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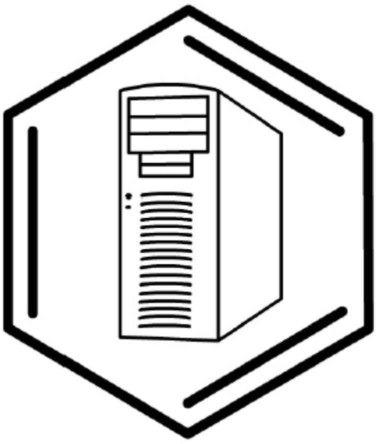
UKRAINIAN-AMERICAN LABORATORY OF COMPUTATIONAL CHEMISTRY



BOOK OF ABSTRACTS

Methods and Applications of Computational Chemistry

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3RD INTERNATIONAL SYMPOSIUM

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Methods and Applications of Computational Chemistry

3rd International Symposium

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Quantum Chemistry and Materials Science

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Main problems of the use of quantum chemistry methods in modeling the formation, structure, and properties of functional materials for micro- and nanoelectronics and photonics are considered. Simulations of the deposition and growth of thin films with the use of quantum chemical calculations and the kinetic Monte Carlo method, modeling of the structure and electronic properties of surfaces and interfaces of dielectric and semiconducting films, modeling of surface reactions, prediction of possible structure of polymorphous materials, prediction of properties of luminescent materials. Modeling of materials for the sensing layer of optical chemosensors is considered as an example of the general strategy of multiscale atomistic modeling of hierarchically constructed nanostructured materials for organic nanophotonics. The main steps of such modeling are considered: modeling at the molecular level, modeling at the supramolecular level, and modeling at the level of nanoparticles. Problems arising at each step of modeling are analyzed, and current approaches to their solution are discussed. It is shown that multiscale atomistic simulation at the modern theoretical level allows the main functional properties of materials for micro- and nanoelectronics and photonics to be described and predicted with adequate reliability.

Addressing Challenges of the First Part of the 21th Century: Merging Nano- and Bio- Chemistry

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NSF Interdisciplinary Nanotoxicity CREST Center, Department of Chemistry, Jackson State University, 1325 Lynch St, Jackson, MS 39217-0510

This talk highlights the most significant achievements and challenges related to our recent studies on DNA fragments and nanomaterials. Among studied species are DNA bases, fullerenes, carbon nanotubes, metal and metal oxide clusters. Application of computational techniques allows obtaining detailed information on changes of the DNA fragment properties interacting with fullerene and gold particles. Possible applications of nanospecies for hydrogen storage, DNA protection and damage, and nerve agent detections and decomposition are discussed. Also novel developments in prediction properties of nanospecies and in the risk assessment of nano-size materials will be reviewed.

Problems in the Computational Studies of Transition-Metal Clusters with 3d Electrons. Mn_2

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Computational studies of transition-metal clusters are still a challenge to theorists. The main problem is that the CASSCF expansion of the wave function does not contain a principal configuration, which should be HF configuration, and a large number of reference configuration in the CI procedure must be treated equally. Thus, the multireference approach is, in general, mandatory. The arising calculation problems we illustrate on the simplest system: the dimer Mn_2.

A large number of Mn_2 calculations were performed by the DFT method. In the most of studies the ferromagnetic ground state was predicted, with S = 5, in one the ground state has S = 1 and in two S = 0. While experiment and all *ab initio* multireference calculations predict the antiferromagnetic ground state with S = 0. There are two reasons for this contradiction: 1. The 3d clusters should be treated by the multireference methods, although the DFT method is a single reference and what is more, it is a single-determinant approach. 2. As was proved in Ref [1], the electron density of an arbitrary N-electron system is invariant with respect of the total spin, hence the conventional Kohn-Sham equations are the same for all values of S. The procedures for multiplet structure developed up-to-date modified only exchange functionals and use the correlation functionals not corresponding to the total spin of the state. Thus, the DFT results obtained by these procedures are very unsafe, their predictive value is doubtful.

All MR *ab initio* calculations of Mn2 performed up-to-date predict antiferromagnetic singlet ground state and all were performed by different versions of MR PT2. In the present study [2] we employ the MR methods: MR CISD, MR CISD+Q, and ACPF and calculated the complete potential energy curves for all 6 spin states, dissociating on the Mn atoms in ground state, and six excited undecets states, dissociating into one atom in the ground state and another in the first excited state. The Balabanov-Peterson augmented correlation consistent basis set, aug-cc-pVQZ, was used. The total number of configurations in the CI treatment was 9 x 10^9 (4 x 10^7 after contraction). The ground state being the singlet , X $^1\Sigma_g^+$, with the binding energy D_e = 1.3 kcal/mol (0.06 eV) and R_e = 3.6 A. The calculated exchange coupling constant J is in a good correspondence with experiment. It was proved that the binding in the Mn_2 dimer is of van der Waals type.

[1] I.G. Kaplan, J. Mol. Struct. **838**, 39 (2007); Int. J. Quant. Chem. **107**, 2595 (2007).
[2] D. Tzeli, U. Miranda, I.G. Kaplan, and A. Mavridis, J. Chem. Phys. **129**, 154310 (2008).

Shaping the Key to Aromaticity

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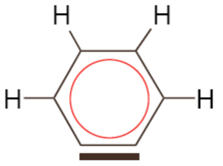
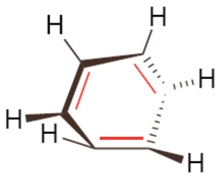
Like flavors in the daily life, aromaticity remains non-univocally appraised in the chemistry context. Both perceptions are not observables in the strict sense, but both rely on molecular recognition processes, where "shape complementarity" is measured by binding affinity to olfactive cell receptors, or by resonance energies (REs) with respect to Dewar-type acyclic references (or multi-component versions thereof).[2] A shared interpretation of the interaction now requires a rigorous analysis. Regarding aromaticity (resp. antiaromaticity) of π-conjugated molecules as their *tendency* to resist to (resp. accomodate) the *loss* of the cyclic character of the conjugation, under constraint or relief of external perturbations, a critical analysis of the performance of various chemical schemes, from Breslow's RE's[1] to Malrieu's ACE's,[2] will be developped.

Since the reference of the perturbation is not precised *a priori*, except by being "as identical as possible" to the considered cyclic system but just "acyclic", a formal analysis must implicitely refer to discrete topological models of molecules, namely to the Lewis chemical graphs. The topological resonance energy (TRE) proposed by Aihara and Trinajstic in the 70’s thus rigorously extracts the pure cyclic effects of the conjugation. Nevertheless, the computing complexity and lack of direct chemical interpretation of the TRE acyclic reference discouraged a wide use of TRE in the organic chemist community. Both the calculation and interpretation of TRE will be revisited in light of a cross-reference between Hückel and Möbius rings within the HMO framework.[4]

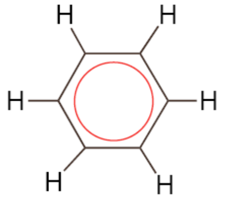
Whereas the orthgogonal π-systems of conjugated alkynes are currently treated independently, the topological influence of triple bonds on TRE values will be illustrated in the case of aromatic ring *carbo*-mers.[5]



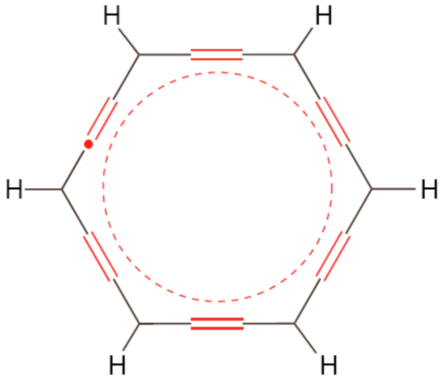
TRE (benzyne) = 0.256



TRE (Möbius benzene) = –0.799



TRE (benzene) = 0.263



TRE (*carbo*-benzene) = 0.089

[1] M. J. S. Dewar, C. de Llano, *J. Am. Chem. Soc.* **1969**, *91*, 789.
[2] M. K. Cyranski, *Chem. Rev.* **2005**, *105*, 3773.
[3] R. Breslow, E. Mohacsi, *J. Am. Chem. Soc.* **1963**, *85*, 431
[4] (a) J.-P. Malrieu, C. Lepetit, M. Gicquel, J.-L. Heully, P.W. Fowler, R. Chauvin, *New J. Chem.* **2007**, *31*, 1918. (b) J.-P. Malrieu, M. Gicquel, P.W. Fowler, C. Lepetit, J.-L. Heully, R. Chauvin, *J. Phys. Chem. A* **2008**, *112*, 13203.
[5] (a) J. Aihara, *J. Am. Chem. Soc.* **1976**, *98*, 2750. (b) I. Gutman, M. Milun, N. Trinajstic, *Croat. Chem. Acta.* **1976**, *48*, 87.
[6] J. P. Malrieu, P. Fowler, C. Lepetit, R. Chauvin, to be submitted.
[7] (a) R. Chauvin, C. Lepetit, *Acetylene Chemistry*, Chapt.1, p.1-50, F. Diederich, P. J. Stang, R.R. Tykwinski Eds, Wiley, Weinheim, **2005**. (b) V. Maraval, R. Chauvin, *Chem. Rev.* **2006**, *106*, 5317.

Energetic Aspects of Cyclic π-Electron Delocalization

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For nearly two centuries aromaticity has remained one of the central concepts in chemistry and through ever wider application, is now increasing in importance.[1] As many other important chemical concepts called by Coulson *Primitive Patterns of Understanding in Chemistry*[2] (*e.g.* electronegativity, van der Waals radii, Lewis acidity/basicity, molecular diagrams, ionicity *etc.*) it is not a directly measurable quantity and can be defined only by convention. All aromaticity definitions refer to cyclic π-electron delocalization as the most basic phenomenon.[3]

From energetic perspective a common measure of its extent in a given system is resonance energy or aromatic stabilization energy.[4] According to the Pauling-Wheland definition, the RE is the extent to which a real molecule is stabilized relative to the energy of its most stable (virtual) resonance contributor. ASEs measure the "extra" stabilization due to cyclic π-electron delocalization of an aromatic system over appropriate conjugated reference counterparts. It has been pointing out that the effect of aromatic stabilization, while being among the largest deviations from additivity found chemically, is at most a few percent of the total atomization energy for typical aromatic systems, what in turn causes difficulty in isolating it from other important effects which stabilize/destabilize a molecule.[5] Many methods have been employed to evaluate REs and ASEs. Isodesmic reactions conserve the number of bonds of each formal type, *e.g.* C-H, C-C, C=C, while allowing the relationships among the bonds to vary. Homodesmotic evaluations aim to balance hybridization differences as well. The discrepancies in estimated values of aromatic stabilization energies are either due to differences in the choice and definition of reference molecules and the defining equations, so the energies may be perturbed by additional effects such as strain, topological charge stabilization, hybridization, heteroatom interactions, anomeric effects, hyperconjugation, and/or inaccuracies in the energies both experimental and theoretical employed.[5]

The lecture is focused both on critical analysis of various model approaches of the estimation of the extent of π-electron delocalization and its analysis for few families of π-electron compounds such as five-membered heterocyclic systems,[6] linear polyacenes,[7] nonplanar benzenoid hydrocarbons[8] and their nonalternant analogues such as isocoronene[9] or fullerenes.[10]

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[1] see *e.g.* Two thematic issues of *Chemical Reviews* devoted to Aromaticity (P. v. R. Schleyer, Ed. **2001**, *101*, 1115–1566), or to Delocalization pi and sigma (P. v. R. Schleyer Ed. **2005**, *105*, 3433–3947).

[2] McWeeny in preface to *Coulson's Valence*, Oxford University Press: Oxford, 1979.

[3] a) V. I. Minkin, *Pure Appl. Chem.*, **1999**, *71*, 1919–1981. b) T. M. Krygowski, M. K. Cyrański, Z. Czarnocki, G. Häfelfinger, A. R. Katritzky, *Tetrahedron* **2000**, *56*, 1783–1796. c) Z. Chen, S. C. Wannere, C. Corminboef, R. Puchta, P. v. R. Schleyer, *Chem. Rev.,* **2005**, *105*, 3842–3888.

[4] M. K. Cyrański, *Chem. Rev.* **2005**, *105*, 3773–3811.

[5] M. K. Cyrański, P. v. R. Schleyer, T. M. Krygowski, H. Jiao, G. Hohlneicher, *Tetrahedron*, **2003**, *59*, 1657–1665.

[6] M. K. Cyrański, T. M. Krygowski, A. R. Katritzky, P. v. R. Schleyer, *J. Org. Chem.* **2002**, *67*, 1333–1338.

[7] M. K. Cyrański, B. T. Stępień, T. M. Krygowski, *Tetrahedron* **2000**, *56,* 9663–9667.

[8] a) G. J. Bodwell, J. N. Bridson, M. K. Cyrański, J. W. J. Kennedy, T. M. Krygowski, M. R. Mannion, D. O. Miller *J. Org. Chem.* **2003**, *68*, 2089–2098. b) M. A. Dobrowolski, M. K. Cyrański, B. L. Merner, G. J. Bodwell, J. I. Wu, P. v. Ragué Schleyer, *J. Org. Chem.* **2008**, *73*, 8001–8009. c) J. I. Wu, M. A. Dobrowolski, M. K. Cyrański, B. L. Merner, G. J. Bodwell, Y. Mo, P. v. R. Schleyer, *Mol. Phys.* **2009**, *107*, 1177–1186.

[9] A. Ciesielski, M. K. Cyrański, T. M. Krygowski, P. W. Fowler, M. Lillington, *J. Org. Chem.* **2006**, *71*, 6840–6845.

[10] M. K Cyrański, S. T. Howard, M. L. Chodkiewicz, *Chem. Comm.* **2004**, 2458–2459.

Intermolecular Interactions with Participation of π-System in Supramolecular Complexes and Molecular Crystals

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Conjugated systems represent one of the most widespreading source of weak intermolecular interactions in supramolecular complexes and molecular crystals. The most well known example of such interactions is stacking interactions between bases in nucleic acids. However, during last decade it was recognized several new types of intermolecular interactions with participations of π-systems. In particular, this concerns formation of the X-H…π hydrogen bonds, halogen bonds, different types of stacking interactions etc.

In particular, presence of the lone pair and p_z-AO at the nitrogen atom of aromatic heterocycle creates the possibility for formation either the X-H…N or the X-H…π hydrogen bonds. Investigation of character of hydrogen bonding in polyhydrated complexes of adenine and guanine reveals existence also area of mixed X-H…N/X-H…π hydrogen bonds where both lone pair of the nitrogen atom and π-system make significant contribution into total energy of hydrogen bonding.

Recently it was demonstrated that halogen atoms can form stable halogen bonds with electron rich heteroatoms or molecular fragments, for example, π-system of aromatic rings. Investigation of crystal structure of complexes of fluorenonophane with haloforms reveal also the formation of stable halogen…π bond which may be considered as some kind of halogen bonds. Analysis of intermolecular interactions in crystals of halogen derivatives of trityl alcohols demonstrates that halogen bonding provide 30-100% into total energy of interaction between molecules. However, analysis of character of halogen…π interactions in some complexes clearly indicates that these interactions may be also repulsive depending on orientation of halogen atom with respect to π-system.

Quantum Chemical Topology Description of the Nature of Chemical Bonds and Chemical Reactions

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Since many decades understanding the nature of chemical bonds was one of the most important goals of chemistry. In recent years very powerful tool for theoretical analysis and interpretation of chemical bonds is an approach called generally as Quantum Chemical Topology (QCT). In the framework of QCT, which contain several theoretical formalisms, two methods are especially popular among chemist: theory named as Atoms in Molecules (AIM) proposed by Bader [1] and topological analysis of Electron Localization Function (ELF) formulated by Silvi and Savin [2] on definition of ELF in formulation of Becke and Edgecombe [3]. Not going into details, the ELF is relative measure of electron localization associated with the spherically averaged conditional same-spin pair probability density and therefore is very interesting theoretical tool for study of nature of chemical bonds. In recent years very attracting approach to study the nature of chemical bond is topological analysis of the Electron Localizability Indicator (ELI) proposed by Kohout [4].

In the lecture, analysis of the nature of chemical bonds for selected group of molecules using the topological analysis of ELF and ELI methods will be presented. Some examples of recently discovered protocovalent bond will be discussed, which constitute a new class bond family distinct from the covalent and ionic bonds.

