RNA, both *in vivo* and *in vitro*. In addition, it is known to interact *in vitro* with DNA, forming a complex at its RNA transcription sites.[4] This occurrence is belived to effectively inhibit RNA transcription, preventing its synthesis for a period of two to three hours, beginning four to five hours after tyrocidine addition, although it will not stop RNA synthesis once it has commenced. This interaction of DNA with tyrocidine can be offset by the addition of linear gramicidin, after which time RNA transcription will resume.[3]

The interaction between tyrocidine and DNA was inferred from the results of studies which involved the quenching of tyrocidine fluorescence in the presence of DNA. The fact the fluorescence quenching of tyrocidine is reduced in the presence of gramicidin seems to indicate that the DNA-tyrocidine interaction is nullified in its presence. This occurrence is believed to arise due to a hydrophobic force-sponsored interplay of

gramicidin with tyrocidine.[1,5]

Further research on the tyrocidine-DNA interaction was undertaken by means of studying the hypochromicity of the DNA at 257 nm. The increase in DNA hypochromicity at this wavelength with tyrocidine addition suggests that the absorbance of DNA decreases with increasing tyrocidine concentration. Gramicidin, however, does not bring about DNA hypochromicity, yet causes the DNA-tyrocidine complex to dissociate at lower temperatures than when it is not present. From this, one may infer that gramicidin causes the DNA-tyrocidine complex to dissociate.

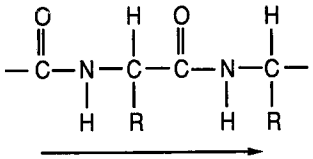
Similar studies with hypochromicity, wherein various base-enriched DNA strains are reacted with tyrocidine, have demonstrated that DNA abundant in cytosine-guanine bases exhibits increased hypochromicity with decreasing tyrocidine concentration. This indicates that cytosine-guanine rich DNA complexes preferentially with tyrocidine over DNA rich in adenine-thymine bases, which demonstrates negligible hypochromicity change.[1] Hence, it has been demonstrated that tyrrocidine binds externally to DNA, albeit by virtue of interactions as of yet unknown.[5] For this reason, discovering the lowest-energy conformations of of both tyrocidine and the complex it forms with DNA shall prove critical to comprehending the nature of their biological interactions.

II. Theory:

In order to gain insight into the structure of the polypeptide tyrocidine and the nature of the study described herein, it first becomes necessary to comprehend the structure of amino acids, the base molecular units of which tyrocidine is constructed. The general form of an amino

acid linkage, or general peptide chain, may be seen in Figure 1.

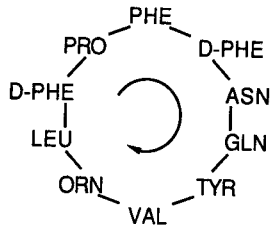
FIGURE 1: A generic amino acid linkage



The backbone of each amino acid residue is composed of an amine group (HN-) bonded to an alpha carbon (-C^{α}-), which is, in turn, bonded to a carbonyl group (-CO). In addition, the alpha carbon is bonded to a hydrogen atom and a side chain (-R) group, which, alone, serves to differentiate each amino acid, except in the case of proline, which has a hydrocarbon ring side chain bonded to both the alpha carbon and the amine nitrogen.

In forming a peptide chain, amino acids are linked from the carbonyl carbon (C') to the amine nitrogen atom, with the arrow of figure 1 indicating the direction of the amino acid linkages. Tyrocidine, then, is a cyclic decapeptide formed from the amino acids phenylalanine (PHE) and its stereoisomer (D-PHE), asparagine (ASN), glutamine (GLN), tyrosine (TYR), valine (VAL), ornithine (ORN), and leucine (LEU). Its amino acid sequence may be seen in Figure 2, where the arrow indicates the direction of its amino acid linkages.

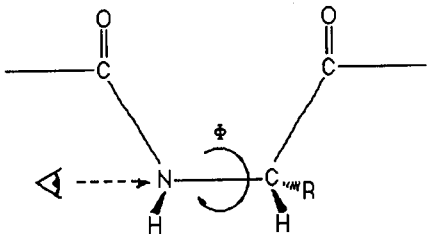
FIGURE2: The structure of tyrocidine



The method by which one quantifies the orientations of atoms relative to one another in space becomes a critical concept when one undertakes a study of molecular conformations. A particularly useful method of bringing order to the myriad of conformations a molecule can assume involves the concept of the dihedral angle. Dihedral angles are discerned by looking down the axis of a bond about which rotation can occur and noting the rotation about the bond, in degrees, relative to the other bonds surrounding it. This notion is illustrated in Figure 3, where an observer is seen envisioning the dihedral angle Φ about a peptide N-C^{α} bond.

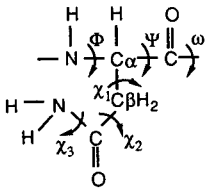
From the foregoing definition, it should be obvious that three bonds exist along the backbone of a peptide to which dihedral angles may be assigned, and that more such bonds may exist in its side chain, depending upon the structure of the R group in question. In the nomenclature of peptides, each dihedral angle in an amino acid is given a different designation, using characters from the Greek alphabet, as follows:

FIGURE3: Determination of the dihedral angle Φ in a peptide chain



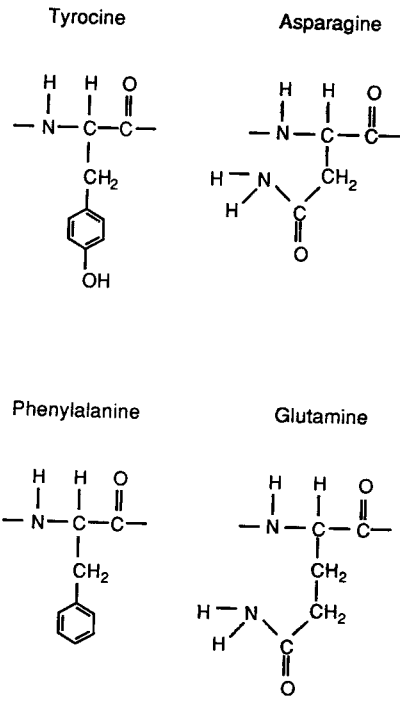
(a) the N-C^{α} bonded dihedral angle is termed Φ; (b) the C^{α}-C' dihedral angle is designated Ψ; (c) the C'-N dihedral angle is termed ω; and (d) any dihedral angles present on the side chain of the amino acid are designated χ, and numbered in increasing order from the beta, or side chain connecting, carbon (C^{β}) outward. The dihedral angles present in the amino acid asparagine may be seen in Figure 4.

FIGURE4: The set of dihedral angles found in asparagine



The structural formulas of the four fundamental amino acids of tyrocidine with which this project was concerned may be seen below in Figure 5.[5]

FIGURE 5: Structural formulas of amino acids present in tyrosine



III. Experimental:

Dihedral angles perform a fundamental role in determining the conformational energy which a certain molecule is able to possess at a particular moment in time. Since the most preferable conformation can attain in a specified state is, by definition, the conformation with the lowest total energy, it is, therefore, feasible to design a computer program which calculates total conformational energy as a function of varying dihedral angles. The program employed in pursuing this research was ECEPP (Empirical Conformational Energy Program for Peptides), and did, indeed, function in just such a manner. ECEPP calculates total conformational energy (E_{tot}) by virtue of calculating the following potential energy functions and summing them: (a) the electrostatic energy (E_{es}); (b) nonbonded energy (E_{nb}); (c) hydrogen bonded energy (E_{hb}); (d) general torsion energy (E_{tor}); (e) cystine bridge torsional energy (E_{cystr}); and (f) a loop-closing potential for S-S bond energy (E_{loop}).[7] An equation for the total conformational energy of tyrocidine may be written thus:

(1) $$E_{tot} = E_{es} + E_{nb} + E_{hb} + E_{tor}$$

due to the fact that there are no cystine peptides in tyrocidine, rendering the last two potential energy functions unnecessary for consideration in this study.

The approach utilized in calculating electrostatic energies with ECEPP involves partial charges obtained using the CNDO/2 (Complete Neglect of Differential Overlap) molecular orbital method. The CNDO/2 theory operates upon all valence electrons, while applying zero differential overlap and explicitly considering electron interactions.

