perform a 100 ps molecular dynamics simulation at 900K. 100 conformations of the peptide were taken from the dynamics trajectory for every 1 ps. Rms graphs were used to classify the 100 minimized conformations into five conformations families.
The five conformation families were compared with the conformation from 2D nmr studies. RMS values obtained are between 2.0A and 4.0A. By studying the representative conformations of each family on graphics, the conformation group with the least rms value was found similar to the nmr structure. Conformational search by combining distance geometry and molecular dynamics has not been seen in literature. The primary purpose of this study was to obtain the model of a de novo peptide or protein.In future, more constraints from theoretical design and motif alignment will be added in distance geometry. Moreover, criteria will be developed to indicate the preferable conformation.

PS-05.01.14 ELECTROSTATIC EFFECTS IN PROTEIN: COMPARISON OF TK METHOD AND FDPB METHOD. **By Yanli Wang*, Luhua Lai & Xiaojie Xu, Department of Chemistry , Peking University, Beijing, China**

Two approaches for calculating electrostatic effects in proteins are compared. Both TK methods which is based on Tanford-Kirkwood theory and FDPB method which is based on finite-difference Poisson-Boltzmann equation are applied to calculate the pKa values of the charged residues. All of the results are compared with the experimental data. It is shown that TK method gives better results than FDPB method, especially for the residues near the surface of the molecule, and RMS between calculated data and experimental data are 2.55 and 0.99 respectively. It is found that the results from TK method are closely related to the accessibility of a residue. For the residues with accessibility higher than 0.67, the absolute values of difference between experiment and calculation are below 0.50, on the other hand , for most of the rest residues , the difference values are above 0.90. It is interesting that the two approaches compensate each other, and this phenomenon is also related to the accessibilities of the charged residues. For deeply buried residues, the calculated results from FDPB method are more accurate than those from TK method, whereas for residues near the surface of the molecule, TK method can give more accurate results than FDPB method. This can been seen from the calculated results for the residues GLU_35, ASP_8, ASP_52, LYS_97. The possible reasons are discussed, as well as the virtues , limitations of the two models.

PS-05.01.15 THE DESIGN OF TEMPLATE ASSEMBLED PARALLEL FOUR-HELIX BUNDLE PROTEIN. by Yu Luo*, Zhenwei Miao, Luhua Lai, Xiaojie Xu, Department of Chemistry, Peking University, Beijing 100871, CHINA

The packing of the hydrophobic surfaces of the four helices forming the parallel four-helix bundle were investigated using crude energy function: $E=(R/R0)^9 - 1.5*(R/R0)^6$. Based on the crystal structure of a leucine zipper protein-GCN4, 4-fold symmetry was proposed for this bundle protein. Monte Carlo technique was used to obtain the optimal orientations and displacements of the four helices with respect to the main axis of the bundle.
Single Helices of standard alpha-helix geometry were built using QUANTA/CHARMm. Up to 10 heptad repeat sequences were devised with hydrophobic side chains at position 1,4 and 5. The most frequently occurring rotamers of side chains were used. The hydrophilic surfaces were approximated by alanines. Inspection of the optimal geometry of the bundles showed that isoleucine and valine at position 1 and 5 were less favorable than leucine. Taken also into account the electrostatic interactions, we designed three 16-residue helix sequences and one contrast sequence. One of the three helix sequences were synthesized and high helicity observed.

PS-05.01.16 CONSTRAINT PEPTIDE CONFORMATIONAL ANALYSIS BY MONTE CARLO SIMULATED ANNEALING. by Leyu Wang*, Qiaolin Deng, Luhua Lai, Yuzhen Han, Xiaojie Xu, Department of Chemistry, Peking University, Beijing 100871, CHINA

Distance geometry and molecular dynamics method are currently employed in determining molecular structures with inter-atomic distances from NMR NOESY experiment. Because of the flexibility of peptide, distances obtained from NMR are usually not sufficient to confine its structure. Both distance geometry and molecular dynamics method will bias in the conformational space at this circumstance. Constraint Monte Carlo simulated annealing was established to solve this problem.
Distance constraints were included into the ECEPP force field by introducing an energy term of $E'=K(R-R0)^2$. Monte Carlo simulated annealing was performed in dihedral angle space. Conformational analysis on a pentapeptide with eight inter-atomic distances was carried out as a test. The resulting conformations agree well with experimental data.

