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Protocyanin is a complex pigment extracted from flower petals of blue cornflower, *Centaurea cyanus*. The components of protocyanin were recently demonstrated to be anthocyanin (AN), flavone glycoside (FL), Fe^{3+}, Mg^{2+} and Ca^{2+} ions[1]. For X-ray structure determination, protocyanin was reconstructed from the components and crystallized in space group $P2_12_12_1$ with unit cell dimensions of a = 29.7, b = 49.2 and c = 78.3Å. Two protocyanin molecules are contained in an asymmetric unit. Data were collected on the beam line 6A at Photon Factory KEK to1.05 Å resolution.

The refined molecule has pseudo three-fold symmetry and four metals align along the pseudo three-fold axis in order of Ca^{2+}, Fe^{3+}, Mg^{2+} and Ca^{2+}. The four metals are coordinated to six AN and six FL molecules. The inner Fe^{3+} and Mg^{2+} ions are each coordinated to three AN's, respectively, while the outer two Ca^{2+} ions are each coordinated to three FL's. Both AN and FL molecules are self-associated with each other as AN-AN and FL-FL in pair and this hydrophobic association also exists between AN and FL molecules, building copigmentation stacks. Protocyanin is a tetra-metal (Fe^{3+}, Mg^{2+}, $2Ca^{2+}$) nuclear complex, a new type of supramolecular pigment.

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Keywords: X-ray structure analysis, pigments, biological molecular complexes

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Crystal Structures of the Fungal Metabolite Oosporein

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Oosporein is a symmetrical red coloured 2,5-dihydroxybenzo-quinone derivative biosynthesized by a broad variety of soil borne fungi. The compound, being known for almost six decades, is the major secondary metabolite of the entomopathogenic fungi *Beauveria brongniartii* which is successfully applied as a biological control agent against the European cockchafer *Melolontha melolontha*. In the course of isolating and purifying pure oosporein from biological cultures we obtained a dioxane solvate and a non-solvated form which were characterized with different solid state analytical techniques including X-ray diffraction.

The molecular geometry of oosporein is x-shaped with a dihedral angle of 67.8 and 79.9° in the non-solvated form and the dioxane solvate respectively. Surprisingly the two forms crystallize in the same space group (monoclinic, C_2/c) showing a similar O-H...O network. The non-solvated form shows two dimensional O-H...O tetrameric layers which are off stacked leading to a densely packed structure. In the dioxane solvate one solvent molecule is involved in the O-H...O hydrogen bond network resembling the overall network of the anhydrous form. This pseudo-tetrameric arrangement results in a large channel along the c-axis which is occupied by highly disordered dioxane molecules.

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Keywords: oosporein, natural organic molecules, crystal structure

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Xanthone Derivatives: Conformational Study and Development of Force Field

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Xanthone derivatives extracted from herbs are important components of homeopatic antibacterial, mycotoxic and cytotoxic medicines. Synthetic substituted xanthones tested against broad spectrum of biological activities revealed: antiinflammatory, cytostatic, antimycotic, and cardiovascular activities. In a series of newly synthesized substituted xanthones, two constitutional isomers, 2-methyl-2[2-(methyl)-6-xanthonoxy]-propionic acid, 2-methyl-2[4-(methyl)-6-xanthonoxy]-propionic acid, and racemic (RS)-2-[2-(methyl)-6-xanthonoxy]-propionic acid have shown differentiated antiinflammatory action.

The crystal structures of xanthone derivatives were solved using both single-crystal diffraction and HRPD data recorded with synchrotron radiation. In order to find the native, optimal structures of xanthone derivatives in their natural environment of lipid bilayer, additional force field parameters were obtained using X-ray diffraction data and *ab-initio* calculations.

Keywords: xanthone, *ab-initio* calculations, synchrotron radiation

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Diffraction and Computational Studies of Hydrogen Bonded Base Paired Systems

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Diffraction methods are often utilised to gain a greater insight hydrogen bonding interactions. In work to date the advantages of single crystal variable temperature x-ray and neutron diffraction, coupled with the imaging capabilities of Fourier difference maps, as complementary techniques for anomalous hydrogen bonding investigations have been highlighted [1]. In addition, recent advances in computational chemistry have enabled calculations to be carried out both on isolated molecules and in the periodic (i.e. crystalline) environment [2].

The main aim of this poster is to discuss the use of complementary methods to promote a better understanding of hydrogen bonding within carboxylic acid dimers and nucleic acid base paired systems. One particular system of interest is 3',5'-di-O-acetylthymidine and various techniques have been utilised to determine the presence of anomalous hydrogen behaviour. A crucial part of this has been a multiple temperature high resolution study carried out on station 9.8 at SRS, Daresbury. Alongside experimental work, recent computational work will highlight how these new methods can augment traditional experimental results. Overall it is hoped that the research presented will again highlight the importance of complementary techniques in crystallographic research.