Employment of the CNDO/2 method yields overlap normalized partial charges for every atom in the amino acid residues studied. Although the usefulness of the partial atomic charges obtained by this treatment have been brought under question, the method remains a popular one, due mainly to its ability to prcduce these parameters while retaining a set molecular geometry.[8]

Calculation of the atomic charges was carried out by virtue of studying numerous molecular conformations, in order to combat conformation-peculiar steric interactions and, thus, to give assurance that the resulting values can typify a wide range of molecular geometries. In applying the method, the total charge of a given residue is assigned a value of zero, with the charges on each of the residue backbone (N, C', H, C^{α}, O) atoms assigned the same value for a particular non-proline peptide in the molecule. The determination of atomic charges then proceeds for each residue as peptide backbone and side chain dihedral angles are varied, after which time the charges are averaged over a set of conformations and rounded off to dispel small differences.The calculation of conformational electrostatic energy U_{el} (denoted E_{es} in ECEPP) utilizes the atomic charges of an atom pair, q_i and q_j, in the formula:

(2) $$U_{el}(r_{ij}) = (332.0q_iq_j)/(Dr_{ij}),$$

where r_{ij} is the distance between interacting atoms, D is the 'effective dielectric constant' of the system (assigned a value of 2 in all computations), and 332.0 is a conversion factor which serves to yield values of U_{el} in units of Kcal/mol. The only variable in the formula is r_{ij}, due to the fact that it is the sole term which is dependant upon the

dihedral angles obtained by a particular conformation.[8]

As important as electrostatic energy is in determining the total conformational energy possessed by a molecule, it only dominates in areas about atoms which lie within three bond lengths. When two atoms are separated by at least three bonds, or when hydrogen bonding is present in a molecule, the nonbonding repulsion and dispersion forces begin to dominate in effect, and so must be computed. When studying the multi-atom forms of polypeptides, then, it becomes most essential to consider any interactions which might occur between the various sections of these large, cumbersome molecules. Indeed, in molecules such as peptides, atoms may behave as independent bodies relative to one another, even bending around and upon themselves, owing to the large numbers of rotational degrees of freedom between these interacting atoms.[8]

Calculation of the nonbonded repulsion and dispersion attraction energies, U_{NB} (or E_{nb} in ECEPP) is carried out by utilizing a Lennard-Jones 6-12 potential, which has proved to yield results more valid than older 'hard-sphere' potentials. The method initially used was later modified so as to better compensate for vibrational contributions in order to better reflect the results predicted for Hartree-Fock and Thomas-Fermi-Dirac repulsion potentials. The equation by which the U_{nb} present between two atoms may be calculated is:

$$U_{NB}(r_{ij}) = (FA^{kl})/(r_{ij}^{12}) - (C^{kl})/(r_{ij}^{6}) \quad (3)$$

where r_{ij} is the distance between interacting atoms, and C^{kl} is a factor resulting from the investigation of interatomic dispersion forces by the Slater-Kirkwood method. The A^{kl} term in the equation is the repulsive

coefficient as obtained from crystal computations. Investigation of repulsive force constants yielded the value of the term F, which is 0.5 for 1-4 type interactions and 1.0 for all others.[8]

Hydrogen bonding is an interatomic phenomenon wherein a hydrogen atom acts to form a link between two strongly electronegative atoms, most commonly F, O, or N.[9] It should come as no surprise, then, to learn that hydrogen bonding can occur in peptides, involving amine nitrogens and carbonyl carbons, as well as any such atoms which may reside on side chains. Hydrogen-bond energy, U_{HB} (E_{hb} in ECEPP), is calculated by use of the following equation:

$$(4) \qquad U_{HB}(r_{H\text{-}X}) = (A'_{H\text{-}X})/(r_{H\text{-}X}^{12}) - (B_{H\text{-}X})/(r_{H\text{-}X}^{10})$$

where $r_{H\text{-}X}$ represents the distance between the interacting atoms. The terms $A'_{H\text{-}X}$ and $B_{H\text{-}X}$ are coefficients which specifically apply to different combinations of hydrogen-bonding atoms.[8]

Experimental studies have discovered that barriers to molecular rotation exist about peptide backbone and side chain bonds in certain peptides. Although the previously defined energy parameters have been found to invoke some degree of these rotational barriers, a distinct function of general torsion energy has been formulated in order to account for these occurrences. The elucidation of such a function was impeded by the absence of experimental barrier data for the dihedral angles Φ and Ψ, as diffraction studies have only been performed for the angle ω. The equation by which torsional energy, U_{TOR} (or E_{tor} in ECEPP), is calculated

may be seen to be:

(5) $$U_{TOR}(\theta) = (U_0/2)(1 \pm \cos n\theta),$$

where U_0 is the n-fold barrier height, defined to be the discrepancy between the computed interaction energy and the observed rotational energy.[8]

With a discription of the program's method of energy calculation now in place, it seems that a discussion of the methods by which peptide conformational data is entered into the program to be processed toward an energy minimum would be the next sensible step. The process, then, by which the eventual calculation of the lowest energy conformation of a specific polypeptideis achieved involves a progressive 'building up' of the desired molecule from its component amino acids. A set of lowest energy conformations has been determined by Vasquez et. al. for each of the 20 naturally occurring amino acid residues by using ECEPP.[10] Each set of conformations (known as a Single Residue Minima, or SRM), which is represented in terms of molecular dihedral angles, may be linked together in any order in the computer's memory, which contains a specific representation of each amino acid structure, as differentiated by their side chains.

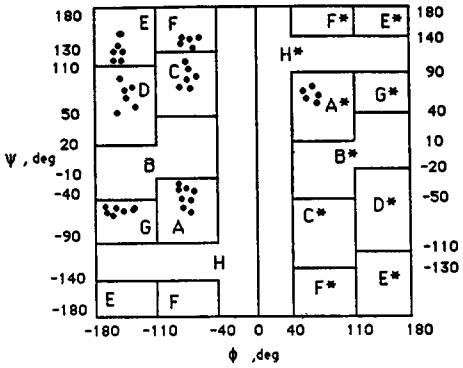
For purposes of facilitating the rate at which calculations are performed by the program, several theoretical assumptions are made. The first of these is inherent to the structure of the ECEPP. As was previously noted, a fixed set of bond lengths and bond angles was selected from crystal data and constrained to remain unchanged during energy calculations, since X-ray crystallographic studies show very little change

between peptides. This one operation greatly simplifies the energy calculations, as a comparatively small number of variables now need to be operated upon. In addition, the assumption seems to be an acceptable one, as comparative studies have shown only moderate discrepancies between results carried out by utilizing, and disregarding, the assumption.[8]

Another assumption which has found wide use in conformational energy studies is to fix the value of the dihedral angle ω at 180^{o} for all SRM, since analyses of various non-proline peptides show virtually no change in ω from 180^{o} for their lowest energy conformations.[8] Hence, the only variables utilized by the program ECEPP are the peptide backbone dihedral angles Φ and Ψ, and whatever χ angles exist on its side chain. Since these angles are the only variables which need to be altered as the minimum energy conformation is sought, it would seem sensible to examine the area wherein these minima might be found in order to bring about the elimination of any unfavorable conformations which might be found, if such a technique is possible.

A popular method by which the conformational space of a set of SRM may be depicted is by plotting the values of SRM dihedral angles versus one another in order to highlight regions in which physical properties (such as conformational energies) are similar. Figure 6, below, illustrates the Φ-Ψ conformational space map of ASN. The nomenclature involved in naming the regions reads as follows: A is the region which contains the right-handed α-helix; B is the bridge region; C contains the C_7^{eq} hydrogen-bond ring; E possesses the extended conformations; H is the high-energy region; and D, F, and G were so named in order to preserve continuity. The astrices on the right-hand side labels denote the fact that

FIGURE 6:[11] Φ-Ψ conformational space map of ASN



the right and left sides are inverse mirror images.[12] One may conclude that two conformations have similar Φ and Ψ values if those conformations are labeled with the same conformational space designations; thereafter, one may undertake additional analyses to determine if one conformation can be eliminated.

