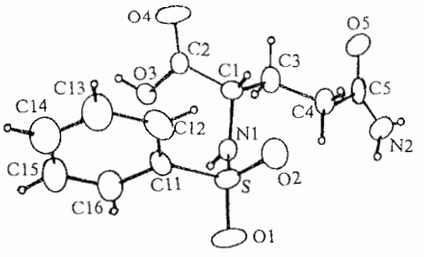

Table 2. Atomic Coordinates and thermal parameters

Atom	x	y	z	B_{eq}(Å^2)
S	0.8620(1)	0.44883(4)	0.46625(4)	2.405(9)
O(1)	1.1268(4)	0.4436(2)	0.4542(1)	3.56(4)
O(2)	0.7031(4)	0.3836(1)	0.4294(1)	3.34(4)
O(3)	0.6549(4)	0.5735(1)	0.6627(1)	3.77(4)
O(4)	0.2590(4)	0.5334(2)	0.6489(1)	3.91(5)
O(5)	0.4541(4)	0.1992(1)	0.7448(1)	3.61(4)
N(1)	0.8226(4)	0.4434(1)	0.5639(1)	2.09(4)
N(2)	0.8366(6)	0.1533(2)	0.7097(2)	3.58(5)
C(1)	0.5734(5)	0.4352(2)	0.5993(2)	2.13(4)
C(2)	0.4804(6)	0.5204(2)	0.6385(2)	2.56(5)
C(3)	0.5714(6)	0.3634(2)	0.6660(2)	2.85(5)
C(4)	0.6466(8)	0.2728(2)	0.6326(2)	3.53(6)
C(5)	0.6411(7)	0.2046(2)	0.6999(2)	2.90(5)
C(11)	0.7621(5)	0.5546(2)	0.4323(2)	2.71(5)
C(12)	0.5520(6)	0.5628(2)	0.3840(2)	3.73(6)
C(13)	0.4798(8)	0.6473(3)	0.3586(2)	4.62(8)
C(14)	0.6122(9)	0.7200(2)	0.3823(2)	4.66(8)
C(15)	0.8187(9)	0.7112(2)	0.4295(2)	4.79(9)
C(16)	0.8962(7)	0.6282(2)	0.4554(2)	4.00(7)

PS-04.04.07 HYDROGEN BONDING PATTERNS IN X-RAY DIFFRACTION STUDIES OF NEUROPEPTIDES, Judith. L. Flippen-Anderson and C. George and J. Deschamps, Laboratory for the Structure of Matter, Naval Research Laboratory, Washington, D. C. 20375-5341, USA

Hydrogen bonding is arguably the most important intra- and intermolecular cohesive force at work in determining the overall geometry, as well as the mode of recognition and association, of biological molecules. Polypeptides exhibit the same types of hydrogen bonding found in proteins: backbone - backbone, backbone - side-chain, side-chain - side chain, water - backbone, water - side-chain, and water-water. The X-Ray structures studied to date on Enkephalin and its analogs have contained from 0.5 to 6 co-crystallized water molecules per peptide molecule. The water molecules are an integral part of the overall peptide structure in that they not only fill structural cavities but they stabilize the geometry of the peptide itself. In fact, no unprotected neuropeptides have been crystallized without included solvent molecules, and there are even common patterns of solvation in their structures. In addition, some of our new structures have been found to contain internal clusters of water molecules which hydrogen-bond extensively within the cluster but have either minimal or only van der Waals interactions with the peptide molecules. While extensive studies have been performed on the hydrogen bonding patterns in nucleic acids and proteins few comparable studies have been made on linear and cyclic peptides. We have begun to compile this important information to aid in understanding the connection between molecular structure and biological activity in neuropeptides. Supported in part by ONR and NIDA.

04.05 – Conformation Analysis

PS-04.05.01 STRUCTURAL CHARACTERIZATION OF TWO POTENT ANTICONVULSANT 1,5-SUBSTITUTED-3-PYRAZOLIDONE COMPOUNDS. By Qing-chuan Yang*, Hui-juan Xu, Lu-hua Lai, You-qi Tang, Department of Chemistry, Peking university, Beijing 100871, China

Since 1-Alkyl-3-pyrazolidone was reported to be an inhibitor of γ-aminobutyrate-transaminase(White, H.J. et al.,J. Neurochem, 1982, 39: 271) , the 3 - pyrazolidone was expected to have anticonvulsant activity. 46 of 3 - pyrazolidone compounds with different substituents were studied (Lei, X. P. et al. , Acta Pharmaceutica Sinica, 1990, 25 : 684) . The pharmacological experiments showed that the anticonvulsant activity of 3 -pyrazolidones with a butyl group at 1-position of the ring were more potent.

The structural characterizations of 1-butyl-5-(p- fluophenyl) -3 -pyrazolidone (I) and 1-propyl-5-(p-methylphenyl))-3-pyrazolidone (II) were revealed by single-crystal X-ray diffraction methods.

Crystal data:

Compound I, $C_{13}H_{17}N_2OF$, triclinic, space group P $\bar{1}$, a 8.831(4), b 11.737(5), c 14.001(5) Å , α 113.19(3), β 91.77(3), γ 97.48(3)° , V 1317.2(9) Å^3 , Z=4.

Compound II, $C_{13}H_{18}N_2O$, monoclinic, space group P $2_1/c$, a 13.838(6), b 8.186(1), c 11.291(2) Å , β 104.52(3)° , V 1238.2(6) Å^3 , Z=4.

The conformations of the five membered rings of the two compounds are near to half-chair. The N(1) atoms at 1-position of the ring are sp^3-hybridized and the N(2) atoms at 2-position of the ring are sp^2-hybridized. The lone pairs of electrons on N(1) atom are clearly protophilic. There are conjugated systems consisted of carbonyl group and N(2) atom in the five membered rings. The C- N bonds between the carbonyl group and N(2) atom are partial double bonds. Therefore, the electron - withdrawing capability of 1- position substituted group might affect the electron distribution on the carbonyl O atom which is suspected to be a center of biological activity.

PS-04.05.02 CONFORMATIONAL ANALYSIS OF PYRAZOLIDONE-3-TYPE COMPOUNDS AND 3D-QSAR STUDY. By H.J. Xu*, L.H. Lai, Q.C. Yang, X.J. Xu, Department of Chemistry, Peking University, Beijing 100871, China.

Pyrazolidone-3-type compounds showed anticonvulsant activity. A series of 1,5-substituted-3-pyrazolidones were synthesized and their anticonvulsant activities were tested.

Single crystals of four compounds were obtained and their crystal structures were determined based on the X-ray diffraction data. Coordinates for 22 test compounds were generated by adding appropriate substituents to the crystal structure of 3-pyrazolidone ring with MMP2. The electronic properties of these compounds were analyzed with MNDO.

A comparative molecular field analysis (CoMFA) method was conducted to correlate the anticonvulsant activities with their structural features. The atomic charges were calculated by the method of Gast-Huck and the molecules were aligned by superimposing the 3-pyrazolidone ring. Results from a CoMFA analysis of 22 compounds correlate well with cross-validated r^2=0.757.

