PS05.02.03 STRUCTURE AND CONFORMATION OF SEQUENTIALLY RELATED PEPTIDES: CRYSTAL STRUCTURE OF L-PHENYLALANYLGLYCYLGLYCINE (FGG). T. Srikrishnan and Seth Hoffman, Center for Crystallographic Research and Department of Biophysics, Roswell Park Cancer Institute, Buffalo N.Y. 14263

A systematic structural investigation of sequentially related peptides is of great importance for the elucidation of the structure-function relationship of peptides and in deducing the possible conformations of polypeptides. Although GGG has an extended anti-parallel ß-structure, crystal structures of other tripeptides of the sequence GGX and XGG show a wider range of conformations ranging from the extended, many kinds of folded conformations to a few helical conformations. In this line of investigation, the crystal structure of FGG was undertaken in our laboratory. Crystals of FGG ($C_{13}H_{17}N_3O_4$), grown by slow evaporation from an aqueous ethanol solution, are orthorhombic, space group $P2_12_12_1$, with the following cell dimensions: a= 5.459 (5), b=15.299 (6), c=16.047 (6) Å, V= 1340.2 Å^3, D_o= 1.38 g/c.c, D_c= 1.384 g/c.c and Z=4. Complete three dimensional data was collected on a CAD 4 diffractometer (2643 reflections, 2305>3σ). The structure was solved by the application of direct methods and refined to a final R factor of 0.031. The molecule exists as a zwitterion in the crystal. The peptide units are trans planar (ω_1= -178.6 and ω_2 = 175.6 °). The peptide backbone is folded with the torsion angles of Ψ_1 = -116.7, ω_1= -178.6, Φ_2= 88.8, Ψ_2=29.4, ω_2= 175.6, Φ_3= -135.6 and Ψ_3= -8.2°. For the phenyalanine side chain, χ_1= 123.4 and χ_2= -56.3°. The molecules are linked together intermolecularly in an infinite sequence by head to tail hydrogen bonds, as is typical of charged peptides.

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PS05.02.04 STRUCTURAL FEATURES OF STEREOISOMERIC ANALOGS OF CYCLOTETRADEPSIPEPTIDE [-(MeVal-Hyi)2-]. G. Tishchenko, Institute of Crystallography, Moscow Russia

DLLD(1),LDLD(2),DDDL(3),LDDD(4), DDDD(5), LLDD(6) stereoisomers of c[-(MeVal-Hyi)2-] were investi- gated by X-ray structure analysis. Cycles 1-5 have slightly elongated forms, asymmetric in 3,4, 5, centrosymmetric in 1, with C2 pseudoaxis in 2. The cycle 6 is square. Ester groups are trans in all cases, amide - cis in 1-5 and trans in 6. C=O groups are disposed in pairs under and above mean cycle plain in 1,6; on one side of it in 2,3. One C=O group (of Hyi2 in 4, of Val3 in 5)is directed inside the cycle, opposite to three others.In all molecules, exept 3, experimental conformations are close to calculated ones with minimal total energy. There is the conformation with energy slightly differing from minimal one in 3. The calculation was not carried out for the unique all-trans conformation 6.In crystal 5 there are two independent molecules with very close conformations. The most pronounced difference between these molecules is the side chains orientation of the residue 4 (trans and gauche). Experimental phi,psi-points are situated mainly near k and p-q minima on conformational maps for the model compounds Ac-L-MeVal-OMe and Ac-D-Hyi-NMe2. Exept the residues MeVal in 6, Hyi in 3, MeVal3 and Hyi2 in 5. This result agrees well with phi, psi-points arrangement near the other minima on conformational maps: l and r for 6 and 3, l and r simultaneously for 5 (minimum r is weak), as well as with yealds of cyclization reactions of the linear molecules. If for 1,2,4 yeald is 70-75%, for 3 and 6 40-45%, then for 5 it is only 8%. All structures were solved by direct method with full-matrix least squares refinement. R-factors are 0.066, 0.086, 0.11, 0.055, 0.051 and 0.049 for structures 1-6 respectively.