With regard to the designation of χ dihedral angles in a set of SRM, if a dihedral angle χ_n has a value of $30^o < \chi_n < 90^o$, it is termed 'gauche +' (G+); if $-30^o < \chi_n < -90^o$, the angle is termed 'gauche -' (G-). A dihedral angle χ_n is, however, termed 'trans' (T) if it has a value $-150^o < \chi_n < 150^o$. By convention, if the two χ_n lables are identical for a given conformation, the two dihedral angles may be regarded as similar.

If, for two given SRM conformations, the preceeding two criteria are

met, a final test may be employed in order to decide whether one of the conformations can be discarded. In this test, if all dihedral angles Φ, Ψ, and χ_n in the two conformations are found to be equal to within 30^o, then either of them, but not both, may be discarded from the SRM list. This three-step method is the final assumption which the operator may employ in order to increase the program efficiency.

Once the smallest set of each residue's dihedral angles have been isolated, they are combined such that all conformations of the first listed residue are 'mixed' with every conformation of the second listed residue in the order in which they occur in the tyrocidine peptide chain. For an illustration of this process, see Table 1.

TABLE 1: Illustration of the ECEPP conformational mixing process

	Input	Output
Peptide 1, SRM:	A	AD
	B	AE
	C	BD
		BE
Peptide 2, SRM:	D	CD
	E	CE

Finally, after the mixing is completed, the resulting polypeptide is treated as if it were linear and each end has a group attached to it in order to 'cap off the bonds' and complete the molecule. The two end groups employed by the program are an amino-$COCH_3$ and a carboxyl-$NHCH_3$, which fit on the 'front' and the 'back' of the polypeptide, respectively.

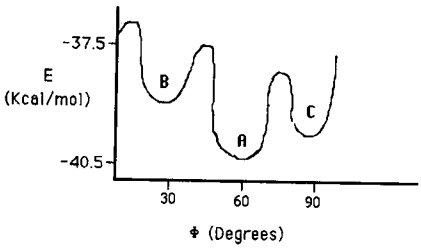
Once the molecule is constructed (both as input data and as

represented in the program), ECEPP calculates E_{tot}, as previously described, for the first conformation in the input list. Following this, the subroutine MINOP of ECEPP changes the value of each dihedral angle by 0.001^{o}, computes E_{tot} for the new conformation, and discards whichever of the two conformations has the larger energy (and its E_{tot}). This operation, called an 'iteration', can be carried out a controllable number of times for each conformation before moving on to the next. Once the specified number of iterations is carried out for each conformation in the list, the resulting data, which consists of the lowest energy conformations calculated from the input conformations and their energies, is saved to a file where it may be examined later. The data desired as output from this project are the conformations (and corresponding energies) which have been processed through 50 iterations and ordered from lowest energy to highest. Conformations which succeed in being minimized through 50 iterations and possess conformational energies within a 3 Kcal/mol range of the lowest energy species are retained for use in further computations. However, any conformation in the final list which has a minimum energy within 0.1 Kcal/mol of another and has all dihedral angles within 3^{o} of another may be eliminated as well, since experience has shown that such small conformational differences will produce nearly identical results under further minimization.

A 50-iteration standard of computation has been adopted since it has proven to be, roughly, the smallest number of iterations which will take a conformation sufficiently near its true energy minimum so that further iterations will only produce negligible minimization (typically a value of $E \leq 0.1$ Kcal/mol). Along similar lines, a 3 Kcal/mol range of output data is retained because the possibility exists that, when iterations are performed on conformation sets, a particular conformation

will be minimized toward a local minimum (wells B and C in Figure 7), rather than the true global minimum (well A in Figure 7). If this occurs during the minimization of a dipeptide, whereafter the data is used to minimize a tripeptide with a different global minimum, the conformation will be unable to 'escape' from the well. This complication is referred to as the 'multiple minima problem' and is the reason why a range of low energy values must be retained for further analyses.[13]

FIGURE 7: Energy wells in a peptide for its dihedral angle Φ



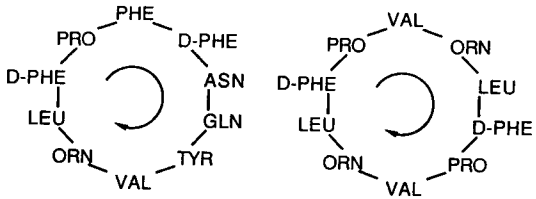
With regard to the actual construction and minimization of the tyrocidine molecule, it was carried out in a stepwise process, wherein SRM were combined to produce dipeptides, the earliest being PHE-DPHE, ASN-GLN, and GLN-TYR, for which it was assumed that a beta bend was located between GLN and TYR[11] (later analyses indicated that a beta bend was more likely present between PRO and DPHE[14]). As a result, the dipeptide GLN-TYR was later recalculated. The output from the dipeptide was combined with the SRM of ASN to yield ASN-GLN-TYR. following the

minimization of the tripeptide, its output was mixed with that of the dipeptide PHE-DPHE to yield the pentapeptide PHE-DPHE-ASN-GLN-TYR, and minimization calculations were again performed. The goal of the research is to achieve a gradual construction of the decapeptide in such a stepwise fashion.

The reason that the tyrocidine molecule is not constructed all at once is due to the astronomically large number of conformations which would be produced (~4.9 $x10^7$ for the pentapeptide mentioned above), thus prohibiting the problem's solution within any reasonable frame of time. Hence, by limiting conformations as one progresses from dipeptide to tripeptide to pentapeptide, large numbers of these conformations will be eradicated in much less time. In addition, fortunate circumstances will, hopefully, further simplify the problem at hand. Half of the amino acid structure of tyrocidine is identical to the cyclic decapeptide gramicidin-S, as can be seen in figure 8.

The lowest energy conformation of gramicidin-S has been calculated previously using ECEPP.[16] It is the hope of our research team that once the lowest energy conformation of the 5 amino acid chain PHE-DPHE-ASN-GLN-TYR has been calculated, that the distance between the ends of PHE and TYR will be on the order of that between the ends of PRO and VAL in gramicidin-S, 20 $\mathring{A}$. If this is the case, it will strongly suggest that the lowest energy conformation of tyrocidine may be obtained by merely joining the two halves of the conformation together.

FIGURE 10: The structures of tyrocidine and gramicidin-S



Tyrocidine Gramicidin-S

IV. Results:

The lowest energy conformations selected from the SRM of ASN, GLN, and TYR (29, 61, and 16 conformations, respectively) for use in this study have been displayed in Appendix A. Initial mixing (as per Table 1) of the SRM of GLN and TYR yielded a set of 976 conformations, which were used as input for the minimization of the GLN-TYR dipeptide. The 88 conformations listed in Appendix B were selected as final output of the computation and underwent mixing with the selected ASN minima to yield a set of 2552 conformations. The resulting tripeptide input data was then minimized to yield a final output of 86 conformations, which may be seen in Appendix C.

In order to create the tyrocidine-specific pentapeptide desired, it was necessary to obtain a set of lowest energy conformations for the dipeptide PHE-DPHE. This set, calculated by another researcher,[15] may be

seen in Appendix D. Once mixed with the tripeptide output, a set of 9718 pentapeptide conformations was created, which, after minimization, yielded a final set of 11 lowest energy conformations, which have been listed in Appendix E. The calculation of the cartesian coordinates corresponding to the three lowest energy conformations of the pentapeptide (as per Appendix E) was carried out by the subroutines GENER, GNAMIN, GNCARB, and GNSIDE of ECEPP. Using these coordinates, the computer program CHEM3D was able to depict these pentapeptide conformations in both space-filling (normal) form and in bond-illustrated form; both types of depictions can be seen in Appendix F.

V. Discussion:

Having calculated a set of lowest energy conformations for the pentapeptide PHE-DPHE-ASN-GLN-TYR, it now becomes desirable to determinine the likelihood of a particular conformation being the one which is sought after. One method which may be used to bring about this end for conformations which differ significantly in energy is statistical analysis. As can be seen from Appendix E, the pertinent lowest energy conformations calculated for the pentapeptide possess values of E_{tot} which are substantially different from one another; hence, a statistical investigation should prove to be of value in this instance.