Quantum chemical studies of chemical reactions usually are restricted for determination of reactants and transition state. Very little attention is paid to the analysis of chemical bonds which are important during the chemical reaction. In the lecture, mechanism of H-abstraction in the reaction between ethynyl radical and ammonia will be analyzed from a point of view of the Bonding Evolution Theory (BET). It will be presented, that the transition state structure is not associated with any topological change of ELF.

[1] R.F.W. Bader, Atoms in Molecules. A Quantum Theory, Oxford University Press, Oxford, 1990.
[2] B. Silvi and A. Savin, Nature, 371 (1994) 683.
[3] A.D. Becke and K.E. Edgecombe, J. Chem. Phys., 92 (1990) 5397.
[4] M. Kohout, Int. J. Quantum Chem., 97 (2004) 651.

Looking for the Bonding Descriptors Based on Electron Density

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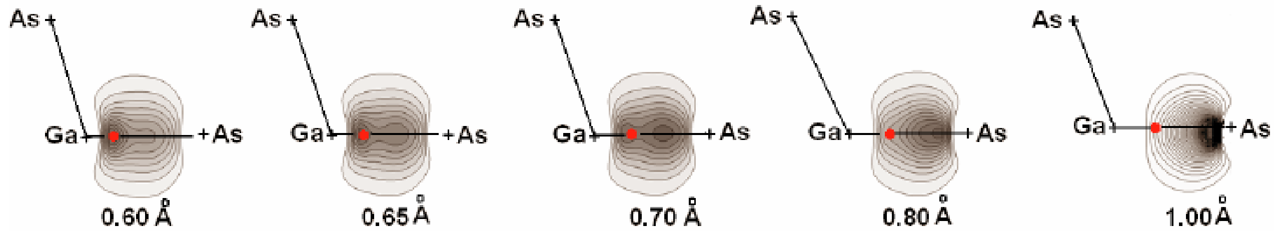
Many present-day structural models portray a crystal (and a molecule) as a 'sea' of electron density with immersed nuclei. This picture is close to the quantum mechanical description however it takes away from classical canons, which consider a crystal/molecule as a set of atoms linked by a network of chemical bonds. Therefore, great efforts were made to establish which atoms, in terms of electron density, are directly bonded and which are not. Additionally, numerous attempts to quantify the atomic and molecular interactions were undertaken. As a result, a language used to interpret the electron density pictures now represents the sophisticated and often contradicting mixture of classical and quantum concepts. Certain progress in diminishing the contradictions has taken place in the last few years; in particular, quantum-topological analysis of the electron density was expanded to include the electrostatic potential and the electron localization function. The experimental electron density was also introduced in the DFT formulae: it allowed extracting the total, exchange and correlation energy densities and integrated electronic energy characteristics from the X-ray diffraction experiment.

There is a question whether these developments provide new insights on the nature of atomic and molecular interactions. In search of an answer to this question we shall consider the most recent results dealing with the bonding descriptors based on the electron density and its derivatives and equally applicable to theoretical and experimental densities. We shall discuss the descriptors which reflect the properties both the atoms and bonds as the electronic total, exchange and correlation energy densities, electric inner-crystal field and Fermi hole density. All of them are derived by using certain approximations; therefore the limits of their applicability will be discussed as well.

This work is supported by Russian Foundation for Basic Research, grant 07-03-00702.



Manifestation of the bond ionicity in crystalline GaAs: the approximate Fermi hole density “jumps” from the Ga atomic basin to As one when the reference electron is moving along the bond line

Magnetism in Novel Metallofullerenes and Ultrashort Carbon Nanotubes

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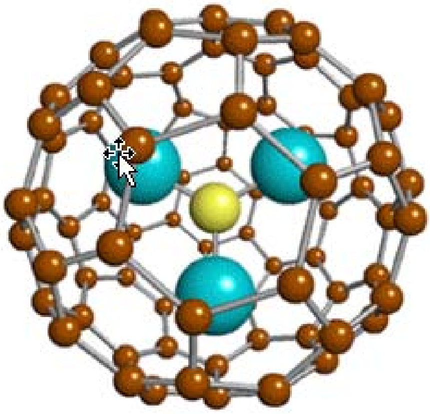
Within in the current effort of designing novel nanomaterials, carbon nanostructures occupy a special place. This is due to the broad range of their properties which can be tuned to match an equally broad variety of actual or potential applications. While carbon nanostructures have been established as promising candidates for new electric devices, applying their magnetic properties has been envisaged only in the recent past. Thus, novel magnetic resonance imaging (MRI) contrast agents can be fabricated by enclosing small clusters of lanthanide atoms into fullerene cages. Further, finite carbon nanotubes exhibit intrinsic magnetism and could be of great interest for the emerging field of molecular spintronics.

In this contribution, I will present density functional theory results on magnetism and associated electronic phenomena in two classes of recently manufactured carbon nanomaterials, namely fullerenes enclosing trimetallic nitrides and short single walled nanotubes (SWNTs) of the zigzag type. In particular, my presentation will focus on metallofullerenes of composition $M_3N@C_{80}$ with M = Sc, Sm, Gd, Lu, as well as semiconducting SWNTs of the type (10,0). In both cases, the nature and the origin of magnetic features will be discussed in the context of the geometric and electronic structure of the considered species.



Structure Harmonics in Slater Basis Sets: Strategy and Applications for Metabolic NMR

Philip E. Hoggan

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This work uses exponential type functions (ETFs) as a basis set satisfying the nuclear cusp condition. The choice of Coulomb Sturmian basis functions is motivated by the fact that they constitute a complete set without continuum states. They also orthogonalise the Coulomb attraction [1].

Structure harmonics, arising from Resolutions of the Coulomb operator introduced by Gill greatly simplify the requisite integrals [2].

The code structure is modular with many pre-calculated coefficients stored and retrieved from look-up tables. This includes Gaunt coefficients, optimal exponents, normalization constants and atomic integrals [3-4].

Efficient orbital rotation techniques are implemented to facilitate the use of a DIM (Diatomics in Molecules) strategy [5-6].

Finally, applications to precise evaluation of NMR chemical shifts of *in situ* metabolites are given to illustrate why Sturmians are far superior to Slater type orbitals in this case [7].

[1] C. A. Weatherford, E. Red and P. E. Hoggan, Mol. Phys. 103 2169 (2005) and references therein.
[2] P. M. W. Gill and A. T. B. Gilbert. Resolutions of the Coulomb Operator. II The Laguerre Generator. *Chem. Phys.* 356 (2009) 86.
[3] D. Pinchon and P. E. Hoggan, Int. J. Quantum Chem 107 (2007) online.
[4] Ja. Avery and Jo. Avery, Hypersperical harmonics and generalized Sturmians, Kluwer, Dordrecht. 2007.
[5] D. Pinchon and P. E. Hoggan, J. Phys. A. 40 (2007) 1597-1610.
[6] N. Absi and P. E. Hoggan, Int. J. Quantum Chem 106 (2006) 2881-2888.
[7] P. E. Hoggan, Interdisciplinary Science 1 (2) (2009) 114-120.

The implicit electrostatic solvent model with continuous dielectric permittivity function

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The modification of the electrostatic continuum solvent model considered in the present work is based on the exact solution of the Poisson equation, which can be constructed provided the dielectric permittivity ε of the total solute+solvent system is an isotropic and continuous spatial function. This assumption allows one to formulate a numerically efficient and universal computational scheme which covers the important case of variable ε function inherent to the solvent region. The pertaining sort of solution is unavailable for conventional dielectric continuum models which imply that ε is discontinuous on the boundary confining the excluded volume cavity of the solute particle, such as Onsager and Kirkwood models for spherical cavities and the polarizable continuum model (PCM) for solute cavities of general shape. Test computations based on the present algorithm are performed for water and several non-aqueous solvents. They illustrate specific features of this aproach, called "smooth boundary continuum model" (SBCM), as compared to the PCM procedure, and suggest primary tentative results for its parameterization in different solvents. The calculation for the case of a binary solvent mixture with variable ε in the solvent space region demonstrates the novel application field which is provided by the SBCM.

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Analysis of Interactions within Catalytic Sites

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Intermolecular interactions determine numerous practically important physical and chemical properties of biomolecules with parameters considerably exceeding synthetic materials[1]. Due to the large size of biomolecular systems they are still studied by very crude methods, employing mostly empirical force fields or in the best case by supermolecular variational methods which can not provide any insight into the physical nature of corresponding interactions. However, the physical nature of such interactions can be analyzed using variation-perturbation partitioning of intermolecular interaction energy into electrostatic, exchange, delocalization and correlation terms [2-3] defining hierarchy of approximate models useful in rational design of new materials with desired properties.

One of such models — Differential Transition State Stabilization (DTSS) approach [4-5] describes catalytic activity of molecular environment allowing to determine the most important residues and energy contributions involved. Corresponding analysis of protein kinase A[6] and fatty acid amide hydrolase [7] catalytic activity will be discussed.

[1] W. A. Sokalski(ed), Molecular Materials with Specific Interactions: Modeling and
[2] Design, Vol. 4, Series: Challenges and Advances in Computational Chemistry and Physics (series ed. J. Leszczynski), Springer 2007.
[3] W.A. Sokalski, S. Roszak, K. Pecul, Chem.Phys.Lett., 153,153 (1988).
[4] R. W. Góra, W. A. Sokalski, J. Leszczynski, V. Pett, J. Phys. Chem. B **109** (5), 2027-2033 (2005)
[5] B. Szefczyk, A.J. Mulholland, K.E. Ranaghan, W.A. Sokalski, J.Am.Chem.Soc., 126, 16148 (2004)
[6] W.A. Sokalski, J.Mol.Catalysis,30, 395 (1985).
[7] P. Szarek, E. Dyguda-Kazimierowicz, A. Tachibana, W.A. Sokalski, J.Phys.Chem.B, 112,11819 (2008).
[8] E. Chudyk, E. Dyguda-Kazimierowicz, W.A. Sokalski, to be published.

The Peculiarities of the Active Site Formation in Cation-Exchanged High Silica Zeolite Catalysts

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Catalytic properties of cation-exchanged zeolites are associated usually with Broensted acidity of their H-forms or with Lewis acidity and redox activity of metal cations, stabilized at cation positions of zeolite structure. Cationic positions are formed by isomorphous substitution of Si on Al in zeolite lattice, each lattice Al ion enables to stabilize one cation with effective charge +1 (e.g. H^+, Na^+ GaO^+ etc.). The entrapping of a many-valence cation demands, generally speaking, participation of the corresponding number of lattice Al ions. For instance, in the case of two-valence cation (e.g. Zn^{2+}, Ca^{2+} etc.) it can be two lattice Al ions in a frame of one zeolite ring. Evidantly, in the high silica zeolites with small Al/Si ratio, what are often very active catalysts, the number of places with such close assignment of two lattice Al ions should be small. Nevertheless, in this case, as a rule, it is possible to realize the whole exchange capacity of the zeolite. It can be understand if we accept the proposed in [1] model of the localization of two-valence cation near one lattice Al ion with distant placing from second lattice Al cation; it was illustrate on the example of ZnZSM-5 zeolite. It was shown, that such type of active sites should reveal increased Lewis acid strength. Later the formation of similar active sites was proved experimentally. DFT calculations of adsorption and subsequent heterolytic dissociation of H_2 [2], CH_4 and C_2H_6 [3] molecules on the sites were in fine agreement with the experimental studies. Another example of the appearance of the similar type of active sites is formation of binuclear gallium-oxide clusters $[Ga_2O_2]^{2+}$ in gallium-exchanged zeolites from distantly separated two oxo-ions $[GaO]^+$ [4]. It was found that partially hydrogenated form of this cluster can provide catalytic cycle of the dehydrogenation of light alkanes in contrast to oxo-ions $[GaO]^+$. Alternative way of the stabilization of two-valence metal cations in high silica zeolites is the formation of binuclear species with extra-lattice oxygen $[M\text{-}O\text{-}M]^{2+}$. This structure can reveal interesting chemical properties. Recently we have found that such species can accumulate oxygen atoms from molecular oxygen with the formation of structures $[M\text{-}O_n\text{-}M]^{2+}$, n=2-4 [5]. The calculations were performed for $[M\text{-}O\text{-}M]^{2+}$, M=Zn, Ca, localized in mordenite 8-member ring. Such structures could be considered as active intermediates in the oxidation of a substrate by molecular oxygen. High-silica zeolites have a tendency towards stabilization of small polynuclear oxide clusters in zeolite channels due to lower exchange-ion zeolite capacity. The formation of such species is considered for ZnZSM-5 and GaZSM-5 zeolites and their catalytic ability in the dehydrogenation reactions of alkanes are discussed.

[1] A.L.Yakovlev, A.A.Shubin,G.M.Zhidomirov, R.A.van Santen. Catal.Lett. 70 (2000) 175
[2] A.A.Shubin, G.M.Zhidomirov, V.B. Kazansky, R.A.van Santen. Catal.Lett. 90 (2003) 137
[3] A.A.Shubin, G.M.Zhidomirov, V.B. Kazansky, R.A.van Santen. Theor.Chem.Acc.114 (2005) 90
[4] E. A. Pidko, E. J.M. Hensen, G. M. Zhidomirov, R. A. van Santen. Journal of Catalysis 255 (2008) 139
[5] G.M. Zhidomirov, A.V. Larin, D.N. Trubnikov, D.P. Vercauteren. Journal of Physical Chemistry C (2009), in press.

Theoretical Studies of Property Variations in Oligomers Precursors of Conducting Polymers

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Polymers containing carbazole and fluorene fragments in the main chain have attracted much attention because of their unique properties which allow for various photonic applications. To control the electronic and optical properties of such polymers one may introduce electron-rich heterocycles at the terminal polymerization sites to prepare multi-ring electropolymerizable monomers. The studied heterocycles, possessing the ability for electrochemical polymerization, are thiophene, ethylenedioxynothiophene, furane, methylopyrrole, and pyrrole.

The differences between HOMO-LUMO gaps, ionization potentials, and distribution of total atomic spin densities of radical cations of studied molecules can indicate the expected electropolymerization properties. The variation of above properties as the size of oligomers increases provides more precise tool for the modeling of conductive materials. The studies presented are based on molecular orbital calculations using the density functional theory.

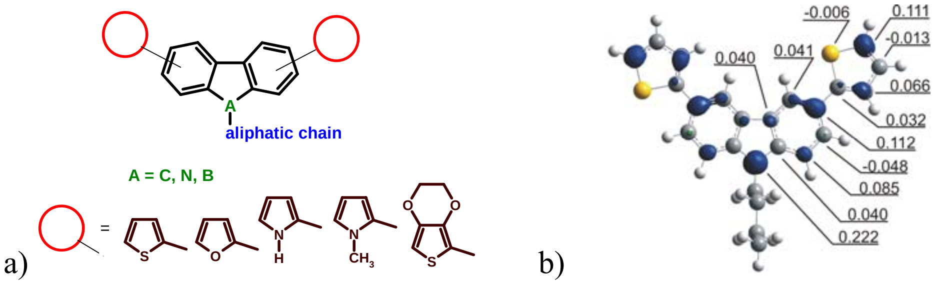

Figure: a) Carbasole and Fluorene derivatives b) Isovalent surfaces (0.004) of spin electron density (in blue) in thiophene carbasole. Atomic electron spin densities are given in electrons.

Devoted to academician Aleksey V.Bogatsky (1929-1983) blessed memory

Crown Ethers Complexes with Chromium(VI) Compounds. Supramolecular Aspects of Structure and Reactivity

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The approaches to synthesis of the crystalline complexes of miscellaneous crown ethers (**CE**) with alkaline and alkaline-earth metals and ammonium halogenochromates (**1**), halogenodiperoxochromates (**2**) and mono-(**3**), di-(**4**) and trichromates (**5**) $M_mCr_nO_{3n+1}$ (m=1 or 2; n=1, 2 or 3) were developed.

On the base of the X-ray analysis of more than 40 complexes, the factors defining their stehiometry and molecular organization (architecture) are discussed.