PS05.02.05 CRYSTAL STRUCTURES OF PEPTIDES DESIGNED TO MIMIC PROTEIN SECONDARY STRUCTURAL ELEMENTS K. R. Rajashankar, S. Ramakumar, V. S. Chauhan, Department of Physics, Indian Institute of Science, Bangalore, India and ICGEB, Aruna Asaf Ali Marg, New Delhi, India

Peptides containing a,ß-dehydroamino acid residues are found to exhibit specific conformational preference and altered biological activity. They are found in many naturally occurring peptides and proteins of microbial and fungal origin. In particular, a,ß-dehydro phenylalanine (ΔPhe), has become one of the most promising conformation restricting residue useful in peptide design. Theoretical and experimental studies on oligopeptides containing ΔPhe residues have demonstrated the potential of ΔPhe residues to induce folded conformation. In order to understand the effect of the number and relative positioning of ΔPhe residues on the overall conformation of peptide sequences, we have carried out a systematic study of a number of peptides containing ΔPhe residue/s. In this paper crystal structure of nine peptides containing ΔPhe residue/s will be discussed, highlighting the utility of ΔPhe as a 'designer residue'. The sequence and conformation of the peptides studied are listed in the table below.

	Peptide Sequence	Conformation
1	Boc^0-Val^1- ΔPhe^2-Phe^3-Ala^4-Phe^5- ΔPhe^6-Val^7- ΔPhe^8-Gly^9-OMe	TR
2	Boc^0-Leu^1-Phe^2-Ala^3- ΔPhe^4-Leu^5-OMe	TR
3	Boc^0-Leu^1- ΔPhe^2- ΔPhe^3-Ala^4-Phe^5-NHMe	TR
4	Boc^0-Val^1- ΔPhe^2- ΔPhe^3- ΔPhe^4-Val^5-OMe	TL
5	Boc^0-Val^1- ΔPhe^2-Ala^3-Leu^4-Gly^5-OMe	AR
6	Boc^0-Pro^1- ΔPhe^2-Ala^3- ΔPhe^4-Ala^5-OMe	B
7	Boc^0-Val^1- ΔPhe^2-Leu^3-Phe^4-Ala^5- ΔPhe^6-Leu^7-OMe	TRS
8	Boc^0-Val^1- ΔPhe^2-Phe^3-Ala^4-Leu^5-Ala^6- ΔPhe^7-Leu^8-OMe	TRS
9	Ac^0- ΔPhe^1-Val^2- ΔPhe^3-Phe^4-Ala^5-Val^6- ΔPhe^7-Gly^8-OMe	A/TRS

PS05.02.06 CONFORMATION OF CYCLOSPORIN IN DIFFERENT CRYSTAL FORMS. Michal Husák, Jan Ondrácek and Alexandr Jegorov, Department of Solid State Chemistry, Prague Institute of Chemical Technology, Technická 5, 166 28 Prague 6, Czech Republic, Galena Co., R & D., Branisovská 31, 370 05 Èeské Budìjovice, Czech Republic

Cyclosporin is a general name for the cyclic undecapeptides related to the structure of cyclosporin A: *cyclo*-[MeBmt-α-Abu-Sar-MeLeu-Val-MeLeu-Ala-D-Ala-MeLeu-MeLeu-MeVal], where MeBmt is (*2S,3R,4R,6E*)-3-hydroxy-4-methyl-2-methylamino-6-octenoic acid. Cyclosporin A has been successfully used as an immunosuppressant in the field of organ transplantation (Consupren®, Galena, Sandimmun®, Sandoz) and moreover some of its derivatives exhibit some potential for the treatment of multidrug resistance and even of AIDS. Despite the intensive investigations, the details of their mechanism of action still remains obscure. Since the solid state conformation of cyclosporin could be used as a starting point for molecular dynamic simulation, a study of two new cyclosporin crystal forms was undertaken.

Two new solid state modification of cyclosporin are reported. The first one is the structure of cyklosporin A arlasolve solvate (a = 15.521(2), b=20.833(3), c=12.949(3) Å , β= 100.21(1)°, $P2_1$, Z=2). The second one is the structure of cyclosporin H monohydrate (a = 12.338(1), b=18.964(1), c=11.111 Å , β= 96.21(1)°, I2, Z=4) the degradation product of cyclosporin A having as [D-MeVal] instead of the original L-amino acid.

Conformation of the title compounds has been compared with 3 known solid state conformations of cyclosporin A, and 2 types of conformation of cyklosporin complexed either to cyclophilin or with