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Keywords: hydrogen bonds, diffraction methods, computation

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Polymorphism of Crystalline Amino Acids. The Role of Non-covalent Interactions

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The crystals of amino acids are interesting from several points of view – as drugs, as molecular materials (e.g. piezo- and ferroelectrics), but also as biomimetics. Understanding the effects of pressure, temperature, and various chemicals on the crystal structures of these

compounds can give a better insight into the properties of hydrogen bonds and of other, weaker, non-covalent interactions in these systems. This can, in turn, be helpful for getting a better understanding of the conformational changes induced by temperature, pressure, or chemicals in the biopolymers built from amino acids (peptides). In the contribution we shall illustrate this by the results of recent X-ray single-crystal and X-ray powder diffraction, Raman and IR-spectroscopy studies at variable temperatures and pressures, as well as of the DSC and adiabatic calorimetry studies from 5K to the decomposition temperatures.

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Keywords: hydrogen bonds, high pressures, low temperatures

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Neutron Diffraction Structure of the β-Cyclodextrin Ibuprofen Complex at 15K
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The structure of the inclusion complex of β-cyclodextrin (β-CD) with ibuprofen has been determined as part of a study of β-CD complexes with non steroidal anti-inflammatory drug molecules and similar organic compounds. Ibuprofen is a hydrophobic molecule but becomes soluble in water by complexation with β-CD. This complex forms dimers in the crystalline state. Very often β-CD complexes crystallize as dimers linked head to head by hydrogen bonds between secondary hydroxyls. These dimers form infinite two dimensional layers in a C2 unit cell. The extended crystal structure is built up by linking together the layers in different packing modes. As well as the substantial pharmaceutical interest of describing the interaction between the drug and the CD molecule in the crystalline complex, one of our goals was to investigate how the nature of the guest and the solvent molecules influences the packing mode in the crystal, how the hydrogen bonding interactions are important in the supramolecular structure, and how order-disorder phenomena observed in analogous compounds can be explained. In these studies, we have used X-ray and neutron diffraction data, as well as X-ray diffuse scattering patterns. The results of the X-ray diffuse scattering analyses will not be described here. Here we report the first neutron diffraction structure of a dimeric β-CD complex (at 15K) and the comparison with the Synchrotron X-ray structure (at 300K).
Keywords: β-cyclodextrin-ibuprofen, neutron diffraction, order-disorder

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Electrostatic Properties of Two Precursors of Potent HIV-1 Integrase Inhibitors
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New AIDS therapy developments focus on the integrase inhibition in order to block the virus replication. Quinoline derivatives are potent drugs in this novel chemotherapy [1]. These molecules are formed by a quinoline moiety connected to a hydroxylated aromatic ring through a spacer fragment. This latter plays an important role in both inhibition and toxicity of the drugs. We have carried out the study of electrostatic properties of the two main precursors. These properties are derived experimentally from high-resolution X-ray diffraction experiments and from quantum mechanics calculations at Hartree-Fock level. The topological features of the electron density of precursors are carefully analyzed. The atomic charges and the electrostatic potential are discussed to highlight the correlation between the drug activity and the electronic structure.

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Keywords: electron density, electrostatic properties, drug structure-activity relationships

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Crystal Structures of Potential Sweeteners. The Kier Glucophore Geometry
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We compare molecular geometry and interactions of new potential sweeteners which were designed using chemical modification of a known sweet compound [1] and bioisosteric replacement. We determined crystal structures of three arylsulfonylalcanoic acids and one bioisoster containing a tetrazole instead of the carboxylic group. Unfortunately, last of them occured to be bitter. However, it is not very surprising since the sweet and bitter tastes are strongly related.

According to the geometrical model of glucophore given by Kier, there are three fundamental fragments of a sweet compound which interact with a sweet taste receptor [2]. A sweetener should contain a donor and an acceptor of hydrogen bond and a fragment which can be involved in hydrophobic interactions [3]. Distances between those fragments define a glucophore. However, the geometry of our sweet compounds in the crystalline state do not agree with the Kier model.

We observed a pair of very strong hydrogen bonds in sweet compounds building a dimer *via* inversion centre whereas in tetrazole the dimeric structure does not occur. That can explain why the bioisoster is bitter.

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Keywords: sweetener, dimer, hydrogen bond

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Chloroquine Derivatives. Conformation and Intermolecular Interactions
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Crystal structure of hydroxychloroquine (OHClQ) sulfate has been determined: a=10.5437(3)Å, b=8.8532(2)Å, c=22.0923(8)Å, α=90°, β=101.426(1)°, γ=90°, $P2_1/c$, Z=4, in order to compare its conformation and intermolecular interactions to those in the crystalline chloroquine (ClQ) phosphate [1] and quinine salicylate (QSal) monohydrate [2].

Molecular conformations of OHClQ and ClQ are comparable in both salts; the differences between corresponding torsion angles are not greater than 10°. Each of the nitrogen atoms is a proton donor in the intermolecular hydrogen bonds with the oxygen atoms of sulfate or phosphate anions. While the parameters of the N1-H1···O and N3-H3···O bonds are similar, the distance N···O within the bond N2-H2···O is much shorter in the case of OHClQ. The -OH group of OHClQ forms an additional H-bond with the oxygen atom of SO_4^{2-}.

The comparison of the hydrogen bonds formed by OHClQ and ClQ with those of quininium anion in QSal shows that these antimalarial molecules may interact with their putative receptor in a similar way.

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Keywords: antimalarials, chloroquine, intermolecular interactions