Independently of a stehiometry of these complexes and anions nature, as well as composition, dentaty, structure and configuration of **CE**, the structurally "rigid" fragment which determine a form of macrocycle in the complex and, as a consequence, a distance (**δ**) of metal cation from the mean plane of **CE** oxygen atoms, may be not only 1,2-phenylene but 1,2-cyclohexene. The parameter **Δ*l*** (characterizing the cation translation relative to the center of **CE** cavity) “responds” to a changing of “extra-ligand” composition – *e.g.* comparison of $\boldsymbol{l(\mathrm{K{-}O_{CE}})_{av}}$ and **Δ*l*** parameters allowed to realize the peculiar classification (screening) of studied complexes, in crystal structure of which a cation orientation is determined very largely by an initial **CE** conformational flexibility. However, among investigated complexes (including “sandwiches”) value of $\boldsymbol{l(\mathrm{Cr{-}O})_{av}}$ is noticeably on the decrease as value of $\boldsymbol{l(\mathrm{K{-}O_{Crown}})_{av}}$ increases and is symbate to changing of **δ** and Δ*l* values.

It was revealed that the whole complexes **1-5** selectively oxidize the benzyl (**BAlc**), allyl, furfuryl and amyl alcohols and cyclohexanol to corresponding aldehydes (ketone). The influence of solvent, cation and anion-oxidant nature, as well as a size of macrocycle, its composition and structure on the rate of the subject reaction is discussed. For instance, in contrast to complexes **1**, under the oxidation by complexes **2** the "sensibility" of studied alcohols to influence of substituents polarity (ρ^*) is by order of magnitude smaller and has opposite character.

The correlations between rates of **BAlc** oxidation and structural parameters **δ**, **Δ*l***, $\boldsymbol{l(\mathrm{M{-}O_{CE}})_{av}}$ and $\boldsymbol{l(\mathrm{Cr{-}O})_{av}}$ were revealed. On the base of obtained results the possible mechanisms of alcohols oxidation by complexes **1-5** are proposed.

The kinetics of complexes **1** decomposition up to complexes **2** is studied. It is revealed that orders and constants of the rates of an initial complex loss and a product accumulation do not depend practically on **CE** composition and structure. At the same time a character of the **CE** noticeably affects the differences between the contributions of enthalpy and of entropy components to a free energy of activation. The factors influencing the thermal stability of complexes **2** and possible mechanisms of their decomposition are discussed.

It was developed that the main factors defining **CE** activity in phase-transfer catalysis of **BAlc** oxidation by suspension of potassium chlorochromate in dichloromethane are the optimal size of a macrocyclic polyether and its form and also **CE** interaction with a surface of $KCrO_3Cl$ particles. On the base of 3D QSP(A)R-analysis results the structural fragments of so-called "productive conformations" of **CE** and main factors defining their activity as catalysts on interphase conditions are revealed.

This work was supported by Ukrainian Foundation of Fundamental Investigations (Project F7/463-2001) and National Academy of Sciences of Ukraine.

Assessing the Environmental Impacts of High Nitrogen Explosives: A Computational Chemical Approach

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High Nitrogen Explosives (HNEs) are high energy-density materials that are currently being investigated as possible replacements for the more traditional, yet environmentally-challenging, explosives such as RDX and TNT. HNEs are crystalline organic materials that contain more nitrogen than carbon as the backbone for the structure. Early testing of the detonation properties of this class of explosives shows desirable characteristics such as very high detonation velocity along with low impact sensitivity. Little is known about the environmental fate and impact of these materials at any point in its lifecycle history from manufacture, through deployment to retirement from use.

Ab initio computational chemical methods are being used to develop a comprehensive model for the environmental fate of HNEs. Hydrazinebistetrazole (HBT) and 2,2-diamino-1,1-dinitroehtylene (FOX7). Environmentally-relevant physical properties for these two compounds have been predicted. Optimized structures have been obtained for HBT and FOX7 in the gas phase and in water using a Conductor-like Polarizable Continuum Model (CPCM) and the BVWN5 functional and a 6-31+G(d,p) basis set. Results from the prediction of degradation mechanisms under alkaline conditions will be discussed.

Extrapolation of the PES using first and second derivatives

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The Born-Oppenheimer (BO) potential energy surface (PES) is required in many common calculations, such as reaction rates, cross sections, molecular spectra or dynamics. Due to its computational cost, the PES is calculated in an approximated fashion. In the analytic representation of the PES, it is costumary to include only a limited number of couplings between the coordinates -in our case, the vibrational normal modes- that represent the PES. Notwithstanding, PES including more than two mode-couplings are limited to small molecules.

In this work a procedure for the generation of BO *n*-mode PES from lower mode-couplings is presented. The procedure relies on the Taylor expansion for the *m*-mode PES ($m < n$) to extrapolate in the directions of higher mode-couplings. The formulation is general for any extrapolation from*m*mode to *n*-mode couplings and can be applied to the energy or any other molecular property surface for which derivative information is available. The method depends only on an analytical parameter free weight factor that satifies important limiting conditions and controls the contribution from each direction to extrapolate. In order to illustrate the approximation, anharmonic vibrational energies values are presented for a collection of triatomic and tetraatomic molecules. Our results indicate that the use of second-derivatives information on the *n*-mode PES provides with an extrapolated PES with a quality similar to that provided by the (n + 1)-mode PES.

[1] Toffoli D., Kongsted J., Christiansen O. *J. Chem. Phys.* 127, 204106 (2007)
[2] Matito E., Toffoli D., Christiansen O. *J. Chem. Phys.* 130, 134104 (2009)

An *ab initio* Molecular Dynamics Study on the Initial Chemical Events in Nitramines: Mechanism and Kinetics of Thermal Decomposition of CL-20

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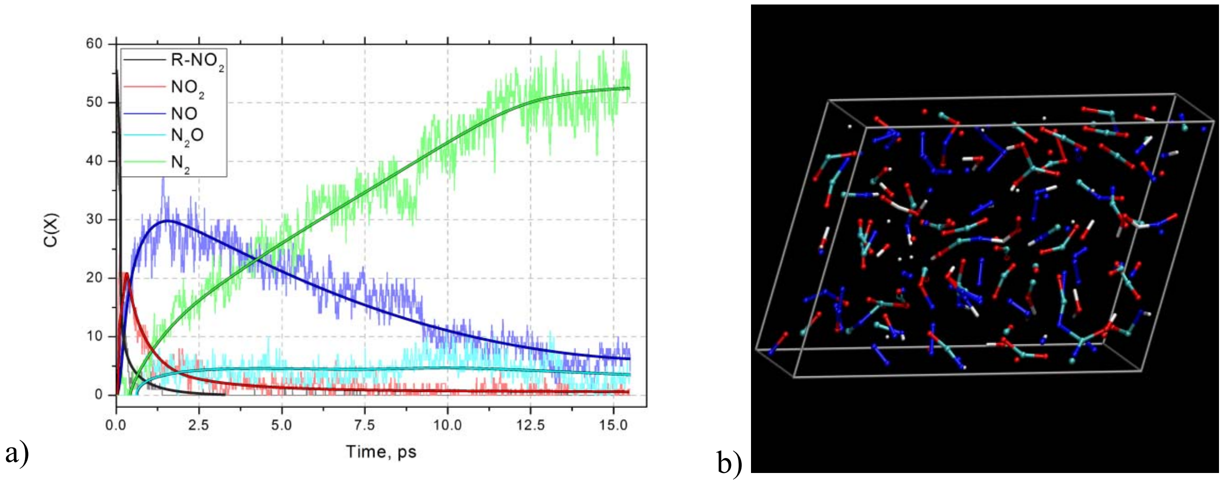
CL-20 (2,4,6,8,10,12-hexanitro-2,4,6,8,10,12-hexaazaisowurtzitane or HNIW) is a high-energy nitramine. To improve atomistic understanding of the thermal decomposition of CL-20 in gas and solid phases, we performed a series of *ab initio* molecular dynamics simulations using CPMD technique.

We found that during unimolecular decomposition, unlike other nitramines, CL-20 has only one distinct initial reaction channel—homolysis of the N–NO_2 bond. We did not observe any HONO elimination reaction during unimolecular decomposition, whereas the ring breaking reaction was followed by NO_2 fission. Therefore, in spite of limited sampling, that provides a mostly *qualitative* picture, we proposed here a scheme of unimolecular decomposition of CL-20. The averaged product population over all trajectories was estimated at 4 HCN, 2–4 NO_2, 2–4 NO, 1 CO, and 1 OH molecule per one CL-20 molecule. We concluded that obtained results demonstrate that AIMD simulations can provide detailed information about chemistry and kinetics of energetic materials under extreme conditions.



a) b)

Figure. a) Time evolution of initial CL-20 (R-NO_2), key reaction products N_2, N_2O, NO, and NO_2 for T=3000K, as calculated from simulations of the big (1×1×2 unitcells) model. Thick spline trendlines corresponds to the actual concentration data of matching color behind. b) Trajectory snapshot of reaction products for T=3000 K at time 15.5 ps.

Molecular Dynamics and Signal Transduction

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Long time-scale (50-100 nanosecond) molecular-dynamics simulations have revealed the mechanism of induction of the tetracycline repressor (TetR), which has become the archetypical signal-transduction system. TetR is responsible for the major mechanism of resistance of Gram-negative bacteria to the tetracycline class of antibiotics. It regulates its own expression and that of the tetracycline antiporter (TetA), a membrane-bound channel that pumps tetracyclines as their complexes with Mg^{2+} out of the bacterial cell and protons in. The available X-ray structures included a so-called flexible loop region that was not resolved, but proved to play a key role in the induction mechanism. [1] Remarkably, the TetR binding pocket shrinks by 40% of its volume on binding a tetracycline and becomes predominantly hydrophobic. [2]

Mutations of TetR are known that exhibit the reverse phenotype (i.e. they are induced in the absence of tetracyclines, but not in their presence). We were able to determine the origin of this effect for the G95E mutant, which shows the reverse phenotype. [3] Similarly, we have been able to deduce the mechanism of induction by the TetR-inducing peptide (TiP), which induces TetR by a different mechanism to that found for tetracyclines and can induce in the absence of Mg^{2+}.

The simulations indicate that the time scale of the induction event in TetR is far shorter than originally thought, so that we can observe allosteric changes directly and reproducibly. The implications of these results for the pre-equilibrium mechanism of induction will be discussed.

[1] H. Lanig, O. G. Othersen, , F. R. Beierlein, U. Seidel and T. Clark *J. Mol. Biol.*, **2006**, *359*, 1125-1136.

[2] H. Lanig, O. G. Othersen, U. Seidel, F. R. Beierlein, T. Exner and T. Clark *J. Med. Chem.*, **2006**, *49*, 3444-3447.

[3] U. Seidel, O. G. Othersen, F. Haberl, H. Lanig, F. R. Beierlein and T. Clark, *J. Phys. Chem. B*, **2007**, *111*, 6006-6014.

Explicit Hydration of Nucleic Acid Bases

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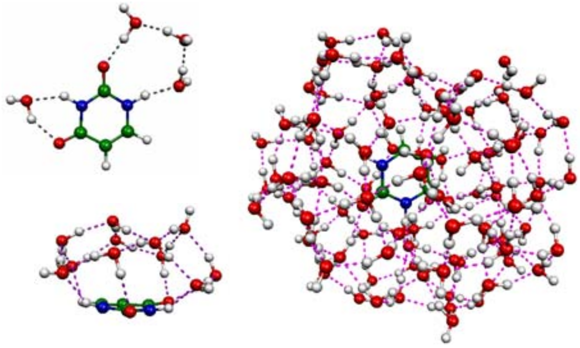
A thorough understanding of the hydration properties of the nucleic acid bases is of uttermost importance because of their relevance to the structure of DNA. Both microhydrated and fully hydrated clusters are of interest. The small hydrated clusters are an intermediary between gas-phase and fully hydrated bases, thereby providing a better understanding of the intricate effects of hydration. In addition, small hydrated clusters are known to play important roles in many biological processes. We have studied nucleic acid bases in environments ranging from microhydration (up to four water molecules),[1] via intermediately-sized hydrated clusters (comprising up to 16 water molecules)[2,3] to fully hydrated bases (surrounded by 50 and 100 water molecules).[4] The hydration model employed was found to have a major impact on the hydration properties.



[1] T. van Mourik, Phys. Chem. Chem. Phys. **3**, 2886-2892 (2001).
[2] V.I. Danilov, T. van Mourik and V.I. Poltev, Chem. Phys. Lett. **429**, 255-260 (2006).
[3] T. van Mourik, V. I. Danilov, E. Gonzalez, A. Deriabina and V. I. Poltev, Chem. Phys. Lett. **445**, 305-308 (2007)
[4] V. I. Danilov, T. van Mourik, N. Kurita, H. Wakabayashi, T. Tsukamoto and D. M. Hovorun, J. Phys. Chem. A (Letter) **113**, 2233–2235 (2009).

Problems with Delocalized Cations in Stacked Purines

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Numerous calculations have been performed on one-electron oxidation of stacked purines. In single crystals of the purine nucleotides, the cation is always localized on a single base. In calculations performed with DFT there is a tendency of the purine cation to be delocalized over several bases in the stack. Attempts have been made to see if methods other than DFT can be used to calculate localized cations in stacks of purines, and to relate the calculated hyperfine couplings with known experimental results. To calculate reliable hyperfine couplings it is necessary to have an adequate description of spin polarization which means that electron correlation must be treated properly. UMP2 theory has been shown to be unreliable in estimating spin densities due to overestimates of the doubles correction. Therefore attempts have been made to use quadratic configuration interaction (QCISD) methods to treat electron correlation. Calculations on the purine bases will be presented to show that with QCISD methods it is possible to calculate hyperfine couplings in good agreement with the experimental results. This technique is then used to explore localization/delocalization of the cation in stacks of purines.

Low-Energy Electron Attachment to DNA Fragments

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Nucleic acid bases, nucleosides, nucleotides, and dinucleoside phosphates are the subunits of DNA to be studied practically by reliable theoretical methods. Exploring electron attachment to these subunits of DNA single strands provides significant progress toward definitive predictions of the electron affinities of DNA single strands. The adiabatic electron affinities of the nucleobases, nucleosides, nucleotides, and oligonucleotides are found to be baes dependent. The geometric features, molecular orbital analyses, and the charge distribution studies for the radical anions of these species demonstrate that the excess electron in these anionic systems is dominantly located on the nucleobase moiety with the exception for the guanine related compounds. The investigations demonstrate that the vertical detachment energies (VDEs) of the radical anions of the oligonucleotides are significantly larger. Consequently, reactions with low activation barriers, such as those for O—C σ bond and N-glycosidic bond breakage, might be expected for the radical anions of the oligonucleotides.

From Simple Molecules to Biomolecules: a Hierarchy of Complexity. Some Applications on the Electron Addition on Dichalcogen Bond

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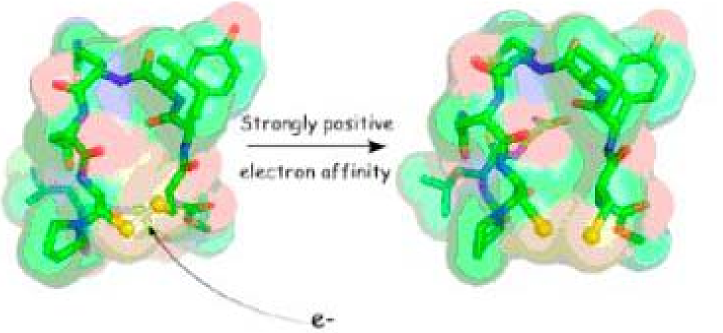
Electron addition on biomolecules is a fascinating reaction, which has raised much interest in the scientific community these last ten years, in relation with its utmost importance. Far from being only a fictitious prototype reaction, experimental results have ascertained the key role of free, low-energy electrons. They are intrinsically able to cause specific damages on proteins (disulfide bridge).

An ultimate understanding of these many-complicated processes will only come from synergetic experimental and theoretical approaches. Intensive research efforts have managed to offer a satisfactory view of model systems. The next step to restore the complexity of such systems is to take into account the biological environment, which falls into the range of hybrid methods. This surrounding can have a dramatic effect: It is known that the electron affinity of dimethyldisulfide molecule is very weak (≈0 eV). Substitutions by other alkyl groups or even aryl groups don't change this value by a significant amount. Surprisingly, the one of biomolecules (for example, the thioredoxin family) can be quite large (≈2 eV).

In this lecture, we will give some answers to understand this huge variation. Analysis of various effects (ring strain[1], electrostatic[2], mutation[3], chalcogen substitution[4], competition and selectivity[5], …) by means of several theoretical tools, ranging from orbital interpretation to hybrid computations mixing molecular mechanics and quantum mechanics[6], will be deeply detailed.