The statistical method employed in the examination operated in a manner which treated the energy of each conformation as the sole dependent variable. The probability, $P(E_i)$, of the pentapeptide occupying a particular energy, E_i (and, thus, the corresponding conformation), is expressed as a percentage in the following formula:

(6) $$P(E_i) = [e^{-(Ei)/RT}]/Q,$$

where R is the gas constant, 1.987 $x10^{-3}$ Kcal/Kmol, and T is the temperature, taken to be 300K for this study. The symbol Q denotes the canonical partition function, which operates over the range of all 11 pentapeptide energy minima (E_n, n = 1-11) considered. The equation which defines Q may be seen below:

(7) $$Q = \Sigma_n \; e^{-(En)/RT}$$

Equation (7) was used to calculate the probability of existence for each of the 11 lowest energy conformations listed in Appendix E. The conformations (as denoted by their energy minima) and their probabilities may be seen in Table 2.

TABLE 2: Energy minima of the pentapeptide and their percent probabilities of occurring

CONFORMATIONAL ENERGY, Kcal/mol	PERCENTAGE PROBABILITY
-53.841	51.8
-53.244	19.0
-52.742	8.2
-52.466	5.2
-52.368	4.4
-52.306	3.9
-52.223	3.4
-51.853	1.8
-51.501	1.0
-51.349	0.8
-51.144	0.6

As was mentioned previously, the interatomic distance between the PRO and VAL ends of the symmetric pentapeptide in gramicidin-S was found by theoretical studies to be roughly 20 Å. From this, one can infer that the distance between the PHE and TYR ends of the pentapeptide PHE-DPHE-ASN-GLN-TYR should also have a length near that of 20 Å, if a proper joining is to be made between the two pentapeptides. Along these lines, the same ECEPP subroutines which compute the cartesian coordinates to enable depiction of molecular conformations also produce a readout of these parameters. By virtue of consulting the output data, one may gather the cartesian coordinates for the N atom on PHE, (X_N, Y_N, Z_N), and the C' atom on TYR, (X_C, Y_C, Z_C), the two end atoms of the peptide. Using these points, it is possible to calculate the distance between the ends of the pentapeptide, r_{P-T}, by employing the following formula:

$$(8) \qquad r_{P-T} = ((X_C-X_N)^2 + (Y_C-Y_N)^2 + (Z_C-Z_N)^2)^{1/2}$$

Values of r_{P-T} have been calculated for the three lowest energy conformations (as denoted by their energy minima) and can be seen in Table 3, below.

TABLE 3: End-to end distances in the three lowest energy pentapeptide conformations

CONFORMATIONAL ENERGY, Kcal/mol	END-TO-END DISTANCE, Å
-53.841	11.13
-53.244	11.15
-52.742	11.39

Although it was not performed here, another test of validity for a conformation involves analyzing the distances between hydrogen atoms and the nearest oxygen and nitrogen atoms in a peptide in an attempt to locate hydrogen bonds. The notion behind undertaking such an analysis is rooted in the fact that the presence of hydrogen bonds in a conformation will tend to increase its stability. Equation 8, above, may be used to discern whether these corresponding distances are no greater than 2.3 $\mathring{A}$, the maximum length of a hydrogen bond between two appropriate atoms.

Initially, a spirit of optimism prevailed when it was learned that 11 pentapeptide conformations were isolated from a starting field of 9718, as this implied a grand minimization of a very specific set of peptides. The probability of 51.8% obtained for the lowest energy pentapeptide conformation in Table 2 indicates, by its high value, a strong likelihood that this arrangement is correct, since its probability of occurrence is over 2.5 times that of the next most likely candidate. In fact, judging solely by this criterion alone, it is highly unlikely that any conformations other than the three lowest in energy are proper. The values of ~11 $\mathring{A}$ calculated for the end-to-end distances are less encouraging, but need not be terribly upsetting, when one considers that this may infer the presence of a large degree of stability to facilitate such close packing; after all, one can assume that less stability should be lost in 'unraveling' a conformation than in 'bunching it up.' Overall, the results of this study seem quite favorable, and it is my firm belief that good data has been produced with which the project may be successfully taken further.

APPENDIX A

Final SRM Selected for Asparagine*

-161.000	160.000	63.000	99.000	-179.000
-76.000	78.000	-62.000	98.000	180.000
-161.000	145.000	-173.000	-100.000	180.000
-74.000	-33.000	-60.000	98.000	-179.000
-162.000	148.000	-171.000	20.000	179.000
-74.000	134.000	-176.000	-101.000	180.000
-72.000	125.000	-176.000	22.000	179.000
-72.000	-38.000	-179.000	-104.000	180.000
-79.000	80.000	-64.000	-82.000	-179.000
-78.000	79.000	-63.000	-7.000	180.000
-146.000	149.000	-60.000	102.000	180.000
-156.000	39.000	51.000	-88.000	176.000
-167.000	-54.000	177.000	-103.000	180.000
-71.000	148.000	59.000	-80.000	179.000
-72.000	-33.000	-64.000	12.000	180.000
-149.000	35.000	60.000	-18.000	-179.000
-78.000	-23.000	59.000	83.000	177.000
-170.000	-52.000	31.000	77.000	-178.000
-151.000	35.000	56.000	99.000	-179.000
-78.000	157.000	63.000	84.000	177.000
-80.000	70.000	54.000	-56.000	179.000
-79.000	-16.000	180.000	-97.000	-175.000
-72.000	-36.000	-175.000	38.000	178.000
-149.000	-56.000	-66.000	102.000	180.000
54.000	45.000	-54.000	-23.000	-179.000
57.000	43.000	-155.000	90.000	-176.000
-167.000	-53.000	179.000	84.000	-179.000
-167.000	-54.000	180.000	27.000	179.000
54.000	51.000	-168.000	23.000	179.000

*The dihedral angles listed here are in the following order: PHI, PSI, CHI 1, CHI 2, CHI 3.

Final SRM Selected for Glutamine*

-157.000	138.000	-177.000	58.000	-101.000
-79.000	76.000	-65.000	-178.000	100.000
-72.000	134.000	-177.000	59.000	-100.000
-161.000	160.000	57.000	180.000	-100.000
-76.000	-33.000	-67.000	180.000	-99.000
-79.000	76.000	-64.000	-68.000	103.000
-71.000	-40.000	-173.000	175.000	97.000
-80.000	76.000	-66.000	-179.000	-3.000
-70.000	-40.000	-172.000	176.000	7.000
-133.000	151.000	-72.000	-73.000	-75.000
-82.000	76.000	-62.000	-67.000	-77.000
-77.000	82.000	-170.000	178.000	-4.000
-81.000	77.000	-75.000	70.000	-105.000
-78.000	138.000	-66.000	-179.000	100.000
-77.000	-33.000	-73.000	73.000	27.000
-76.000	-35.000	-67.000	-179.000	-8.000
-156.000	135.000	-171.000	175.000	101.000
-80.000	77.000	-65.000	-68.000	-28.000
-73.000	104.000	-177.000	62.000	77.000
-160.000	-56.000	-175.000	176.000	99.000
-80.000	-33.000	-77.000	67.000	73.000
-76.000	-31.000	-65.000	-67.000	104.000
-86.000	144.000	-61.000	-66.000	-77.000
-136.000	151.000	-66.000	-175.000	99.000
-76.000	99.000	-160.000	-73.000	105.000
-76.000	83.000	-171.000	67.000	32.000
-80.000	145.000	-67.000	-69.000	-26.000
-160.000	157.000	71.000	-66.000	-75.000
55.000	46.000	-57.000	-176.000	102.000
-136.000	152.000	-65.000	-175.000	-3.000
-155.000	40.000	53.000	174.000	100.000
-161.000	-54.000	-179.000	63.000	82.000
53.000	49.000	-66.000	74.000	-105.000
-70.000	-41.000	-172.000	65.000	-103.000
-80.000	135.000	-73.000	72.000	28.000
-159.000	-56.000	-174.000	176.000	13.000
-70.000	-44.000	-173.000	-83.000	-37.000
-157.000	133.000	-139.000	-65.000	102.000
54.000	45.000	-59.000	-178.000	-101.000
-155.000	110.000	-159.000	-73.000	106.000
57.000	51.000	-159.000	-177.000	-101.000
-136.000	-59.000	-68.000	-175.000	-97.000
-161.000	161.000	61.000	82.000	39.000
-71.000	-23.000	73.000	-170.000	101.000
-65.000	151.000	72.000	-169.000	100.000
-159.000	-56.000	-173.000	-82.000	-46.000
-76.000	100.000	-162.000	-78.000	-72.000
54.000	45.000	-58.000	-177.000	4.000
-150.000	33.000	39.000	58.000	-98.000
55.000	45.000	-54.000	-62.000	-70.000
-155.000	131.000	-163.000	-78.000	-40.000
57.000	48.000	-158.000	-178.000	-17.000
-157.000	167.000	37.000	59.000	-108.000
53.000	48.000	-67.000	74.000	69.000
-152.000	37.000	56.000	-80.000	-56.000
-65.000	153.000	69.000	97.000	68.000
57.000	47.000	-158.000	71.000	18.000
60.000	79.000	-153.000	-66.000	101.000
-80.000	67.000	54.000	141.000	102.000
-75.000	-18.000	71.000	96.000	-108.000
63.000	174.000	-52.000	-175.000	101.000

*The dihedral angles listed here are in the following order: PHI, PSI, CHI 1, CHI 2, CHI 3.

