In continuation of our recently started research program (Kopf, J., Köll, P., Morf, M., Zimmer, B. and Jarchow, O., 1990, Abstract PS-05.04.25, IUCr XV, Bordeaux, France) we have determined the crystal and molecular structures of previously not treated pentitols, hexitols, heptitols and several higher alditols up to decitols including peracetylated derivatives in most cases. Contrary to the above mentioned assumptions, our investigations show that the avoidance of 1,3-parallel interactions between the heavy atoms O and C is not a dominating factor in determining the conformations of higher alditols in the solid state. Acetylated alditols in particular are able to adopt "unexpected" conformations. Examples of the structure determinations and further discussions will be given. First results of our respective work have been published already (Kopf, J., Bischoff, M. and Köll, P., Carbohydr. Res., 1991, **217**, 1; Kopf, J., Morf, M., Zimmer, B., Bischoff, M. and Köll, P., Carbohydr. Res., 1992, **229**, 17 and Köll, P., Morf, M., Zimmer, B., Kopf, J., Berger, A., Dax, K. and Stütz, A. E., Carbohydr. Res., 1993, in press).

**MS-06.01.05** **The Use of Composite Crystal-Field Environments Derived from Crystal Packing in Molecular Recognition and the 'De-NOVO' Design of Protein Ligands**

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Information about intermolecular interactions and the mutual recognition of organic molecules can be obtained from their packing in the crystalline state. Structural data has been retrieved from the Cambridge Crystallographic Database [1] to compile composite crystal-field environments about different functional groups, which also occur in proteins and nucleotides. The spatial distribution obtained for these next-neighbor contacts can be used to map-out putative interaction or recognition sites, e.g. about amino acid residues oriented towards the binding site of a given protein. Although influenced by packing forces, these composite environments show systematic patterns which reflect preferred interaction geometries of the functional groups under consideration with their neighboring groups, e.g. hydrogen bonding partners. A detailed analysis reveals differences and similarities in the structural properties of these functional groups which allows guide-lines to be devised for the consequences of mutual functional group replacements. Similar, but substantially less detailed, distributions can be obtained from crystallographically determined ligand/protein complexes (Brookhaven File [2]) for the spatial orientation of ligand functional groups about amino acid residues. These demonstrate that the properties observed in low-molecular weight structures are also representative for the sought-after spatial orientation of interactions between ligands and their receptor proteins [3]. The crystallographically determined binding geometries of three inhibitor/enzyme complexes are compared with the distributions of putative interaction sites predicted from corresponding composite field environments. In some cases, the observed positions of ligand atoms interacting with the proteins coincide with a region which is also frequently occupied by similar bonding partners in organic crystal structures, however, interaction geometries are also found which fall close to the limits of the ranges observed in the small molecule reference data. The information contained in the different composite crystal-field environments can be translated into rules which serve as guide-lines for an automatic docking of small molecule fragments into the active site of proteins [4].

[1] Allen F.H., Kennard O., Taylor R., Acc. Chem. Res. (1983) 16 146
[2] Bernstein F.C., Koetzle T.F., Williams G.J.B, Meyer E.F. Jr., Brice M.D., Rodgers J.R., Kennard O., Shimanouchi T., Tasumi T., J. Mol. Biol. (1977) 112 535
[3] Klebe G., Mietzner T., (1993) in "Organic Crystal Chemistry" ed. Jones D.W., Oxford Univ. Press
[4] Böhm H.J., J. Comp.-Aided Mol. Des., (1992) 6 61-78 and 593-606

**MS-06.01.06** KEY ROLE OF SPECIFIC INTERMOLECULAR INTERACTIONS IN FORMATION OF ORGANIC CRYSTAL STRUCTURES

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Some contacts of atoms (for ex., CN···Cl, O···C=O, I···I, CH···O) display properties, which could not be described by conventional additive models (such as van der Waals radii, transferable atom-atom potentials, superposition models of electron density, etc.). We call them specific intermolecular contacts (SIC). The rise of SIC is one of the important factors determining the structure of a molecular crystal. Different ways to take into account the influence of SIC on the packing of molecules were considered:
1) the addition of SIC energy for the refinement of depths of minima after the energy minimization by atom-atom potential method,
2) the use of the special potentials and/or virtual atoms,
3) the energy minimization under the condition of fixed SIC geometry,
4) a priori construction of packings which contain setted SIC to use the packing as a starting point in energy minimization.
An application of the last way for uracil and its derivatives gave us initial models which were very close to real structures.
The use of donor-acceptor approach based on localized orbitals interaction in the second order of perturbation theory allowed us to reproduce the surface of potential energy for Cl...Cl SIC (contrary to the electrostatic approach).

**MS-06.01.07** STRUCTURES OF UNSTABLE INTERMEDIATES IN THE CRYSTALLINE STATE REACTIONS

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If the structural change in the process of reaction could be "observed" directly by X-ray analysis, the mechanism would be easily made clear. Such a reaction should proceed in a crystal with retention of crystallinity, which is called as crystalline state reaction.