[1] E. Dumont, P.-F. Loos, X. Assfeld, Chem. Phys. Lett., 2008, 458, 276.
[2] E. Dumont, P.-F. Loos, A. Laurent, X. Assfeld, J. Chem. Theory and Comput. 2008, 4, 1171.
[3] E. Dumont, P.-F. Loos, X. Assfeld, *J. Phys. Chem. B*, 2008*, 112*, 13661.
[4] E. Dumont, P.-F. Loos, A. Laurent, X. Assfeld, Int. J. Quant. Chem. 2009, in press.
[5] E. Dumont, A. Laurent, P.-F. Loos, X. Assfeld, J. Chem. Theory and Comput. 2009, submitted.
[6] P.-F. Loos and X. Assfeld, J. Chem. Theory Comput. 2007, 3, 1047.

The promise (or not) of quantum chemistry in QSAR

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Quantitative Structure-Activity relationships (QSAR) link the (biological) activity of a molecule to its structure, where this structure is expressed in terms of a number of mathematical constructs called molecular descriptors. Via a series of statistical manipulations, the above mentioned link is expressed in some (usually a linear) regression equation. Clearly, if a very good QSAR model can be found, one could dream of predicting (biological) activity for molecules not even synthesized and in this way predict whether such a molecule is worth considering or not.

Unfortunately, and despite the advances made in the last decades, good predictive models that fulfill all requirements that a QSAR model should meet, are not so easy to obtain. One of the sources in which improvement could be sought lies in the molecular descriptors.

It is a direct consequence of quantum mechanics and thus quantum chemistry that there is an ultimate descriptor, namely the wave function or the electron density of the molecule. This entity namely contains all there is to know about the molecule, so including its (biological) activity.

In this lecture we will critically examine whether quantum chemistry really is such a fruitful source of information in QSAR. In this context we will show how quantum chemistry can help to obtain (and justify) different molecular descriptors characterizing e.g., aromaticity or the atom in the molecule and we will show several examples where sometimes quantum chemical descriptors do work, but others where it brings very little added value.

Elaboration of HiT QSAR for Analysis of Mixtures of Compounds

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Nowadays the usage of mixtures of compounds becomes more and more popular in the different fields. For example, combining virus inhibitors might overcome the disadvantages of monotherapy. Thus, anti-HIV agents possessing the same mechanism of action are combining in order to overcome resistance to single drugs or synergistic combinations of picornaviruses replication achieve the same antiviral effect at lower concentrations than those required if drugs were used alone.

Usually the interaction of the mixture with biological target cannot be described as just average between interactions of it parts because the last ones have different reactivity in such cases. It is especially applicable for the mixtures of compounds with synergetic or anti-synergetic action.

Thus, the main goal of our study was elaboration and application of Hierarchical QSAR Technology (HiT QSAR) based on simplex representation of molecular structure (SiRMS) approach to QSAR analysis of molecular mixtures and ensembles. At that case binary mixture would be represented by molecules of both components. Bounded and unbounded simplex descriptors would be used for description of such system. It is necessary to indicate whether the parts of unbounded simplexes belonging to the same molecule or to different ones. In the last case such unbounded simplex will reflect the structure of not single molecule as bounded ones, but will characterize a pair of different molecules. Actually unbounded simplexes of this kind are structural descriptors of the mixtures of compounds. Theirs usage allows analyzing synergism, anti-synergism or competition in the mixture interaction with biological target. Obviously that such approach is suitable for different nD QSAR models, where n = 2-4. If in the same task both mixtures and single compounds have been considered, individual compounds would be represented in usual manner and descriptors of mixture would be weighted depending on its composition. Thus mentioned above approach has been named by authors as "double nD QSAR". Although such methodic is suitable only to binary mixtures, it can be easily extended for more complicated tasks.

The application of "double nD QSAR" approach is demonstrated on following examples:

- Phosphorus-containing chiral AChE шnhibitors, where racemate represents 1:1 mixture of (R)- and (S)- isomers and AChE inhibition was expressed as decimal logarithm of the reaction rate coefficients ($lg(k_i)$, $M^{-1}sec^{-1}$);
- Toxicity of ester sulphonates, phenols, aliphatic n-alcohols and their binary mixtures tested against Daphnia magna in various ratios, IC_{50}, µmole/ml;
- QSAR analysis of in vitro inhibitory effects of dual combinations of picornavirus replication inhibitors. This task was the most challenging and interesting because of presence of highly synergistic and anti-synergistic effects depending on the combination and even the ratio of compounds in the mixture.

Reliable QSAR models were obtained in every study using modified simplex approach. Thus, double nD QSAR models could be used as a potent tool for QSAR analysis of action of mixtures of compounds.

Enumeration of Substituted Derivatives with Fixed Symmetries — an Attempted Improvement of the Normalizer-Based Approaches

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In contrast to traditional methods making it possible to simply enumerate substituted derivatives of a given chemical structure, the corresponding techniques producing the numbers of derivatives with fixed symmetries are less known and essentialy more sophisticated. The most advanced of these techniques [1-3] are based on the following, quite obvious idea: (1) to find some number(s) associated with those substituted derivatives whose symmetry is equal or exceeds that of the preselected point group and then (2) to apply some sort of the Inclusion-Exclusion technique to (sets of) results corresponding to all groups in question. All these techniques require to initially compute total lengths of orbits with the prescribed stabilizer groups and aren't based on the famous Pólya Theorem [4]; on the other hand, they typically use quite complicated inverses of mark tables at the final stage.

Another attractive way needs to directly compute numbers of orbits with the prescribed stabilizers; in this case, the equivalence of substitution products can be taken into account by means of the Pólya Theorem. V.R. Rosenfeld [5] was the first one who used for that purpose the well-defined normalizer groups acting on sets of orbits formed by a preselected (sub)group. This author declared his approach to be general and supplied it with proofs of several theorems on applicability of Pólya's and Inclusion-Exclusion techniques. In our recent paper [6], we have suggested theoretically similar but simpler alternative to Rosenfeld's normalizer-based method; in our approach, Pólya's technique was applied to automorphism groups of the easily constructed orbit partition graphs and then followed by stepwise calculation procedure at the final stage. Although this approach was demonstrated to successfully solve several typical enumeration problems, in the adamantane case, our and also Rosenfend's method were shown to produce some erroneous results (namely, those for C_s-derivatives). The applicability of both methods was attributed [6] to the so-called relevance of orbit partitions.

In this poster, we summarize our attempts to recognize the sources of errors and then to improve both techniques. The results show that, for any preselected group, equivalence of the corresponding "not-less-symmetrical" derivatives is correctly taken into account. But equivalence of the same derivatives is not taken into account for some other groups, i.e., those having a selected group as their (first, second, etc.) normalizer. For this reason, the numbers of "extra" duplicates should be computed and then subtracted from the corresponding numerical values (obtained by means of the Pólya technique for well-defined subgroups). As a result, the improved procedure becomes more complicated — it requires that all closed subgroups and chains of normalizer groups be recognized and some additional calculations be performed. This procedure is shown to correctly enumerate fixed-symmetry adamantane derivatives with achiral substituents; the solution to other enumeration problems is also demonstrated.

[1] W. Hässelbarth, Theoret. Chim. Acta 67 (1985) 339-367.
[2] A. Kerber, Algebraic Combinatorics Via Finite Group Actions, B.I.-Wiss.-Verl., Mannheim 1991.
[3] S. Fujita, Symmetry and Combinatorial Enumeration in Chemistry, Springer-Verl., Berlin 1991.
[4] G. Pólya, Acta Math. 68 (1937) 145-254.
[5] V.R. Rosenfeld, MATCH Commun. Math. Comput. Chem. 43 (2001) 111-130.
[6] S.S. Tratch and N.S. Zefirov, Russ. Chem. Bull. Int. Ed.. 57 (2008) 235-252.

Prediction of Animal Toxicity Endpoints Using a Combination of Chemical and Biological *in vitro* Descriptors of Molecules

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A wealth of available biological data for environmental chemicals or drug candidates requires new computational approaches to link chemical structure, short-term bioassay results, and chronic *in vivo* toxicity responses. We advance the predictive QSAR modeling workflow that relies on effective statistical model validation routines and implements both chemical and biological (i.e., in vitro assay results) descriptors of molecules to develop *in vivo* chemical toxicity models. We have developed two distinct methodologies for in vivo toxicity prediction utilizing both chemical and biological descriptors. In the first approach, we employ biological descriptors directly in combination with chemical descriptors to build models. Obviously, this approach requires the knowledge of biological descriptors to make toxicity assessment for new compounds. Our second modeling approach employs the explicit relationship between *in vitro* and *in vivo* data as part of the two-step hierarchical modeling strategy. First, binary QSAR models using chemical descriptors only is built to partition compounds into classes defined by patterns of *in vitro – in viv*o relationships. Second, class specific conventional QSAR models are built, also using chemical descriptors only. Thus, this hierarchical strategy affords external predictions using chemical descriptors only. We will present the results of applying both strategies to ToxCast Phase I data. Our studies suggest that utilizing *in vitro* assay results as biological descriptors afford prediction accuracy that is superior to both the conventional QSAR modeling that utilizes chemical descriptors only or in vivo effect classifiers based on in vitro biological response only. We will discuss how our models can be used to prioritize compound selection for in vivo studies.

Molecular Design of Neuroprotectors

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Important steps of drug design involve the search for and optimization of lead compounds using molecular modeling and quantitative structure-activity relationships (QSAR) techniques. The joint application of those approaches allows researchers to save time significantly on the step of the selection of candidate compounds for preclinical studies.

In the present paper the role of molecular modeling techniques, in silico screening and QSAR in the development of new neuroprotective drugs is discussed. The molecular models of ionotropic and metabotropic glutamate receptors, $GABA_A$ and $GABA_C$ receptors, adenosine receptors of several subtypes and their complexes with agonists, antagonists, ion channel blockers and modulators as important biotargets of neuroprotective compounds are considered and analyzed. The influence of structural modifications of ligands on their interaction with particular types of receptors and the design of compounds selectively and efficiently interacting with a given receptor subtype is discussed.

Minimum Principles and Asymmetry in Hartree-Fock and Density Functional Theory

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Both, the Hartree-Fock approximation (HF) and density functional theory (DFT) are based on minimum principles. However, the resulting many electron wave functions, which are single Slater Determinants, do not have the same symmetry as the exact eigenstates. This is apparent in the case of the spin symmetry, which is always present in the Hamiltonian of the many electron systems unless a nonuniform external magnetic field is applied. Even in the case that the number of spin up orbitals is equal to that of spin down, the corresponding up and down potentials are not the same, leading to asymmetric solutions. We discuss this phenomenon and exploit it to get lower energy solutions, with energy less than that of HF or DFT. Further, we get solutions with the proper symmetry, i.e. from the asymmetric states we get eigenstates of $\mathbf{S}^2$ which have energy less than that found by DFT and HF.

To what Extent are Thermodynamic Properties of Water Argon-Like?

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Surprising properties of water in its liquids states are well known. Among them, the special attention is usually paid to the non-monotonous temperature dependence of density, the large values of dielectric permittivity and the local structure, close to that in hexagonal ice. All these as well as other surprising properties are connected with the existence of H-bonds in water.

However, the role of H-bonds should noticeably change with temperature. Let τ_H be the average lifetime for typical local configurations of H-bonds. In the wide temperature interval, from the melting point T_m to the critical one T_c, τ_H has the same order of magnitude as the soft collision time: $\tau_H \sim a/\upsilon_T$, where a is the interparticle spacing and υ_T is the thermal velocity of a molecule. This conclusion about the temperature dependence of τ_H is practically self-evident if we take into account the behavior of the kinematic shear viscosity of water. For temperatures $T > T_m$, the latter has the same order of magnitude as for argon.

Our analysis shows that in the wide temperature interval the main thermodynamic properties of water are argon-like. In particular, for the fraction volume and the evaporation heat per molecule such a similarity takes place practically in the whole temperature interval $315K < T < 550K$ for liquid states. At $T < 315K$, i.e. in the supercooled and normal states joined to the melting point, the properties of water are determined by clusters, the lifetime τ_c of which is essentially greater than the characteristic time τ_H. At temperatures, closed to the critical point ($550K < T < 648K$), the properties of water are determined by both the fluctuation effects and the dimerization ones. In this region, the lifetime τ_d of dimers is also essentially greater than τ_H.

The similarity of the thermodynamic properties of water and argon in the wide interval $315K < T < 550K$ is naturally explained by the effective intermolecular potential between water molecules, which is obtained from the strongly anisotropic microscopic potential owing to the averaging on the rotation degrees of freedom.

In this report we consider 1) the structure of the averaged inter-molecular potential for water, 2) the closeness in the thermodynamic behavior of normal and heavy water and argon on their coexistence curves and 3) the cause of strong difference in the positions of the melting points for water and its nearest homologue H_2S.

Electronically Excited States in the Multireference State-Specific Coupled Cluster Theory

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The conventional, single reference coupled-cluster singles and doubles (CCSD) theory cannot properly describe most of the electronically excited states because the wave functions of those states usually contain two or more configurations (determinants) that being dominant are also degenerate (or quasidegenerate). Some success in potential energy surface (PES) calculations for excited states has been achieved by using equation-of-motion CCSD (EOM-CCSD) approach, linear response CCSD (LR-CCSD) method, and the symmetry adapted cluster configuration interaction (SAC-CI) method. The above mentioned approaches are all non-state-specific approaches i.e. the excited state wave functions are by-products of the ground state calculations. This means that in those methods the ground state wave function is determined first and then corrections due to an external electric field perturbation are calculated yielding excitation energies. Our multireference state-specific (MRSS) approach to calculate excited states is different because it focuses on a single excited state at a time and does not require precalculation of the ground state. The reference function of such approach includes the superposition of several most important determinants which generated as distribution of the active electrons among the *active orbitals*. The MRSS coupled cluster approach for the simple and frequently encountered case is based at two electrons by two orbitals (designated as I, A) active space. The wave function of the method (eXcited state Complete Active Space CCSD, XCASCCSD) can be written as:

$$\left|\Psi_{\mathrm{XCASCCSD}}\right\rangle = \mathrm{e}^{\mathrm{T}}\left(\delta + \lambda[\mathrm{a}_{\mathrm{A}}^{+}\mathrm{a}_{\mathrm{I}} \pm \mathrm{a}_{\bar{\mathrm{A}}}^{+}\mathrm{a}_{\bar{\mathrm{I}}}] + \gamma\, \mathrm{a}_{\mathrm{A}}^{+}\mathrm{a}_{\mathrm{I}}\mathrm{a}_{\bar{\mathrm{A}}}^{+}\mathrm{a}_{\bar{\mathrm{I}}}\right)\left|0\right\rangle, \qquad (1)$$

where, as usual, $\mathrm{a}_{\mathrm{A}}^{+}$ and a_{I} are second quantized operators. The determinant $\left|0\right\rangle$ and some single and double excitations from it are reference determinants. The cluster operator T generates all single and double excitations from all reference determinants. In our approach all the necessary excitations, which is correspond to wave function (1), generated as higher level excitations from selected "*formal reference*" determinant. Depending on the spatial and/or spin symmetry, δ, γ, and λ can have different values.

Appropriate diagrammatic representation, working equations and corresponding FORTRAN code for XCASCCSD approach have been obtained by using our program package CLUSTER [1]. The set of approaches to general ansatz also has been proposed and tested [2,3]. Our previous calculations have demonstrated a very good ability of the XCASCCSD method to describe PES of ground and excited states of molecular systems as compared with the full configuration interaction calculations. The calculated spectroscopic parameters as well as the energies of vibrational levels of some diatomic molecules in states with different spatial and spin symmetries ($^{1,3}\Sigma^{\pm}$, $^{1,3}\Pi$, $^{1,3}\Delta$) are in good agreement with the experimental data.

[1] D.I. Lyakh, V.V. Ivanov, L. Adamowicz, J. Chem. Phys. **122**, 024108 (2005).
[2] V.V. Ivanov, L. Adamowicz ,D.I. Lyakh, J. Chem. Phys. **124**, 184302 (2006).
[3] D.I. Lyakh, V.V. Ivanov, L. Adamowicz, J. Chem. Phys. **128**, 074101 (2008).