Final SRM Selected for Tyrocine*

-157.000	162.000	60.000	-90.000
-155.000	152.000	180.000	78.000
-146.000	157.000	-62.000	-77.000
-142.000	35.000	-58.000	-78.000
-75.000	-31.000	-179.000	79.000
-78.000	147.000	-178.000	-100.000
-82.000	73.000	-61.000	-71.000
-79.000	81.000	-177.000	-115.000
-84.000	-24.000	-59.000	-70.000
-162.000	-53.000	170.000	72.000
-143.000	27.000	54.000	94.000
-161.000	-53.000	172.000	-106.000
-150.000	-54.000	-70.000	103.000
-81.000	-20.000	72.000	83.000
48.000	46.000	-51.000	107.000
48.000	47.000	-167.000	-115.000

*The dihedral angles listed here are in the following order: PHI, PSI, CHI 1, CHI 2.

APPENDIXB

Final Dihedral Angles and Energy Values for the Dipeptide GLN-TYR*

```
 -80.892 108.757-179.701  57.712-101.953-136.115  26.388  56.647
 -60.290-0.22585E+02
 -70.506 108.755-179.091  58.132-100.516 -87.718 -23.536 -53.303
 -63.195-0.22493E+02
 -60.460 -36.732-173.294 177.668  -0.092-126.842  36.589 -54.309
 -71.637-0.22143E+02
-156.322 118.820-179.416  58.200-102.916-145.003  30.574 -54.407
 -80.426-0.22143E+02
 -59.964 -35.217-172.987 175.162 101.395-111.560  31.093 -45.039
 -58.798-0.21601E+02
 -76.742  97.690-158.154 -70.088 104.952-138.345  35.982 -59.626
 -59.245-0.21562E+02
 -70.774 -34.376-168.655 179.096  -8.272-139.663 153.925 -60.357
 -66.399-0.21489E+02
 -68.850 116.895-177.546  59.944  63.789 -93.562 157.621 -53.220
 -66.854-0.21438E+02
-156.648 128.164-180.235  56.797-103.244 -91.269 -35.350 -56.927
 -71.235-0.21297E+02
 -71.744 109.785-180.377  56.912-101.902 -78.098 -31.369-178.312
  80.627-0.21237E+02
-157.160 125.726-180.744  56.494-103.798 -86.459 -36.699-178.678
  79.452-0.21104E+02
 -83.131 127.761-176.316  61.385  60.038-135.599 167.894 -56.087
 -62.242-0.21060E+02
 -68.387 -29.118-171.714 168.015  96.832-134.460  34.575 -58.471
 -67.778-0.21009E+02
 -69.986 -29.461 -69.007 178.036-101.284-139.050  35.002 -53.337
 -75.958-0.20840E+02
-153.288 101.854-156.457 -69.111 104.758-145.038  38.232 -56.368
 -77.496-0.20753E+02
-156.014 125.177-178.617  58.314-102.430-150.891  29.671  54.161
  95.842-0.20653E+02
 -79.678  73.569 -64.957-178.122 100.498-143.837  33.719 -57.522
 -70.074-0.20584E+02
 -72.017 108.685-178.955  57.387 -99.946 -83.895 -22.452  70.013
  83.029-0.20575E+02
 -69.922 111.792-179.758  58.420  68.573 -76.144 151.233 182.130
  79.543-0.20540E+02
 -80.283  73.817 -64.943-177.864 100.556 -85.733 -24.487 -53.886
 -60.031-0.20537E+02
 -78.946  77.969 -65.490-178.660 100.404-145.996 158.158 -60.331
 -70.623-0.20530E+02
 -70.109 111.447-179.776  58.398  68.761 -75.861 151.073-178.203
-101.163-0.20519E+02
 -85.624 135.207-176.437  59.382 -98.548-145.453 156.700 -60.363
 -68.839-0.20496E+02
 -74.579 -31.195 -67.548 179.132-101.165-144.579 156.696 -57.055
 -75.124-0.20471E+02
 -66.171 -43.734-176.160 -98.997 -75.021 -86.630 -23.295 -58.655
 -73.515-0.20462E+02
-156.375 137.310-176.160  58.990 -99.290-147.265 156.239 -57.566
 -82.005-0.20339E+02
-156.696 125.343-178.689  56.718-102.623 -92.834 -27.053  70.184
  84.119-0.20334E+02
 -84.504 137.402-177.658  58.147-100.051-146.836 -52.604 -63.656
 110.364-0.20280E+02
 -80.117  73.239 -64.636 -68.215 102.358 -85.751 -25.117 -53.959
 -59.865-0.20249E+02
 -80.276  73.933 -65.158-178.346 100.058 -83.587  71.101 -56.986
 -62.444-0.20247E+02
 -79.510  73.141 -64.540 -68.199 102.311-143.526  32.930 -57.452
 -69.919-0.20211E+02
 -70.451 -29.780 -68.566-180.093  -8.406-138.596  34.886 -53.752
 -76.113-0.20209E+02
-156.680 138.712-176.053  58.765 -99.637-157.389 160.266  57.194
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-77.857 82.923-175.211 58.440 72.520 -90.599 -32.392 -52.417
-56.393-0.20183E+02
-67.387 -21.672 72.251-170.671 97.357 -99.288 11.515 -56.494
-65.082-0.20111E+02
-78.800 79.996-151.323 -62.242 102.535 -88.066 -28.271 -52.595
-57.002-0.20101E+02
-69.602 -39.740-172.743 178.443 97.133-154.002 162.801 56.118
-99.621-0.20099E+02
-64.262 -43.820-175.202 -99.359 -75.927 -88.159 66.974 -59.472
-74.103-0.20094E+02
-73.149 -26.558 -74.587 72.245 25.836-138.199 33.584 -54.023
-76.331-0.20064E+02
-81.904 73.892 -62.038 -66.052 -76.882 -85.635 -23.449 -53.370
118.763-0.20057E+02
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-70.428-0.20036E+02
-65.848 -23.014 72.381-172.466 96.303-101.494 16.754 -58.558
-61.863-0.20028E+02
-103.298 116.218-178.806 57.464-105.296-146.710 27.404 51.366
 90.925-0.20010E+02
-79.865 73.444 -65.186-179.072 -2.340-143.606 33.629 -57.397
-69.859-0.20008E+02
-87.754 132.641 -64.245-178.670 99.793-145.602 158.680 -59.484
-70.112-0.20005E+02
-62.068 -36.370-172.576 64.966-102.675-130.905 37.297 -54.278
-70.373-0.20005E+02
-81.892 73.677 -62.045 -66.094 -76.936 -85.630 -23.501 -53.828
-61.416-0.19994E+02
-74.075 -33.309 -68.114 179.140 -98.964-157.230 162.305 53.932
-97.374-0.19988E+02
-78.776 77.708 -64.557 -67.775 103.128-145.744 158.486 -60.300
-70.482-0.19982E+02
-67.526 126.711-179.046 57.887-100.030 -93.401 67.804 -56.381