Deterministic Chaos in Oscillating Reactions with Three Component

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Let us consider a system of three reacting chemical components, as one of reactions that serve as an example of non-equilibrium thermodynamics, resulting in the establishment of a nonlinear chemical oscillator, similar to BZ-reaction.

The model is defined by the system of equations

$$A_{n+1} = A_n - k_{AB} \cdot A_n^2 + k_{BA} \cdot B_n^2 + A_{in}$$

$$B_{n+1} = B_n + k_{AB} \cdot A_n^2 - (k_{BA} + k_{BC}) \cdot B_n^2 + k_{CB} \cdot C_n^2$$

$$C_{n+1} = C_n + k_{BC} \cdot B_n^2 - (k_{CB} + k_{out}) \cdot C_n^2,$$

here k_{XY} (X, Y = A, B, C) $\in (0, 1)$.

In general, solutions of the system of equations can be found only numerically. Our investigation of the model showed that the region in the parameters space for which there exist stable phase trajectories is bounded. The system has a stationary solution that can be obtained analytically if A_{in} is small enough.

When A_{in} increases there are two possibilities of further evolution of the system. In the first case, it undergoes a cascade of the period-doubling bifurcations and Feigenbaum scenario of transition to chaos is realized. The ratio of intervals between two successive bifurcations coincides with the universal Feigenbaum constant $\delta_F = 4.669$ with error 1.3 %.

In the second case after the periodic regime, we observed a situation similar to Hopf bifurcation that leads to a quasi-periodic regime and an occurrence of an attractor consisting of two closed curves in the phase space.

Further increase of A_{in} leads to a bifurcation resulting in a chaotic regime. In such a case, there occurs a strange attractor in phase space (Fig.1). We found out that when a quasi-periodic regime is realized, it is possible that a synchronization of the model will occur. In such a situation, a periodic regime in the system occurs with a period depending on the level of synchronization.

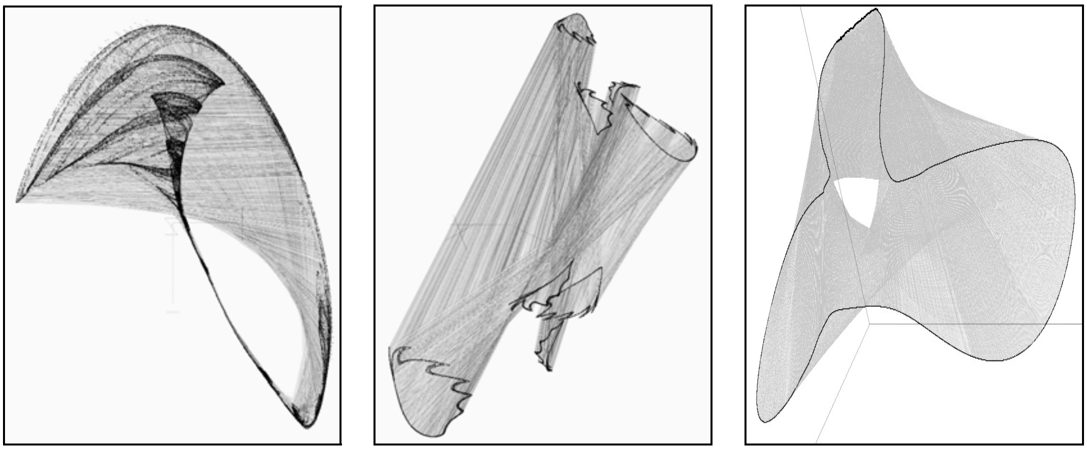

Fig.1. Examples of the strange attractors in phase space of components mass.

[1] A. Herega, in Proceedings of the 4th Siberian Congress on Applied and Industrial Mathematics (INPRIM-2000), Novosibirsk, 2000.

[2] A. Aslanov, A. Herega, T. Lozovskiy, Technical Physics, **51**, No 6, 812 (2006).

[3] A. Herega, T. Lozovskiy, Engineering Simulation, **30**, No 3, 3 (2008) (in Russian).

On the Energy Spectrum and Low-Temperature Thermodynamics of Model Ferrimagnet Having One-Dimensional Magnetic Sublattice of Spin Tube Type

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The one-dimensional magnetic systems exhibit a big variety of unusual physical phenomena such as quantum phase transitions, plateau of intermediate magnetization and others. Therefore, the corresponding quasi-one-dimensional magnetic materials may be of interest for modern nanotechnologies.

We studied analytically and numerically the energy spectrum and magnetic properties of spin tube formed by folding of stripe fragments of decorated rectangular spin-½ lattice with antiferromagnetic isotropic Heisenberg interactions of neighboring spins (Figure 1). This tube has three-site unit cell and can be treated as a collection of L cyclic fragments formed by n unit cells

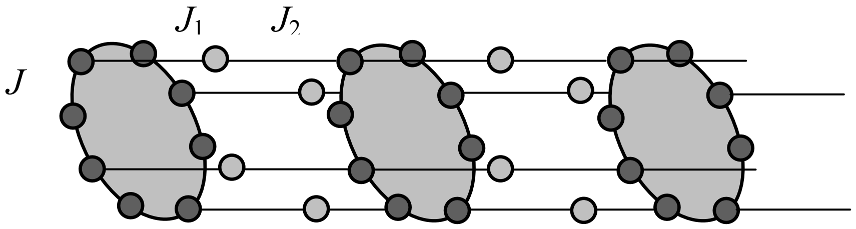

Figure 1. Tube formed by 12 spin cyclic fragment ($n = 4$)

At $L \to \infty$ these tubes should have the ground state which is characterized by spin-wave structure and macroscopic value of total spin $S_0 = Ln/2$. In addition, in this limit, the exact excitation spectra should be gapless for arbitrary positive value of coupling constants. In other words our spin model represents "ferrimagnetic nanotubes" of different diameters. We suppose that such spin structures may be present in quasi-one-dimensional compounds on the base of transition metals.

For weak interaction between cyclic fragments ($J_1, J >> J_2$) the low-energy states of the tube are described well in first order of perturbation theory in J_2 by effective Heisenberg Hamiltonian, which corresponds the uniform spin-$n/2$ chain with ferromagnetic coupling constant J_{eff}. For $n = 5 - 7$ we determined numerically that J_{eff} takes maximum value at $J_1/J \sim 0.5$ (the Davidson method was used). We also found the finite energy gap between the excitations with $S \geq S_0$ and the ground state of these tubes. Due to this gap, the field dependence of tube magnetization should have an intermediate plateau which is increase with the increasing of value of J_2. For arbitrary coupling we estimate the ground state energies per spin $E_0(n)$ of infinite tubes with $n = 2, 3$ by means of simple cluster-expansion renormalization technique and compare the results with the approximate variational estimates. For uniform tubes $(J_1 = J_2 = J = 1)$ we found: $E_0(2) = -0.4779$, $E_0(3) = -0.4719$.

For evaluation of low temperature thermodynamics of infinite tubes with $n = 2, 3$ we used simplified model with Ising interaction between ring segments (dark balls) and additional spins (light balls). The temperature and field dependencies of infinite tube magnetization and magnetic susceptibility were determined numerically by means of transfer-matrix approach for the corresponding Heisenberg-Ising spin Hamiltonian.

Linear Augmented Cylindrical Wave Method For Calculating the Pristine and Chemically Modified Nanotubes

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Every carbon single-walled nanotube (SWNT) can be generated by first mapping only two nearest-neighbor C atoms onto a surface of a cylinder and then using the rotational and helical symmetry operators to determine the remainder of the tubule. With account of these symmetries, we developed a symmetry-adapted version of a linear augmented cylindrical wave (LACW) method. In this case, the cells contain only two carbon atoms, and the *ab initio* theory becomes applicable to any SWNT independent of the number of atoms in a translational unit cell [1]. The approximations are made in the sense of muffin-tin potentials and local-density-functional theory only. We have calculated the total band structures and densities of states of the chiral and achiral, semiconducting, semimetallic, and metallic carbon SWNTs up to the (100, 99) tubule containing the 118 804 atoms per translational unit cell. About 150 functions produce convergence of the band structures better then 0.01 eV independent of the number of atoms in the translational unit cell. Moreover, the electronic structure of double-wall carbon nanotubes (DWNT) consisting of two concentric graphene cylinders is calculated in the terms of the LACW method [2]. In this approach, the electronic spectrum of the DWNTs is governed by the free movement of electron in the interatomic space of two cylindrical layers, by electron scattering on the MT spheres, and by electron tunneling between the layers. The electronic structure of SWNTs embedded in a crystal matrix containing structural defects and impurities are investigated using LACW method too [3,4]. A delocalization of the nanotube electrons into the matrix region results in a strong band-structure perturbation. In the case of armchair nanotubes, the delocalization is responsible for a high energy shift of the states and growth of the electron density of states at the Fermi level. For the semiconducting nanotubes, it causes a decay of the minimum energy gap and the formation of a metallic state.

This study was supported in part by the Russian Foundation for Basic Research (Grant no. 08-04-00262 and 08-08-90411) and Ukraine National Academy (Grant 0 26-08).

[1] P.N. D'yachkov and D.V. Makaev, *Phys. Rev. B* **76**, 195411 (2007).
[2] P.N. D'yachkov and D.V. Makaev, *Phys. Rev. B* **74**, 155442 (2006).
[3] P.N. D'yachkov and D.V. Makaev, *Phys. Rev. B* **71**, 081101 (2005).
[4] P. N. D’yachkov and D.V. Makaev. J. Phys. Chem. Solids. Vol. 69, No 12 (2008).

Spin Catalysis in the Process of H_2S Oxidation with Quinones and Quinoid groups on the Surface of Active Carbon: a Quantum Chemical Insight

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Examination of catalytic oxidation of H_2S is actual and practically important task, since hydrosulphide (H_2S) and lower mercaptanes are known atmospheric pollutants. One of the most used ways of H_2S fixation is an oxidation by molecular oxygen in aqueous solution of quinones (Q) [1]. Alternative way is a catalytic oxidation on active carbon (AC) surface [2-5]. According to the current opinion in carbon chemistry the nature of elementary acts in both processes is similar, since ACs contain quinoid surface groups (Q-groups) [6–8] and. Thus, the generalised reaction of H_2S oxidation implies reaction with Q-groups.

A series of arguments [2,9,10] are provided to support the following 2-stage mechanism of the process:

$$Q + H_2S \rightarrow HQ + S;$$
$$HQ + O_2 \rightarrow Q + H_2O,$$

where Q acts both for quinone and Q-groups on the surface of AC. Therefore, the Q and Q-groups are regenerated in the process and, hence, the overall process may be treated as catalytic one. The elementary acts are not catalytic in a classical paradigm. However, the elementary acts of this process are the subject of spin catalysis [11], since the elementary reactions occurring are spin-dependent and should be sensitive to presence of spin catalysts or intermediate spin-active species. Formation of elementary sulphur and polysulphides has been QC demonstrated. Energetic parameters of elementary reactions have been computed. An impact of multiplicity state of the system on the pass of reactions has been formulated. One can also assume that the oxidative catalysis of the lower mercaptanes passes in analogous way.

[1] V.T. Yavorskii, V.F. Mel'nik, Z.L. Konovalenko, Ya.A. Kalymon, M.A. Menkovskii, Zh. Prikl. Khim. (Russ) 49 (1976) 2110.
[2] R. Steudel, Ind. Eng. Chem. Res. 35 (1996) 1417.
[3] F. Adib, A. Bagreev, T.J. Bandosz, Langmuir 16 (2000) 1980.
[4] T.J. Bandosz, Carbon 37 (1999) 483.
[5] S.V. Mikhailovsky, Yu.P. Zaitsev, Carbon 35 (1997) 1367.
[6] M.A. Fryling, J. Zhao, R.L. McCreery, Anal. Chem. 67 (1995) 967.
[7] Y.-C. Liu, R.L. McCreery, J. Am. Chem. Soc. 117 (1995) 11254.
[8] J. Lahaye, Fuel 77 (1998) 543.
[9] M. Steijns, F. Derks, A. Verloop, P. Mars, J. Catal. 42 (1976) 87.
[10] M. Steijns, P.Koopman, B. Nieuwenhuijse, P. Mars, J. Catal. 42 (1976) 96.
[11] D. Schröder, H. Schwarz, in Essays in Contemporary Chemistry. From Molecular Structure towards Biology, G. Quinkert, M. V. Kisakürek (Eds.) Helvetica Chimica Acta, Zürich, Switzerland, 2001. P. 131.

Molecular Modelling of Supramolecular Reactions of Organic Peroxides and Onium Salts

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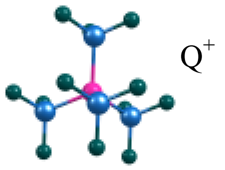
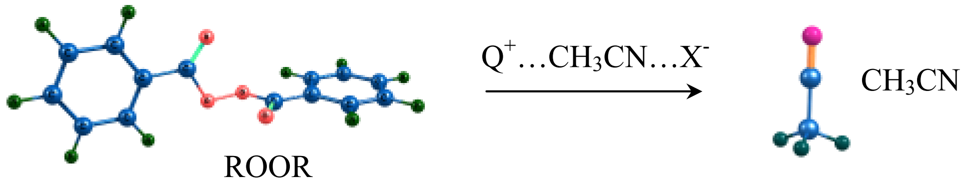
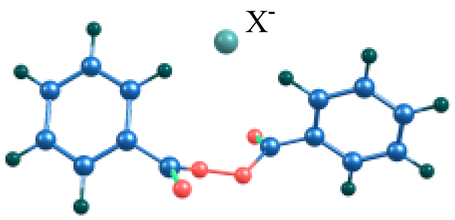
For reaction of the organic peroxides catalytic decomposition in the presence of the quaternary ammonium salts the supramolecular mechanism of the reaction proceeding has been proposed. Quaternary ammonium salts are catalysts of the radical decomposition of peroxides - diacyl peroxides, aralkyl hydroperoxides, cyclohexanone peroxides [1, 2]. Stage of complex formation between the peroxide molecule and the salt has been investigated by NMR spectroscopy and kinetic methods. The anion nature is the dominating factor in the chemical activation of the peroxide molecule, and the quaternary ammonium cation contributes to the structural destabilization of the peroxide.

For investigation of molecular recognition stage of the decomposition reaction of benzoyl peroxide, lauroyl peroxide, dioxydicyclohexyl peroxide, cumene hydroperoxide, tert-butyl hydroperoxide activated by cations, anions, contact and solvent separated ion pairs of the quaternary ammonium halides the semiempirical AM1 and DFT UBHandHLYP methods have been used. Interactions of the solvent separated ion pair of the salt ($Q^+ \ldots CH_3CN \ldots X^-$) with the peroxide molecule (ROOR) leads to the formation of two types of complexes. In complex-bonded peroxide molecule the elongation and weakness of the O-O bond are observed as compared with non-bonded peroxide. The key factor of the peroxide fragment COOC activation in the presence of the quaternary ammonium salt is structural changes of COOC fragment. Molecular modeling of the minimum energy path of the peroxide bond decomposition has shown that the structure of the complex decomposition transition state is similarly to its equilibrium configuration in the reaction ground state.







For the presented complex model the electron transfer in the reaction transition state from the salt anion to the peroxide bond is not observed. The peroxide decomposition in this case will be the catalytic radical-pair reaction. For the alternative model when the peroxide molecule is located in anion and cation strong electrostatic field the electron transfer is observed in the decomposition reaction transition state. It leads to the reaction proceeding accordingly to the oxidative-reductive mechanism.

[1] Turovskyj M.A., Opeida I.O., Turovskaja O.M., Raksha O.V., Kuznetsova N.O., Zaikov G.E. // Oxidation Communications. – 2006. – Vol. 26, No. 2. – P. 249-257.

[2] Turovskyj M.A., Opeida I.O., Kusch O.V., Baranovskyj E.L., Zaikov G.E. // Journal of the Balkan Tribological Association. - 2007. Vol.13, No 1. P. 72-78.

Abnormal Shifts in Raman Spectra of Deuterated Cytidine and 6-Azacytidine: Experimental and Calculated

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Anomalous nucleoside 6-azaC is known as an antimetabolite with wide spectrum of therapeutic activities. By comparison Raman study of 6-azaC dissolved both in H_2O and D_2O it was revealed that some Raman peaks of 6-azaC dissolved in D_2O have manifested abnormal high frequency shifts with respect to their position water solution while the other have been shifted to low frequencies. Similar results were obtained for canonical nucleoside cytidine and its related nucleobase cytosine. In the Table below are listed positions ν and shifts Δν of two most intensive lines in Raman spectra of these 3 compounds as example of normal and abnormal Raman shifts.

Substance		Raman peak positions ν and shifts Δν in H_2O and D_2O solutions, cm^{-1}					
		Normal shifts			**Abnormal shifts**		
		ν(H_2O)	ν(D_2O)	Δν	ν(H_2O)	ν(D_2O)	Δν
6-azacytidine	exp*	759,6	748,8	10,8	1288,9	1302,6	-13,7
	cal**	774,5	761,8	12,7	1292,4	1299,9	-7,5
cytidine	exp	784	773,5	10,5	1244	1247,6	-3,6
	cal	786	773,6	12,4	1266,9	1270,3	-3,4
cytosine	exp	786,8	777,3	9,5	1290,2	1291,3	-1,1
	cal	785,1	772,3	12,8	1296,8	1303,2	-6,4

* – experimental, **– calculated

To discriminate effect of deuterated solvent and deuteration effect of the nucleoside molecule itself we have made recrystallization of 6-azaC and cytidine from their H_2O and D_2O solutions. Raman spectra of 6-azaC microcrystals recrystallized from H_2O solution occurs identical with spectra of the initial 6-azaC microcrystalline sample but in spectra of 6-azaC microcrystals recrystallized from D_2O solution in addition to the initial peak at 760 cm^{-1} appeared peak at 750 cm^{-1} and in addition to the initial peak at 1290 cm^{-1} appeared peak at 1301 cm^{-1}. It confirms noticeable deuteration effect of the nucleoside molecules itself in D_2O solution and existence of abnormal Raman isotopic shift in 6-azaC crystal too. Similar results were obtained for recrystallized cytidine. To the best of our knowledge this is the first observation of abnormal Raman frequency shifts of intramolecular modes under deuteration.

The close similarity of Raman spectra of 6-azaC in crystalline form and solved in different solvents in the region from 500 to 1800 cm^{-1} allows us to assume that parameters of intramolecular modes in crystal and in solutions are approximately the same. Calculations of Raman spectra were performed for free molecules of the above 3 compounds and their water solutions using PCM model, Gaussian 03 package, B3LYP hybrid density functional in 6-31+G (d,p) basis set. In the calculated spectra of 6-azacytidine and cytidine were obtained both normal and abnormal shifts close to the experimentally observed (see the Table) except abnormal shift in spectrum of cytosine.

We assume that abnormal shift occurs due to deuteration of intramolecular H-bonds. To test such possibility we calculated Raman spectra of benzophenone and fully deuterated benzophenone that has no H-bonds and of 2,2′-dihydroxybenzophenone that contains two adjacent OH groups. No abnormal shift occurs for benzophenone in view of excellent agreement of calculated and measured spectra. On the contrary after replacement of OH with OD in the last molecule 1060-cm^{-1} peak moves for 5.4 cm^{-1} to higher frequencies.

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Theoretical Investigations of DEA-NONOate Decomposition Pathways

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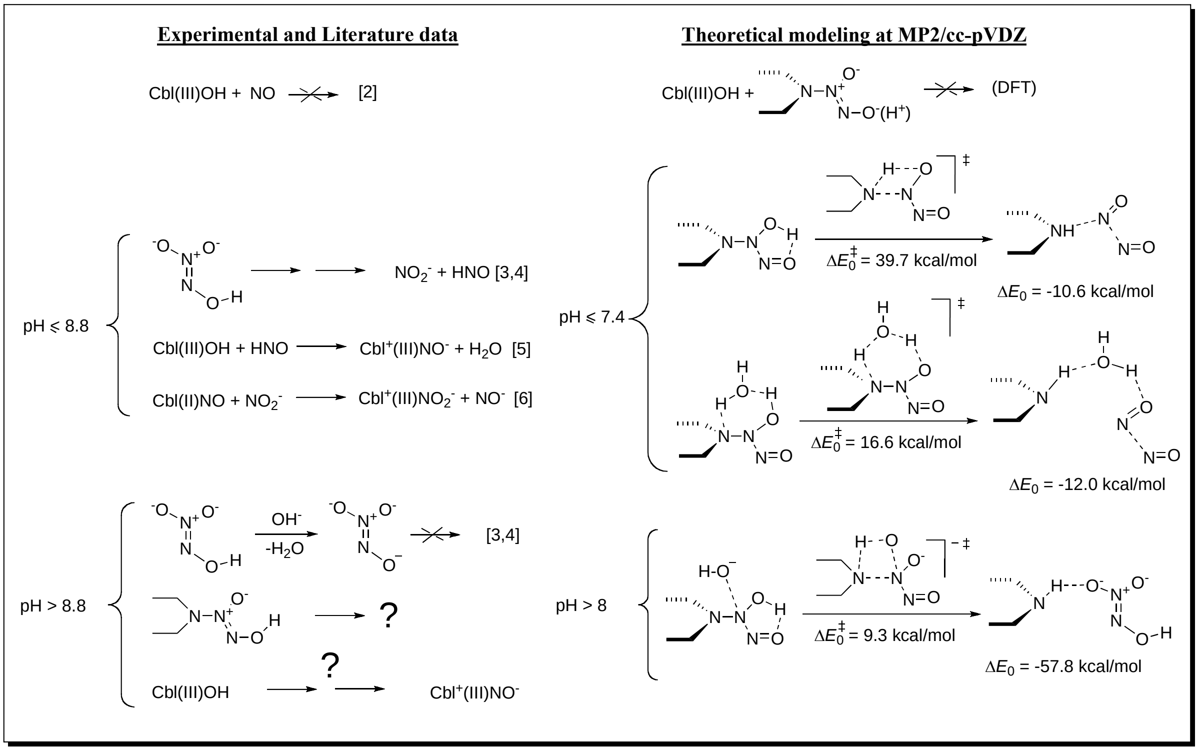
Nitric oxide (NO) is an important bioregulatory agent, and structural studies of the interactions of hemes and heme models with NO have played a major role in elucidating the activation mechanism of the NO-receptor enzyme guanylate cyclase. Emphasis has also been placed on various NO carriers and how such entities function to release NO. Previously it was shown that the Drago $R_2N[N_2O_2]^-$ anions ("NONOates") are smooth nonenzymatic releasers of nitric oxide in physiological media.

The NO derivative of vitamin B12, known as nitrosylcobalamin (NOCbl), has recently attracted a lot of attention in the literature. The first efficient procedure to synthesize NOCbl was reported in 2007 and was based on reaction of the NO donor 2-(N,N-diethylamino)diazenolate-2-oxide (DEA-NONOate) with hydroxycobalamin hydrochloride.[1]

Provided the importance of the understanding mechanisms of such reactions, we have preformed extensive DFT and MP2 calculations on possible DEA-NONOate decomposition pathways and its reaction with NOCbl.



[1] Hannibal, L.; Smith, C. A.; Jacobsen, D. W.; Brasch, N. E. *Angew. Chem*. **2007**, *46*, 5140.
[2] Selçuki, C; van Eldik, R.; Clark, T. *Inorganic Chem.* **2004**, *43*, 2828.
[3] Duton, A. S., Fukuto; J. M., Houk, J. M. *J. Am. Chem. Soc.* **2004**, *126*, 3795
[4] Hughes, M. N.; Wimbledon, P. E. *J. Chem. Soc. Dalton Trans.***1976**, 703.
[5] Our suggestion is based on results from Miranda, K. M. et al. *J. Med. Chem.*, **2005**, *48*, 8220.
[6] Roncaroli, F.; Shubina, T. E.; Clark, T.; van Eldik, R. *Inorg. Chem.* **2006**, *45*, 7869-7876.

The Kinetics of Cluster Formation during the Phase Transition Gas-Liquid in Alcohols

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The processes of the molecular cluster formation of monohydric alcohols (from methanol to hexanol) were investigated by FTIR using the matrix isolation technique in Ar matrices. The transformation of FTIR bands of free hydroxyl groups (3600 – 3800 cm^{-1}) into diffuse bands (3000 – 3600 cm^{-1}), which were assigned to the stretching vibrations of the H-bonded O–H groups in various clusters, was monitored in its initial stage softening the matrices by heating from 20 K to 50 K.

The quantum-chemical calculations of different alcohol clusters were carried out with the program set Gaussian 03 (B3LYP, 6-31G(d,p)). The comparison of the calculated vibrational spectra of the studied alcohols with the experimental IR spectra of alcohol clusters trapped in Ar matrices gives the possibility to determine the cluster structure of investigated alcohols.

The band shape analysis was carried out for all investigated systems. The FTIR bands of alcohol molecules trapped and solidified in the matrices without annealing were found very close to be Gaussian-shaped, whereas the contours of water bands, which presents in the samples as impurity, were perfectly fitted by Lorentz functions. The magnitude of inhomogeneous broadening due to the matrix effect was evaluated from the bandwidth of monomer species. The values of hydrogen bond dissociation time of alcohols in trapped in matrices were evaluated from the bandwidths of dimers, trimers and higher aggregates after broadening factor was taken into account. These data correlate with those directly measured in ultra fast infrared experiments of alcohols in solutions.

Nature of the Positive and Negative Hydration for Single Charged Ions of Alkali Metals in Water Solutions

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The local structure around ions in water-electrolyte solutions is determined by the interaction potentials between them and water molecules. The main aim of this talk is to present the generalized Stillinger-David potential, which describes the interaction between ions and water molecules. It takes additionally into account the polarization of oxygen ions that arises due to the effect of the soft repulsion between ion and oxygen anion at their contact. Due to account of the additional polarization effects the generalized Stillinger-David potential reproduces the results of quantum-chemical calculations with good accuracy.

The proposed potential allows to perform the direct calculations of the interaction energy between doped ions and water molecule surrounding of them. The approximation of the nearest neighbors is used. It is supposed that doped ion is located at the center of the hexagonal cell formed by water molecules, the positions and orientations of which are similar to that for the hexagonal ice (1h). The immediate comparison of the interaction energies for different ions shows the specific role of the ion K^+, in consequence of it plays the key role in the definition of the positive and negative hydration. It is established that the sign of the hydration energy for ions of alkali metals depends, first of all, upon the sign of the configuration part $\widetilde{Z}_q$ of the hydration energy. In its turn $\widetilde{Z}_q$ depends on the difference in the charge distribution for some ion I^+ and K^+.

The main attention in the talk is focused on 1) the construction of the generalized Stillinger-David potential; 2) peculiarities of the interaction of water molecules with different ions and 3) the analysis of the potential surfaces for different ions.

Comprehensive Conformational Analysis of Canonical and Modified Nucleosides: Structure-Activity Relationship. *Ab initio* DFT and MP2 Study

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The aim of this work was to present a comprehensive investigation of structural and vibrational properties of some nucleosides (canonical, minor and modified) by ab initio calculations. The obtained results demonstrate a wide scope of conformational flexibility of nucleosides corresponding to a narrow range of energy (7-10 kcal/mol). Slightly less than one hundred conformers of deoxyribonucleosides are stabilized by some hundred intramolecular H-bonds of various types, i.e. from the strongest (OH...O), to the weakest ones (involving CH groups). It was shown that at 298.15 K, all of the studied nucleosides are characterized by quasi-degenerate global minima on the Gibbs energy landscape, each global minimum corresponds indeed to two conformers. Conformational equilibrium of isolated nucleosides appears to be shifted towards syn base orientation. Moreover, South (S) conformers of sugar dominate over North (N) conformers. The whole set of conformational parameters were estimated and correlations between them were established. Geometrical, vibrational, structural-topological, and energetic features of intramolecular H-bonds in the calculated conformers were determined. Convolution of calculated IR spectra in the ν(O-H) range for all the thymidine and 2′-deoxyuridine conformers appeared to be consistent with the observed low-temperature matrix spectra. Among the full calculated conformational families of nucleosides, only three DNA like conformers were detected related to BI, A and BII forms. In contrast, 2′-deoxy-6-azacytidine (i.e. modified analogue of 2′-deoxycytidine) adopts only an A form like conformation. A close inspection of the above-mentioned theoretical data leads to some conclusions at biological level. In particular, the biological effect of this modified nucleoside may correspond to the inhibition of replicative DNA polymerase caused by an unusual orientation of the sugar residue against the base in the only A form conformer. On the other hand, the close similarity between calculated energetic and geometric characteristics of thymidine and 2′-deoxyuridine DNA like conformers with anti and syn base orientations and transition states of anti→syn interconversion between them, leads to think that the uracil mismatch glycosylase discriminates between the two nucleosides due to the difference in their shapes (methyl group in thymidine instead of hydrogen atom in 2′-deoxyuridine at position 5 of pyrimidine ring), rather than due to the electronic influence of methyl group.

Modeling of Electronic and Molecular Structures of M-DNA Fragments: From monomer to Stacking Oligomers

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Metallized DNA (M-DNA) with transition metal ions placed between nucleic bases has the conductance ability and this is the fact of great interest for nanotechnology To study the molecular structure of M-DNA and conductance mechanisms in it the quantum-chemistry calculations were performed to obtain electronic and spatial structures, thermodynamic characteristics of stacking dimers, trimers and tetramers of nucleic acids base pairs, both with n zinc ions (n=2,3,4) together with hydroxyls and without such ions. The calculations of these properties of GC pairs with Mg^{2+}, Ni^{2+} ,Cd^{2+} and hydroxyl were carried out too. Geometry optimisations of oligomers studied were performed at MP2 level of theory and by using M06 functional, being employed 6-31G* basis sets. The interaction energies were calculated at the usual scheme with including BSSE by using 6-31+G* basis sets.

Calculations performed at MP2 level of theory demonstrated that stacking oligomers of nucleic acid bases with zinc ions have bridges between base pairs. The inter-plane distance in the dimers, in trimers and in tetramers is equal to 3.2Å. The highest occupied molecular orbitals (HOMO) in dimer and trimer of base pairs with zinc ions include MOs of bases being adjacent in the stack .

The interaction energies between base pairs in stacking dimer without zinc ions (AT)(CG) and in stacking dimer with zinc ions $(AT)(CG)\cdot 2Zn^{2+}$ are of 11.0 kcal/mol and 37.4 kcal/mol respectively. H-bond interaction energies in oligomers studied were calculated too.

Middle base pairs in stacking trimers and tetramer studied are more planar in comparison with outer pairs.

Amyloid formation of Two Abl-SH3 Domain Peptides

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Short-peptide sequences drive protein aggregation in amyloid fibrils [1-2]. Based on a homology search we have identified an aggregation-prone region in the Abl-SH3 domain of Drosophila with sequence **DLSFMKGE** (**MK**), and less amyloidogenic human homologous region with sequence **DLSFKKGE** (**KK**).

The antiparallel flat β-sheets consisting of two and ten strands of MK and KK were constructed. We created four single sheet systems: (1) two strands of MK **(2xMK)**, (2) two strands of KK **(2xKK)**, (3) ten strands of MK **(10xMK)**, and (4) ten strands of KK **(10xKK)**. Each of these β-sheet systems was surrounded by a 10 Å layer of water molecules over the solute and subjected to molecular dynamics (MD) simulations with the Amber 8.0 force field in the NPT (constant number of molecules, pressure, and temperature) scheme.

From the results of single sheet simulations [3] we can conclude that the 2xMK β-sheet is more stable than the 2xKK β-sheet, and the 10xMK β-sheet is more stable than the 10xKK β-sheet; this suggests that the MK peptide is more prone to fibril formation than the KK peptide. The increased stability of the β-sheet formed from the the 10xMK system arises because of the interactions between the methionine and the phenylalanine residues of the neighboring strands. Replacement of Met by Lys removes that stability factor.

Neither the two- nor the ten-strand β-sheet systems are not sufficiently stable at 300 K, which means that they should be stabilized by other parallely placed β-sheets to form fibrils. To prove this hypothesis some parallely placed multisheet systems of MK and KK were simulated by MD.

The MD simulation of multisheet sistems revealed that:

⇒ 10x6xMK beta sheet stack is stable, but 10x6xKK beta-sheet stack is not.

⇒ 10x6xMK beta-sheet is stable because of hydrophobic interactions of metionine-phenilalanine and leucine of the neighbouring sheets. Met, Phe, Leu make a hydrophobic core for the stack of beta-sheets.