-71.805-0.19976E+02
-72.409 98.676-178.645 58.901 74.679 -85.078 68.623 -55.535
-59.923-0.19976E+02
-70.693 -36.487-167.504 177.485 94.379-147.857 156.523 -75.989
-65.273-0.19966E+02
-81.631 73.279 -61.889 -66.099 -77.022-143.505 33.768 -57.190
-70.424-0.19966E+02
-80.434 73.590 -65.240-179.101 -2.058 -85.868 -23.839 -53.865
-60.044-0.19960E+02
-75.187 -31.546 -67.088-179.353 -7.208-144.322 156.854 -57.355
-75.200-0.19926E+02
-81.342 77.588 -62.405 -67.090 -77.711-145.876 157.790 -59.857
-71.341-0.19905E+02
-77.015 85.900 -66.076-177.993 100.628-125.733 24.575 -56.352
-55.667-0.19869E+02
-76.500 83.240-170.276 178.312 -3.387-146.465 159.483 -62.472
-68.719-0.19867E+02
-156.004 138.811-177.384 58.032-100.823-148.160 -52.436 -63.320
 98.511-0.19848E+02
-80.996 73.717 -74.429 69.486-104.611-143.947 33.396 -57.376
-70.563-0.19848E+02
-69.195 -40.183-171.356 180.638   8.636-154.381 162.795 54.881
-100.077-0.19846E+02
-80.402 73.880 -65.318-179.027 -2.649 -83.248 71.313 -56.962
-62.482-0.19829E+02
-78.533 77.726-168.976 179.170 -7.217 -86.576 -22.809 -53.159
-57.885-0.19828E+02
-80.897 73.308 -70.954 73.337 25.808 -85.873 -24.462 -53.676
-60.180-0.19826E+02
-81.242 74.201 -74.649 69.259-104.468 -86.238 -24.815 -53.736
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-59.946-0.19809E+02
-157.400 139.164-177.222 58.119-100.600 -80.815 72.116 -59.789
-71.668-0.19808E+02
-81.333 74.614 -65.400 -70.061 -72.729 -84.810 -24.103 -58.543
113.709-0.19806E+02
-160.248 159.950 61.966 83.220 38.684-145.890 40.705 -57.003
-80.516-0.19803E+02
-70.640 -27.564 -67.618 -69.169 103.615-139.474 35.248 -54.345
-75.086-0.19786E+02
-80.169 73.578 -64.182 -67.628 102.797 -83.316 71.217 -56.986
-62.330-0.19785E+02
-79.122 81.624-153.887 -66.739 102.920 -86.163 73.836 -56.578
-61.238-0.19757E+02
-79.863 74.471 -65.232 -68.031 -26.804-143.556 33.544 -57.884
-69.682-0.19752E+02
-80.628 78.734 -74.685 69.523-104.625-146.128 158.632 -60.352
-71.160-0.19730E+02
-92.038 86.706 -64.663-178.236 100.437-154.610 162.308 61.451
-96.618-0.19712E+02
-71.525 -24.684 -67.510 179.164 -99.538 -79.023 -20.890 -58.387
-70.875-0.19708E+02
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-98.151-0.19707E+02
-81.975 73.437 -62.261 -66.857 -77.373 -83.651 70.902 -56.917
-63.786-0.19706E+02
-91.427 136.080 -60.916 -66.977 -77.810-146.353 158.330 -58.774
-73.461-0.19704E+02
-77.687 76.827-168.575 178.812 -4.288-144.246 34.065 -58.956
-68.753-0.19695E+02
-155.429 39.995 53.360 171.630 97.879-142.784 156.588 -57.373
-70.074-0.19692E+02
-82.351 73.362 -69.677 71.990 27.034 -80.768 -23.433 -54.031
-63.733-0.19668E+02
-78.167 78.880-169.241 178.914 -3.064 -82.999 70.893 -56.618
-60.470-0.19655E+02
-77.749 142.307-174.580 58.517 -98.776-146.209 162.235 66.354
-86.889-0.19637E+02
-80.912 73.692 -70.963 73.275 26.106 -83.196 71.483 -56.882
-62.806-0.19631E+02
-155.022 132.728-171.800 175.495 100.374-147.174 158.980 -57.206
-81.881-0.19629E+02
-129.395 137.907 -69.766 -73.579 -78.293-147.169 158.148 -55.500
-82.656-0.19596E+02
-76.493 -25.053 -77.564 66.823 73.400-138.639 33.311 -54.209
-76.622-0.19585E+02

*The dihedral angles listed here are in the following order: for GLN: PHI, PSI, CHI 1, CHI 2, CHI 3; for TYR: PHI, PSI, CHI 1, CHI 2, and an energy value in Kcal/mol.

APPENDIX C

Final Dihedral Angles and Energy Values for the Tripeptide ASN-GLN-TYR*

-72.627 159.419 62.018 -83.546 178.166 -65.413 112.982-178.797
58.397-100.736 -92.590 -23.679 -56.807 -69.326-0.41974E+02
-162.063 151.375-171.597 -99.451 179.620 -53.835 -41.846-177.564
179.120 -12.309-112.580 38.882 -50.920 -74.905-0.41603E+02
-161.762 151.132-168.100 -98.473 179.439 -57.794 -37.275-174.306
175.197 100.800-108.141 32.528 -44.718 -60.754-0.41471E+02
-68.063 -20.769 59.707 -83.434 179.074 -66.203 -24.605 -73.452
78.343 15.452-117.399 25.043 -50.501 -81.129-0.41438E+02
-163.287 163.741 55.696 89.498-177.751 -69.145 106.733-179.108
57.963-100.312 -86.277 -23.106 -57.169 -71.105-0.41331E+02
-71.426 121.625-176.046 3.093 178.658 -59.123 -34.759-175.422
176.860 99.441-106.248 35.513 -45.884 -61.454-0.41328E+02
-161.121 125.167-176.511 4.294 178.675 -60.187 -35.236-175.415
176.873 99.386-106.410 35.123 -45.731 -62.189-0.41019E+02
-69.417 -27.114 -60.758 96.728-179.392 -60.444 -41.212-177.708
-99.386 -74.187 -86.889 -32.891 -57.733 -73.291-0.40954E+02
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*The dihedral angles listed here are in the following order: for ASN: PHI, PSI, CHI 1, CHI 2, CHI 3; for GLN: PHI, PSI, CHI 1, CHI 2, CHI 3; for TYR: PHI, PSI, CHI 1, CHI 2, and an energy value in Kcal/mol.

APPENDIX D

Final Dihedral Angles for the Dipeptide PHE-DPHE*

-156.460	150.479	176.607	71.133	156.458	-151.439	-179.828	102.048
-63.135	107.613	178.612	73.267	75.982	25.277	178.080	100.876
-63.578	100.583	-178.248	75.378	142.436	-25.734	-52.275	86.429
-93.240	-21.818	-177.480	78.804	159.752	-162.476	-53.640	97.361
-81.884	-43.241	178.658	81.187	137.096	-156.393	56.829	66.073
-75.984	99.178	-176.160	76.735	157.987	-158.949	-60.903	88.642
-156.958	159.808	62.392	96.280	158.582	-151.147	-177.269	101.561
-73.542	147.244	179.147	73.100	156.870	-150.534	-179.183	101.946
-64.176	105.503	178.841	72.263	77.610	21.903	-68.833	96.912
-64.254	101.298	-64.325	110.037	78.624	25.783	178.092	100.711
-86.692	-32.149	-58.678	107.102	144.264	-156.775	60.123	71.898
-158.900	-53.387	169.707	75.479	159.261	-161.521	-54.361	95.814
-155.854	154.332	177.784	79.331	76.669	30.827	177.415	99.130
-156.550	154.602	178.902	68.717	164.700	52.408	-172.314	105.431
-156.464	145.677	58.808	93.306	148.217	-160.504	-68.058	89.608
-69.601	-34.319	179.412	80.859	155.521	-152.280	-179.840	101.794
-156.973	153.972	177.413	79.175	79.637	-147.389	176.637	99.521
-159.288	-55.019	168.238	73.781	143.740	-155.867	56.429	76.956
-71.628	-32.340	179.232	77.835	78.352	-79.215	177.160	114.977
-65.495	97.952	-64.233	109.768	81.797	21.896	-69.044	96.749
-157.111	162.382	61.038	91.002	73.737	32.022	178.793	100.006
-155.430	154.389	-178.925	79.457	82.930	20.353	-68.505	97.055
-156.430	154.033	177.689	79.084	78.979	-80.611	176.786	114.138
-72.305	-30.495	179.510	75.360	77.398	-141.424	178.296	99.577
-71.208	148.981	-179.126	79.653	84.477	15.826	-65.873	97.795
-157.981	162.852	61.084	90.917	76.365	-146.792	177.954	100.445
-149.010	-53.625	-67.274	102.059	159.004	-161.516	-57.147	94.031
-67.978	89.614	-64.059	109.583	142.740	-24.211	-55.547	84.611
-142.797	33.664	-57.218	100.589	146.623	-158.311	60.033	80.181
-81.286	71.713	-60.842	107.940	157.251	-160.268	-58.200	89.308
-77.178	-27.891	-59.913	109.182	155.804	-152.320	-179.676	101.701
-73.734	-27.597	179.527	64.635	75.802	35.670	179.003	99.387
-161.713	-55.218	165.958	70.387	74.628	-89.239	179.105	112.569
-142.966	33.690	-57.021	100.493	155.206	-152.370	-179.853	101.568
-161.460	-54.428	168.552	74.825	153.833	-151.403	-179.779	101.589
-80.871	73.689	-61.488	107.453	147.252	-155.857	59.714	80.800
-70.037	150.705	179.805	80.556	80.448	-75.616	175.962	115.049
-84.654	152.818	-57.923	108.485	146.849	-154.164	60.257	73.971
-148.389	-54.444	-67.640	101.947	144.901	-157.084	55.747	79.569
-157.117	157.810	60.388	94.186	162.229	53.019	-171.611	105.352
-77.399	152.196	-179.830	69.468	164.534	52.348	-172.028	105.553
-156.513	153.118	-178.958	80.249	85.850	-157.418	-68.863	96.821
-80.578	73.423	-60.989	107.965	156.079	-150.548	-179.347	101.424
-75.940	-25.030	-178.479	68.623	83.441	23.098	-69.772	96.631
-152.334	117.598	-177.131	84.404	142.890	-26.840	-63.782	79.301
-76.568	151.879	-179.468	79.872	83.390	-143.860	176.687	98.815
-143.077	35.185	-57.028	100.428	75.217	-147.518	178.352	100.473
-80.164	71.928	-60.817	108.118	72.937	-147.758	178.721	100.582
-78.816	-26.362	-59.512	109.024	76.132	-147.198	178.090	100.337
-157.083	163.168	61.153	91.076	80.274	21.249	-69.090	96.950
-77.875	76.933	-177.231	64.468	72.303	-147.654	178.750	100.597
47.557	55.761	-170.002	64.811	149.089	-155.523	60.512	78.950
-83.525	150.865	-59.241	107.962	156.844	-150.810	-179.376	101.490
-142.723	35.936	-56.836	100.449	73.352	32.873	179.217	99.824
-68.959	-31.393	179.775	80.551	162.882	53.010	-171.317	105.646
-101.838	-1.170	-56.394	104.239	143.810	-27.099	-51.486	87.675
-72.294	-30.919	179.947	75.195	87.782	-155.622	-68.696	96.696
-79.177	-25.525	-59.507	108.941	74.093	31.739	178.872	99.851
-156.512	154.691	60.510	91.788	125.759	-14.990	-57.292	91.037
-79.792	70.900	-60.776	108.262	160.046	52.723	-172.317	104.939
-77.319	77.001	-177.538	64.358	160.578	52.657	-172.494	104.793
-150.044	-54.146	-68.204	102.621	156.132	-151.798	-179.493	101.587
-161.496	-56.108	165.255	53.809	59.408	-153.949	-63.431	98.208
-98.580	-8.607	-175.946	74.576	145.700	-27.455	-49.121	91.592
-139.868	31.323	-56.080	100.386	74.805	23.008	-67.356	97.013

-83.245	71.350	-60.395	107.604	69.255	-157.306	-65.181	98.854
-76.747	-24.379	-59.900	109.304	162.994	52.932	-171.250	105.545
-139.862	31.880	-56.379	100.527	145.945	-28.921	-55.454	82.786
-79.511	-24.697	-59.540	108.652	80.335	21.734	-68.332	97.014
-141.537	32.836	-56.439	100.336	68.645	-156.241	-65.993	97.438
-79.389	77.736	-177.260	64.676	69.677	-157.271	-65.942	98.393
-142.121	34.530	-56.853	100.480	161.609	53.094	-171.841	105.324
-77.435	148.282	-60.206	109.204	79.005	-76.981	176.947	115.412
-79.591	-24.587	-59.038	108.948	77.654	-157.172	-67.454	97.392
-150.087	-54.160	-68.432	102.642	76.029	-147.023	178.228	100.371
-150.532	-54.193	-68.715	102.850	73.582	32.011	179.052	99.884
-59.442	-33.715	177.272	72.389	-50.600	-38.058	165.586	114.685
-87.941	150.595	-58.657	107.022	76.418	-144.707	178.340	100.069
-161.934	-54.263	168.960	74.907	160.033	53.366	-171.963	105.432
53.314	34.063	-162.957	66.928	59.806	36.033	-178.313	100.164
-76.890	82.172	-176.329	68.253	165.820	43.883	-55.515	83.968
-161.944	-50.470	171.266	50.991	147.360	-26.954	-47.036	96.320
-74.996	93.132	178.863	66.720	-49.579	-44.721	166.165	114.902
49.072	45.861	-167.132	64.452	158.266	-160.182	-57.539	89.945