⇒ During MD run the Met, Phe, Leu of neighbouring sheets act as conformational switch moving beta sheets by two amino acid steps towards each other.

⇒ Replacement of Met by Lys destroys the hydrophobic core, which is the stability factor of the beta sheets stack. 10x6xKK system maintains beta sheets, but loses interactions between beta sheets.

⇒The calclulacions of six beta sheets confirm the conclusion drawn for single sheet systems: parallelly placed beta-sheets stabilize each other.

This work was supported by NATO Collaborative Linkage Grant LST.CLG.979807, by stipend for I.L. from the "Kasa im. Jozefa Mianowskiego" Fund, Poland, by Latvian Science Council Grant 05.1768, calculations are carried out at the Gdansk Academic Computer Center TASK

[1] Ventura, S., Zurdo, J., Narayanan, S., Parreno, M., Mangues, R., Reif, B., Chiti, F., Giannoni, E., Dobson, C.M., Aviles, F.X. and Serrano L. Short amino acid stretches can mediate amyloid formation in globular proteins: the Src homology 3 (SH3) case. Proc. Natl. Acad. Sci. U S A 2004, 101, 7258-7263.

[2] Ventura S., Lacroix E.and Serrano L Insights into the origin of the tendency of the PI3-SH3 domain to form amyloid fibrils. Journal of Molecular Biology 2002, 332, 1147-1158.

[3] Liepina I., Ventura S., Czaplewski C., Liwo A. Molecular dynamics study of amyloid formation of two Abl-SH3 domain peptides Journal of Peptide Science, 2006, 12, 780-789.

Computer-Aided Design of Novel Protein Kinase CK2 Inhibitors

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CK2 is a ubiquitous, constitutive, essential serine/threonine kinase that is implicated as a regulator of fundamental cellular processes. Abnormal CK2 expression and function is associated with a number of pathologies, including inflammatory, infectious and carcinogenic processes. These facts evoke strong interest in this enzyme as a target for anticancer, anti-inflammatory and anti-infectious drugs.

In this study we represent 4'-carboxy-3-hydroxyflavones as novel inhibitors of human CK2. These inhibitors have been identified via receptor-based virtual screening of in-house collection containing 500,000 compounds.

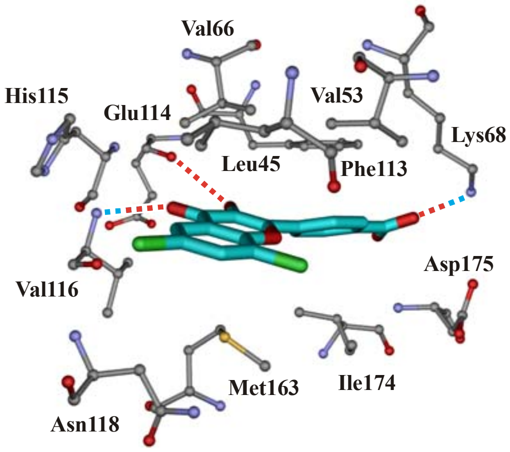

Fig. 1. Binding of 4'-carboxy-3-hydroxyflavone derivative in active site of human CK2. The complex was obtained with molecular docking. Intermolecular hydrogen bonds are indicated as dotted lines.

Analysis of the inhibitor-CK2 complexes obtained with docking allowed to summarize that 4'-carboxy-3-hydroxyflavone derivatives have the binding mode represented at Fig. 1. The binding mode is characterized by formation of three intermolecular hydrogen bonds with amino acid residues Val116, Glu114 and Lys68 as well as by hydrophobic contacts with Val53, Val66, Ile174 and Phe113.

Determination of structure-activity relationships among 4'-carboxy-3-hydroxyflavone derivatives showed importance of hydrophobic substituents in positions 6 and 8 of flavone. The presence of carboxyl group in 4’ position affects the inhibitory activity dramatically. Derivatives having carboxyl group in 2’ or 3’ position were found to be inactive. This could be explained by formation of hydrogen bonds between carboxyl group in 4’ position and Lys68 of CK2 ATP-binding site.

According to the molecular modeling and structure-activity relationships studies, the chemical optimization of 4'-carboxy-3-hydroxyflavones was performed. As a result, the active compound with IC_{50} 60 nM was obtained.

Thus, novel nanomolar inhibitors of human Protein Kinase CK2 were developed. These inhibitors may be of interest for further structural optimization and biological evaluation.

Application of Quantum Trajectories to Collinear Reactive Scattering in the Hydrogen Exchange Reaction

$H+ClH' \rightarrow HCl + H'$

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Molecular dynamics involves the study of elementary chemical rate processes. In order to completely describe these processes, the collision theory must be employed. The main obstacle her is calculation of the reaction probabilities for different initial states. For most heavy particles classical dynamics provides satisfactory results. However, if light particles like hydrogen atoms participate in reactive scattering, rigorous quantum mechanical treatment is needed to correctly describe the dynamics because tunneling may significantly increase the rate of chemical reaction. Unfortunately, due to high demand of computational resources, employment of quantum methods is limited to systems with moderate number of reacting particles. So far the record is 5 particles for the $H_2 + C_2H \rightarrow H + C_2H_2$ reacting system with 9 degrees of freedom. It took about 168 hours to compute one initial reaction probability using the cluster of 64 CPUs [1]. This is due to the exponential scaling of computational resources with the number of degrees of freedom. Therefore alternative quantum methods are of great interest in order to overcome the scaling problem. One of these is hydrodynamic approach to quantum mechanics. The purpose of this work is to use hydrodynamic approach to study collinear collision of light atom with a molecule consisting of one heavy and one light atom. As an investigating system we chose the collinear $H+ClH' \rightarrow HCl + H'$ exchange reaction.

First step in calculating the rate constant within the collision theory is computation of the potential energy surface (PES). For the studied system the electron correlation must be accounted. The PES was computed at the QCISD(T)/6-311++G(3df,3pd) level. Its topology is similar to the BW1 PES in [2]. The barrier height is 18.42 kcal/mole at r_{HCl} = 2,79 Å and the PES has van der Waals wells in the entrance and exit channels starting at r_{HCl} = 5,65 Å.

Dynamical studies consist in propagation of a wave packet on this PES. The reaction probability is computed as a transmitted portion of the wave packet into the product region on the PES. The wave packet propagation was explored by solution of the time dependent Schroedinger equation using finite difference method. The gradient of the phase is extracted from the pre-computed time-dependent wave function and is used in determining the velocities of quantum trajectories. The equations of motion for quantum trajectories are integrated using the Runge-Kutta scheme with adaptive time step.

Unlike classical trajectories, quantum ones can pass into the regions where potential energy exceeds their total energy rendering the tunneling phenomenon [3]. Some trajectories are reflected from the barrier and some are transferred to the product region. Each trajectory carries a portion of the probability. Summing the statistical weights of all transferred trajectories, the reaction probability can be estimated. It gave the relative error 0.93% which is pretty satisfactory taking into account that the total number of trajectories was only 500. An important result of this work is demonstration of possible employment of quantum trajectory method directly without solution of the time-dependent Schroedinger equation. This is due to smooth dynamics of the wave packet unlike the $H + H_2$ system where severe interference produces vortices yielding singularities in the equations of motion.

[1] Wang D., *J.Chem.Phys*. **124** (2006) 201105.
[2] Bian W, Werner H.-J., *J.Chem.Phys.* **112** (2000) 220-229.
[3] Babyuk D., Wyatt R.E., Frederick J.H., *J.Chem.Phys*. **119** (2003) 6482-6488.

Trust, but Verify: Principles of Dataset Curation for Cheminformatics Research

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Preliminary dataset curation is crucial for any cheminformatics analysis (similarity searching, QSAR modeling, clustering, etc.). Despite the common appeal of procedures used for curation, they are implemented or employed differently within different groups. Thus, the main objective of this study is to emphasize the necessity of a standardized data curation strategy, applicable to any ensemble of compounds.

We shall present the most important steps of cleaning every reported data record including: removal of inorganics, counter-ions and mixtures, structural cleaning, ring aromatization, normalization of specific chemotypes, curation of tautomeric forms and the deletion of duplicates. Some general principles acquired from the authors' experience are given for each step as well as some technical advices. Furthermore, several case studies where the initial representation of compounds was incompatible with any modeling exercise are reported and discussed. Results highlight the impact of the cleaning procedures, especially for obtaining more robust and efficient QSAR models.

In addition to well-known OECD principles, the following postulate was formulated: "To facilitate the consideration of a (Q)SAR model for regulatory purposes, it should be obtained using thoroughly prepared dataset." Here the preparation of the dataset means its careful curation and control which are related to representation of both molecular structure (on any level) and investigated activity/property.

Several general rules that in our opinion should be followed in any cheminformatics investigation have been formulated as follows:

- it is highly risky to calculate chemical descriptors directly from smiles strings. It is preferable to compute descriptors (integral, fragments, etc.) from curated 2D (or 3D if necessary) structures.
- the conversion of smiles into 2D structures using Marvin, MOE, ChemOffice, etc, can also produce some structural issues. For that reason, an additional manual cleaning step is always critical despite it being time consuming.
- several tasks such as the aromatization of bonds, salt and mixture removing, are critical but relatively easy to perform using specialized software such as ChemAxon Standardizer.
- even small differences in functional group representations could cause significant errors when generating models.
- duplicates searching and removal is one of the mandatory steps in QSAR analysis. Such search based on chemical name or CAS number only is insufficient; the search must be structure-based.
- since a lot of chemoinformaticians compile experimental data from different sources, the data harmonization is important.
- Nothing can substitute personal participation in the process; some errors that are obvious for human are not obvious for computers.
- After finishing all the above steps, check the accuracy of structures and biological data once again.

Application and Efficacy of Random Forest Method for QSAR Analysis

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Nowadays Random Forest (RF) statistical approach becomes more and more popular. It is caused by its simplicity, quick learning process and following attractive features: i) RF models have no propensity to overfitting, ii) there is no need in pre-selection of descriptors, iii) RF method has its own reliable procedure for estimation of model quality and its predictive ability; iv) obtained models are tolerant for "noise" in source experimental data; v) RF algorithm is effective for processing of large datasets, vi) RF models could be interpretable, vii) it is possible to analyze compounds with different mechanism of actions within one dataset.

Random Forest is an ensemble of decision trees. Thus, resulting RF model can be considered as consensus model with all respective advantages.

Some of aforementioned advantages of RF method were investigated during the QSTR analysis of aquatic toxicity of chemical compounds tested on *Tetrahymena pyriformis* (inverse logarithm of 50% inhibition of *T. pyriformis* growth concentration – $pIGC_{50}$). Dataset included 1093 compounds: training set – 644, test set 1 – 339, test set 2 – 110. Simplex representation of molecular structure has been used. About 6000 2D simplex were calculated and no pre-selection procedure was employed.

Obtained RF model (R^2=0.99, R^2_{oob}=0.81, R^2_{ts1}=0.83, R^2_{ts2}=0.74) was as good as complex consensus model described in literature (R^2=0.92, R^2_{ts1}=0.85, R^2_{ts2}=0.67), but, contrary to the latter, RF model can be interpreted. For example, high impact of lipophilicity and polarizability of investigated compounds on toxicity was determined. It was shown that RF models were tolerant for insertion of irrelevant descriptors (descriptors with random values from the range [0; 1]) as well as for randomization of some part of toxicity values which were representing a "noise". Moreover, fast procedure of optimization of number of trees in the random forest has been proposed. Discussed RF model had comparable or better statistical characteristics than corresponding PLS or KNN models.

RF method was also used for the solution of two following tasks: QSAR analysis of mutagenicity (positive or negative Ames test) and water solubility. In both tasks 2D simplex descriptors were used for molecular structure representation. Mutagenicity dataset included 4361 compounds in the training set and 2181 compounds in external test set. Predictivity of grown RF models (80.5–81.7%) was comparable to consensus model (82.3%) which included 31 various QSAR models (including these RF models). Solubility dataset included 2537 training set compounds and 301 compounds in external test set. In this case RF models were also highly predictive (R^2_{test}=0.80–0.81).

Thus, summarizing everything mentioned above, RF approach was proven as a good tool for QSAR analysis. But it is still necessary to remember about "No free lunch theorem".

QSAR Modelling of Rodent Acute Toxicity

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More than 70000 chemicals are in use today and new ones are permanently synthesized. It is vital to assess the influence of these compounds on human health and environment. Experimental testing is both time-consuming and expensive, and therefore, there is a pressing requirement for accurate *in silico* methods to assess the toxicity. QSAR studies of toxicity chemicals are widely used for this purpose.

In this work we collected the information about 7813 organic molecules with data on acute rodent toxicity. The toxicity end-points are based on the LD_{50} (millimoles/kg) values for the rats with six types of administration: oral, intravenous, intraperitoneal, subcutaneous, inhalation and skin. We used QNA (Quantitative Neighbourhoods of Atoms) descriptors and Self-Consistent Regression for QSAR modeling of acute rodent toxicity. Initial data was randomly divided on training and test sets in proportion 90% and 10%, respectively. Six QSAR models were developed according to the route of administration. Q^2 values for five types of administration exceeded 0.5 and for intravenous type exceeded 0.6. The obtained models were also validated using the test set. Predictions for the test set were performed taking into account the applicability domain for each model. The accuracy of test set predictions for oral, intraperitoneal, subcutaneous, inhalation and skin types of administration exceeded 0.6 and for intravenous type exceeded 0.7.

This work is partially supported by ISTC grant № 3777.

Quantum Chemical Simulation of Metabolism, Toxicity, Carcinogenic Potency, and Biodegradation of Benzene Derivatives

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On the basis of quantum chemical calculations, the dependences of biological oxidation, toxicity, and carcinogenic potency of the mono- and multisubstituted benzene derivatives Ar-XY on the nature of substituents X are studied using an oxenoid model [1,2]. According to this model, the P450 enzyme breaks the dioxygen molecules and generates the active atomic oxygen species (oxens) that readily react with substrates. Using MO LCAO MNDO approach, we calculated the differences ΔE of the total energies of aromatic compounds and corresponding arene oxides with tetrahedrally coordinated carbon atoms. We obtained that the ΔE values determine the positions of the enzyme mediated oxidation, rate of substrate biotransformation, as well as toxicity of the benzene derivatives. In addition to the “dynamic” reactivity index ΔE related to the enzyme-mediated substrate biotransformation, we calculated many standard “static” reactivity indices, such as the energies of the occupied and unoccupied MOs, the effective atomic charges, the free valence indices, and superdelocalizabilities corresponding to the substrate molecules in the starting equilibrium geometry. The arene oxide stability ΔE parameter is shown to be the most adequate characteristic of the biological oxidation process and toxicity of benzenes. The compounds with the low ΔE values are noncarcinogenic. Benzene derivatives with high ΔE values belong to carcinogenic compounds series. The carcinogenicity of amino- and nitro-substituted benzenes is also determined by N-oxidation of amino and reduction of the nitro group. As the phenylhydroxylamines XC_6H_4NHOH and nitrenium ions $XC_6H_4NH^+$ are the common metabolites of nitro- and amino-substituted benzenes and nitrenium ions $XC6H4NH^+$ are the ultimate carcinogens, we use the differences $E_N = E(XC_6H_4NH^+) - E(XC_6H_4NHOH)$ as the second parameter characterizing the carcinogenic activity of amino- and nitro-substituted benzenes. The ΔE parameters were used to describe of metabolism of chlorinated biphenyls by bacteria.

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[1] P.N. D’yachkov, N.V. Kharchevnikova, A.V. Dmitriev, A.V. Kuznetsov, V.V. Poroikov, Int. J. Quantum. Chem. 2007, **107**, 2454.

[2] P.N. D’yachkov, N.V. Kharchevnikova, Z.I. Zholdakova, N.Fjodorova, M. Novich, M. Vrachko, Int. J. Quantum. Chem. 2007, **109**, no 11.