55.360	33.601	-161.235	67.586	62.583	28.897	-70.735	95.629
-147.941	-53.550	-67.089	101.990	141.696	-24.988	-49.049	94.096
-163.826	-50.139	172.160	45.254	95.649	26.386	-68.017	95.439
-86.572	147.287	-58.995	107.191	161.745	52.960	-171.883	105.287
-150.345	-54.030	-67.957	102.793	78.833	22.242	-68.305	96.956
-98.464	-48.186	-60.735	102.059	133.681	-21.049	-61.061	84.984
49.329	44.577	-166.685	64.908	155.567	-151.014	-179.688	101.497
-150.234	-54.206	-68.331	102.708	161.637	53.150	-171.672	105.425
-72.784	137.590	-178.957	60.077	-47.185	-62.454	171.439	115.717
-62.308	-32.396	-63.178	110.801	-51.199	-37.859	164.319	114.067
-100.150	-2.653	-56.928	103.684	165.559	43.929	-57.193	84.123
-79.802	70.370	-60.941	108.281	163.908	44.255	-56.415	82.996
-149.944	-54.082	-67.768	102.664	72.728	-156.552	-67.352	97.326
48.252	48.525	-168.068	64.552	79.909	-74.894	176.573	115.802
-98.252	-12.887	-176.304	75.903	166.623	43.538	-57.484	85.501
50.133	38.525	-165.291	65.459	144.104	-32.118	-54.837	82.438
-139.896	31.355	-56.481	100.587	164.400	44.310	-56.964	82.933
-79.662	73.712	-61.188	108.106	-49.261	-46.772	166.708	115.108
48.651	50.648	-168.155	64.511	84.813	-138.795	177.992	99.194
-142.729	35.285	-56.997	100.492	-49.288	-46.572	166.757	115.144
-161.740	-53.413	169.348	62.316	-48.974	-46.750	168.013	115.676
-159.753	-51.559	171.028	76.062	169.105	42.626	-56.851	88.164
-82.196	144.547	-59.495	108.210	-49.571	-45.415	166.433	115.035
-149.623	-52.803	-66.719	102.455	168.198	42.897	-60.151	87.120
49.518	44.222	-166.495	64.978	161.330	52.920	-172.128	105.136
-156.121	144.205	62.497	94.170	141.251	44.980	-62.828	83.568
-149.899	-54.190	-68.388	102.565	-49.535	-45.323	166.385	115.032
47.973	52.221	-169.582	64.107	-49.091	-44.877	166.715	115.159
48.953	46.798	-167.464	64.197	165.606	44.002	-56.514	83.689

*The dihedral angles listed here are in the following order: for PHE: PHI, PSI, CHI 1, CHI 2; for DPHE: PHI, PSI, CHI 1, CHI 2.

APPENDIXE

Final Dihedral Angles and Energy Values for the Pentapeptide PHE-DPHE-ASN-GLN-TYR*

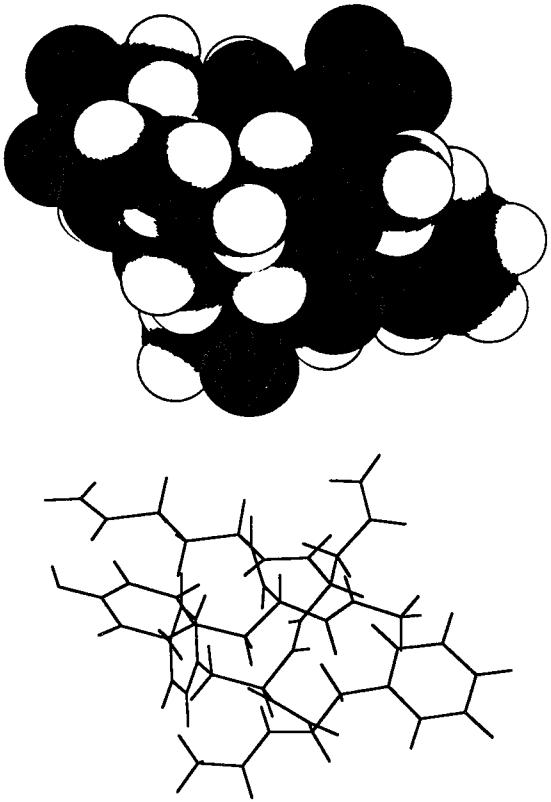
```
-71.356 107.125 179.688  73.586  80.556  19.970 183.831 101.648
-80.985 147.689-178.614  81.192 180.437 -65.501 104.263-178.482
 57.664-100.443 -88.196 -19.991 -48.342 -57.316-0.53841E+02
-72.125 104.724 -62.778 109.308  82.542  19.578 183.956 101.871
-80.299 147.461-178.941  81.154 180.436 -65.457 104.246-178.545
 57.664-100.437 -87.815 -20.319 -48.313 -57.367-0.53244E+02
-81.060 104.674-177.064  76.182 138.809 -23.212 -54.394  88.567
-72.953 137.982-176.852  84.481 179.769 -72.121 115.613-178.595
 57.496-101.697 -90.373 -26.545 -46.031 -54.360-0.52742E+02
-71.209 107.993 179.654  73.823  79.539  21.738 183.633 102.034
-82.599 149.405-175.679-103.500 180.205 -66.771 102.601-178.534
 57.546-100.449 -86.746 -19.717 -48.380 -56.983-0.52466E+02
-59.566 141.436 176.276  74.233 158.425-153.952-176.724 108.062
-168.589 -52.504 178.003-102.140 179.975 -83.556  69.461 -64.733
-70.424 -73.812 -78.826 -27.222 -61.564 -71.159-0.52368E+02
-59.539 -39.478 -66.143 113.460 -54.216 -38.048 163.378 113.639
-79.952 -38.818 -56.153  97.019-179.320 -55.024 -40.704-169.820
182.848 -10.922-112.672  33.078 -46.715 -53.429-0.52306E+02
-59.421 142.138 176.366  74.042 158.660-153.765-176.696 108.118
-168.552 -52.406 177.576-102.397 180.010 -83.429  70.191 -64.653
-70.704 -74.191 -79.855  73.769 -61.952 -71.208-0.52223E+02
-71.995 105.358 -62.784 109.364  81.812  21.281 183.647 102.087
-81.870 149.237-176.030-103.639 180.221 -66.732 102.518-178.554
 57.486-100.480 -86.277 -20.012 -48.358 -56.970-0.51853E+02
-77.550  93.068 -62.797 108.592 139.747 -22.051 -57.265  87.086
-72.998 138.857-176.509  83.654 179.476 -73.538 118.265-178.826
 57.071-102.307 -89.698 -29.204 -45.560 -49.697-0.51501E+02
-80.685 107.405-177.119  77.340 136.106 -21.313 -54.898  89.241
-72.975 138.236-183.619-104.826 180.554 -73.721 111.245-178.643
 57.432-101.773 -87.303 -25.168 -45.307 -54.809-0.51349E+02
-157.595 139.472  61.130  94.770  56.973-132.536 184.735  99.047
-81.558 -19.079 -58.177  99.963-179.226 -81.090  89.024-177.720
 56.108 -98.426 -90.989  -9.111 -55.743 -65.213-0.51144E+02
```

*The dihedral angles listed here are in the following order: for PHE: PHI, PSI, CHI 1, CHI 2; for DPHE: PHI, PSI, CHI 1, CHI 2; for ASN: PHI, PSI, CHI 1, CHI 2, CHI 3; for GLN: PHI, PSI, CHI 1, CHI 2, CHI 3; for TYR: PHI, PSI, CHI 1, CHI 2, and an energy value in Kcal/mol.

APPENDIX F

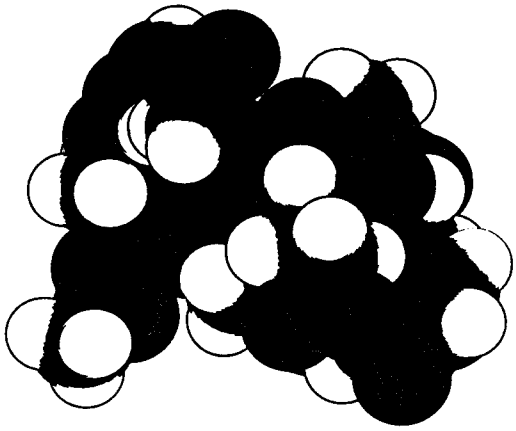
I. Structure of the Pentapeptide

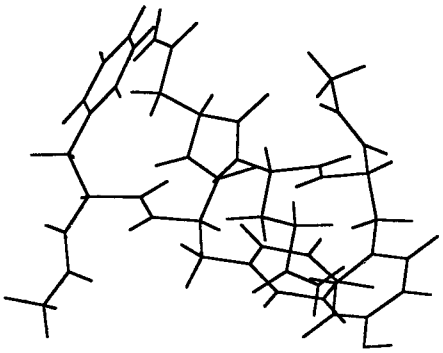
PHE-DPHE-ASN-GLN-TYR with E_{tot} = -53.841 Kcal/mol



II. Structure of the Pentapeptide

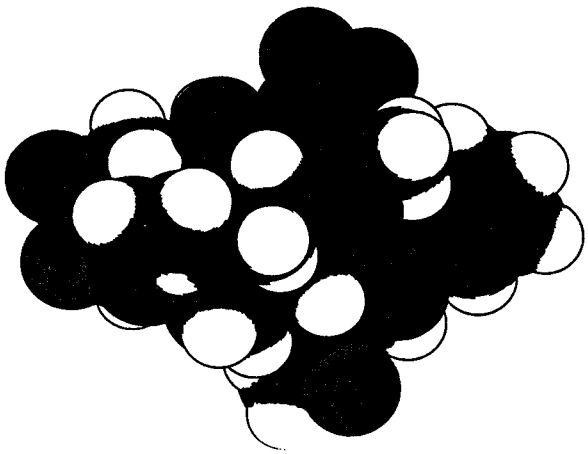
PHE-DPHE-ASN-GLN-TYR with E_{tot} = -53.244 Kcal/mol

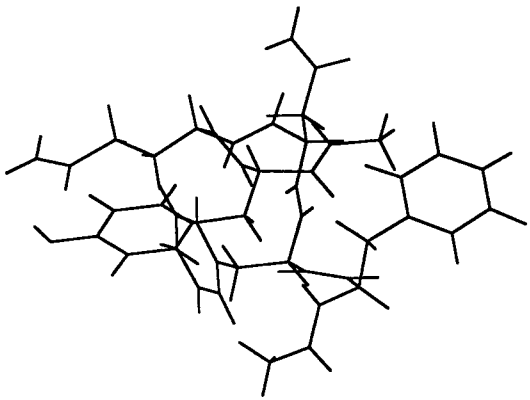




III. Structure of the Pentapeptide

PHE-DPHE-ASN-GLN-TYR with E_{tot} = -52.742 Kcal/mol





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