Creation and External Validation of QSAR Models for Cyclooxygenase/Lipoxygenase Inhibitors

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The study was aimed on evaluation of possibility to create accurate QSAR models on the basis of different sets of compounds tested by different experimental methods for the same biological activity. We created QSAR models for IC_{50} values of ligands interacting with 1,2 cyclooxygenases (COX) and/or 5 lipoxygenase (5-LOX) on the basis of literature source. The models have been tested on the external set from 26 compounds experimentally evaluated on 1,2COX/LOX inhibition. The experimental methods used for testing of the external test set were different from the methods used for evaluation of compounds from the training sets. QSAR models were created by GUSAR software that uses QNA (Quantity Neighbourhoods of Atoms) descriptors for representation of structural formula of chemical compounds and self-consistent regression as a method for creation of QSAR. All QSAR models have R^2 values more 0.6 and Q^2 more 0.5. Number of compounds contained in the training sets varies from 27 to 160. Data on experimental IC_{50} values for the test set were not available during creation of QSARs, and were determined later. Q^2_{ext} and RMSE for the predicted values of the external test after getting the experimental results were calculated for each QSAR model. For the best model of 5-LOX inhibitors Q^2_{ext} value was 0.91 and RMSE value was 0.553. We have analysed the correlation between the accuracy of prediction for the external test and parameters of QSAR models. The similarity between compounds from the training and test sets also as between amino acid sequences of proteins used for experimental testing of compounds from the external test and training sets were calculated. The results of the study will be represented.

Core - and Valence Hole States from Orthogonality Constraints Techniques

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Most commonly used approaches for excited states in use today are based on multireference techniques. Such techniques include configuration interaction, the multiconfigurational self-consistent field method and its ``complete active space'' variant designated CASSCF, multireference perturbation theory and multireference coupled cluster expansions. These methods are cpu time consuming but indispensable in studies of systems where single-configuration methods cannot be applied; for example, when the weight of the Hartree-Fock (HF) configuration in the wave function of the full configuration interaction expansion is less than ~0.9. However, in some particular cases like core-excited states (in which an electron is removed from a core spin-orbital) , the single determinant approach seems to be accurate enough to get reliable excitation energies.

The so-called ΔSCF technique developed by Bagus [1] is a useful tool to calculate, important for quantum chemistry the energy differences, in particular, core- and valence ionization potentials (IPs). According to the ΔSCF method, IPs are determined as the difference between the HF energy of an ionized excited state and the corresponding energy of the ground state of a neutral molecule (atom). In addition, the Fock operator corresponding, e.g. 1s-hole state is constructed on the assumption that the 1s orbital is occupied by *only* one electron. Such core *hole* states are described in terms of open-shells and the unrestricted HF or the restricted open-shell HF methods are used to construct a wave function of the ionized excited state.

In this contribution, in contrast to the conventional ΔSCF methods, the effect of the removal of an electron is achieved by using some orthogonality constraints imposed on the orbitals of an ionized state. *Ab initio* local self-consistent field method [2] and an alternative technique for the constrained variational problem based on an asymptotic projection method [3] have been earlier proposed by us to optimize the electronic wave function under the constraints of orthogonality to one or several arbitrary spin-orbitals. We further develop and compare these methodologies for the construction of ionized *hole* states that are orthogonal to the ground state of the neutral system and correspond to the proper spin symmetry. Then we apply the methods to calculations of vertical IPs corresponding to the excitation of both valence and core electrons. The results of the calculations of the IPs for diatomic and triatomic molecules are in good agreement between each other and with experimental data and state-of-the-art results obtained by other authors.

[1] P.S.Bagus, Phys.Rev., v.139, A619, (1965).
[2] P.-F. Loos and X. Assfeld, Int. J. Quant. Chem. v. 107, 2243, (2007).
[3] V.N. Glushkov and A.Ya. Tsaune , Chem..Phys..Lett, v. 262, 59, (1996).

Reaction Path Hamiltonian Formulated in Frenet Frame

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Reaction path Hamiltonians (RPH) continue to play a key role in dynamical and statistical theories of chemical reaction dynamics. This type of Hamiltonian is used to describe the dynamics within a waveguide (formed by isosurfaces of the potential energy) leading from reactants to products through the collision complex. About 40 years ago Marcus formulated reaction path Hamiltonians. For a collinear A+BC type reaction, Marcus derived both classical and quantum Hamiltonians in terms of two natural collision coordinates (NCC), s and ρ (defining translation along the reaction path (RP) and vibrational displacement away from this path, respectively). Fifteen years after NCC were introduced, Miller, Handy, and Adams (MHA) formulated a RPH in terms of s and the set of normal vibrational coordinates $\{Q_i\}$ representing displacements orthogonal to the RP. In the MHA derivation of the RPH, all coupling was transferred to the kinetic energy expression by diagonalizing the vibrational Hamiltonian at each value of s. In the expression for the classical kinetic energy, two types of coupling terms appear. The first of these, denoted $B_{k,l}(s)$, produce mode-mode coupling and the second type, denoted $B_{k,s}(s)$, produce translation-vibration coupling. Because of these coupling terms, the quantum kinetic energy operator is quite complicated, in general. In contrast, for the RPH derived later in this study, because normal vibrational coordinates are not introduced, coupling terms analogous to $B_{k,l}(s)$ and $B_{k,s}(s)$ do not appear in the Hamiltonian. Coupling arises in both the kinetic and potential energy operators, but the kinetic energy operator is readily formulated and depends upon the reaction path curvatures described below.

In this study, an alternate form of the reaction path Hamiltonian will be derived for nonrotating systems with multiple vibrational modes. This derivation is strongly dependent upon the differential geometry of space curves, as developed independently by Frenet and Serret. With the shape of the reaction path in the N-dimensional space specified intrinsically by at most $(N\text{-}1)$ local curvatures, the Frenet-Serret equations are used to describe the rate at which the moving basis vectors turn and twist with respect to progression along the reaction path. Using these equations, expressions are derived for the classical kinetic energy expression and the quantum kinetic energy operator. The kinetic energy operator depends upon elements of the contravariant metric and these quantities are expressed in terms of the RP curvatures. Using this RPH, Eulerian equations of motion are then derived for the amplitude R and phase S that appear in the polar form of the wave function. These equations are then transformed into a moving grid representation such that ensembles of quantum trajectories can be evolved to describe the reaction dynamics.

For the restricted case of a planar RP, where the second and higher order curvatures vanish, the equations of motion for R and S have been used to study the time-dependent Lagrangian frame dynamics for ensembles of quantum trajectories [1] undergoing reactive scattering. In the first of these studies, trajectory plots and time-dependent reaction probabilities were presented for model reactive systems with up to 25 harmonic vibrational modes. In an extension of these studies, ensembles comprising up to 5000 quantum trajectories were evolved for reactive systems involving up to 200 harmonic vibrational modes [2]. Morse vibrational modes have also been used in reactive scattering models involving up to 25 vibrational degrees of freedom [3].

[1] Wyatt R.E., Babyuk D., *Phys.Rev.E.*, **73** (2006) 046701.
[2] Babyuk D., Wyatt R.E., *J.Chem.Phys*. **124** (2006) 214109.
[3] Babyuk D., Wyatt R.E., *J.Chem.Phys*. **125** (2006) 064112.

On a Solvability Condition for the Optimized Effective Potential Equations

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Nowadays, the optimized effective potential (OEP) based methods are considered to be as a promising technique for constructing local potentials of density functional theory in its orbital-dependent implementation. In particular, the exchange potential is written exactly in terms of an OEP. It is known that exchange-only OEP method, one seeks for a local potential $V_{eff}(r)$ such that the eigenfunctions $\phi_i(r)$ of the Kohn-Sham equation

$$[-\frac{1}{2}\nabla^2 + V_{eff}(r)]\phi_i(r) = \varepsilon_i\phi_i(r) \qquad (1)$$

minimize the same energy functional as the Hartree-Fock approach. This definition leads to the integral OEP equation

$$\frac{\delta E^{OEP}}{\delta V_{eff}} = \sum_i^{occ}\sum_a^{virt}\phi_i^*(r)\phi_a(r)\frac{\langle\phi_a|(V^{HF} - V_{eff})|\phi_i\rangle}{\varepsilon_i - \varepsilon_a} = 0, \qquad (2)$$

whose solution is not straightforward. and suffers from numerical instabilities.

In practice the solutions of Eqs.(1) and (2) are based on a finite basis set implementation. An *orbital* basis set is used to represent the orbitals $\phi_i(r)$ and an *auxiliary* basis set is needed to expand the local potential $V_{eff}(r)$. It was recently demonstrated [1] that the basis set OEP calculations may lead to infinitely many multiplicative exchange potentials that yield the same energy and density, although these potentials can differ dramatically. In addition the corresponding potentials are characterized by unphysical oscillations around the nuclei.

In this communication, using a general result from a theory of equations - *the Fredholm alternative,* we analyze the structure of the basis set OEP equations and formulate a solvability condition for the equations. The solution is constructed as a sum of a unique solution on the subspace of eigenfunctions of the response matrix with non-zero eigenvalues and a solution on a counterpart subspace with singular eigenvalues which depends on arbitrary constants. The restrictions imposed on the exact OEP are used to avoid obtaining infinitely many potentials. We show how to apply this alternative to construct a numerically stable solution free from unphysical oscillations. A performance of our implementation is demonstrated by calculations of the effective potentials for the test systems.

[1] V.N. Staroverov, G.E. Scuseria and E.R. Davidson, J.Chem.Phys. **124**, 141103 (2006).

Hartree-Fock Theory and Constrained Optimized Effective Potential Method for Individual Excited States

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Hartree-Fock (HF) theory is not only a valuable tool to provide useful information about the ground state properties of electronic systems, but is also as a starting point for the development of approaches which deal with correlation. Moreover a comparison of the HF method with the optimized effective potential (OEP) methodology offers a promising route for generating the exchange-correlation potentials and, therefore achieving improved accuracy in density functional theory (DFT). In particular, a comparison of the HF and exchange-only OEP methods for *the ground state* make it possible to treat exactly the ground state exchange energy functional in DFT. However, the extension of the HF and OEP schemes to excited states is more subtle. Attempts to formulate the OEP method for excited states have been done within the framework of the so-called ensemble approach based on the extended Raleigh-Ritz variational principle. Unfortunately, there is far less reported experience, especially for molecules , where a finite orbital basis set choice for an ensemble of states is important to achieve reasonable results.

Recently, an OEP approach for individual states has been proposed and preliminary calculations for excited state energies have been carried out [1,2]. The method is based on an alternative technique for the constrained variational problem developed earlier (see a recent review on this methodology [3]). Specifically, local potentials were derived whose Kohn-Sham determinants minimize the total energies and are simultaneously orthogonal to the determinants for states of lower energies. In this contribution we compare the HF and OEP methodologies for individual excited states having the same symmetry as the ground state. It is shown that this comparison leads to the exchange-only energy functional for excited states which has a similar structure as the ground state one, although the OEPs are different for different states.

[1] V.N.Glushkov, Optics and Spectroscopy, v.99, 684 (2005)
[2] V.N. Glushkov and M.Levy , J.Chem.Phys. v.126, 174106 (2007)
[3] V.N. Glushkov, N. Gidopolous and S. Wilson, Frontiers in Quantum systems in Chemistry and Physics, Eds.:S. Wilson, P.J. Grout, J. Maruani, G. Delgado-Barrio and P. Piecuch; Progress in Theoretical Chemistry and Physics, Springer, Dordrecht, P.423 (2008)

Importance of the Electronic Response of the Surrounding to UV/visible Chromophore Absorption

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Conjugated molecules present the ability to strongly absorb light, and are classified as chromophores. Consequently, these kind of compounds have noteworthy optical properties and are encountered in various systems like dyes, switches, … Their optical properties are now fully understood with a stringent control on subsituent and solvent effects.

The situation is less clear when the chromophore is embedded into a macrocycle, e.g. squarain-tetralactam complex [1] or into a protein like the Green Fluorescent Protein family [2]. Once the chromophore located inside a macromolecule absorbs light, the induced electronic polarization of the environment has to be considered and constitutes a real challenge from the theoretical point of view. Recently, theoretical researches [3] have been lead in order to understand the interplay between the environment and the chromophore, but for such large systems, it is rather difficult to rationalize it.

One way to correctly handled this problem is to use QM/MM methods like the LSCF/MM method developed in our group [4]. We will present the strategy to take into account the environment effects on UV/visible absorption spectra of chromophores by means of a polarizable cotinuum characterized by the relative dielectric constant extrapolated at infinite frequency. Two kind of systems (FIG. 1) will be considered, the self-assembled squarain-tetralactam and the Enhanced Cyan Fluorescent Protein [5]. Both systems possess interesting optical properties, and many applications in biology and medicine like uorescent imaging probes, FRET measurements, cell localizations, …

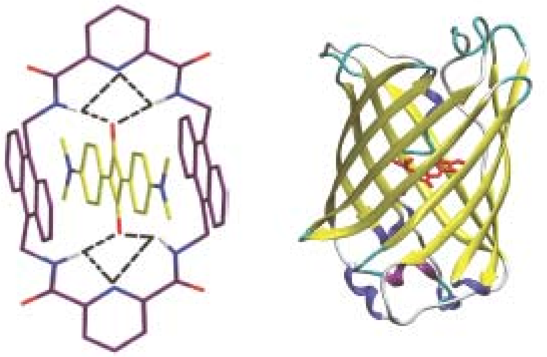

FIG. 1: Squarain-tetralactam complex and Enhanced Cyan Fluorescent Protein

[1] (a) Arunkumar, E.; Forbes, C. C.; Noll, B. C.; Smith, B. *J. Am. Chem. Soc.* 2005, **127**, 3288. (b) Gassensmith, J. J.; Arunkumar, E.; Barr, L.; Baumes, J. M.; DiVittorio, K. M.; Johnson, J. R.; Noll, B. C.; Smith, B. *J. Am. Chem. Soc.* 2007, **129**, 15054.

[2] Tsien, R. Y. Annu. Rev. Biochem. 1998, **67**, 509.

[3] (a) Curutchet, C.; Mennucci, B.; Scholes, G. D.; Beljonne, D. *J. Chem. Phys. B* 2008, **112**, 3759. (b) Dupuis, M.; Aida, M.; Kawashima, Y.; Hirao, K. A. *J. Chem. Phys.* 2002, **117**, 1242. (c) Kongsted, J.; Mennucci, B. *J. Phys. Chem. A* 2007, **111**, 9890. (d) Wanko, M.; Hoffmann, M.; Frähmcke, J.; Frauenheim, T. and Elstner, M. *J. Phys. Chem. B* 2008, **112**, 11468.

[4] Ferré, N.; Assfeld, X.; Rivail, J.-L. *J. Comput. Chem.* 2002, **23**, 610.

[5] (a) Jacquemin, D.; Perpète, E. A.; Laurent, A. D.; Assfeld, X.; Adamo, C. *Phys. Chem. Chem. Phys.* 2009, **11**, 1258. (b) Laurent, A. D.; Assfeld, X. in preparation

Structure and Dynamics of Oxalyl Fluoride in the Ground and Lowest Excited Electronic States

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The structure, conformational and vibrational dynamics of the oxalyl fluoride molecule (O=C(F)–C(F)=O) in the ground and four lowest excited (two singlet and two triplet) electronic states of (n,π*) type were investigated by means of various quantum-chemical methods (MP2, QCISD(T), CCSD(T), CASSCF, CASPT2 with cc-pVTZ and cc-pVQZ basis sets).

For the ground electronic state, the geometrical parameters, vibrational frequencies, and potential function of internal rotation obtained theoretically were found to be in a good agreement with available experimental data. To obtain accurate theoretical estimations of conformer energy difference and barrier to internal rotation, the extrapolation to the complete basis set within Valence Focal Point Analysis procedure (see e.g. [1]) was performed.

According to the results of calculations, for all excited electronic states under study, minima of the Potential Energy Surfaces (PES) correspond to *trans*- and *cis*-conformations. As in glyoxal, the PES of excited states of oxalyl fluoride intersect; the order of states for *trans*-oxalyl fluoride (C_{2h} point symmetry group) is the same as for glyoxal: $\tilde{a}^3A_u, \tilde{A}^1A_u, \tilde{b}^3B_g, \tilde{B}^1B_g$ However, the order differs for *cis*-conformers (C_{2v} point symmetry group): $\tilde{a}^3B_1$, $\tilde{A}^1B_1$, $\tilde{b}^3A_2$, $\tilde{B}^1A_2$ (for glyoxal) and $\tilde{a}^3A_2$, $\tilde{A}^1A_2, \tilde{b}^3B_1$, $\tilde{B}^1B_1$ (for oxalyl fluoride). The information on the stable conformations, symmetry and order of excited states allowed to explain the failure to identify the transitions of *cis*-conformer in the vibronic absorption spectrum of gaseous oxalyl fluoride.

The calculations of vibrational frequencies helped in the assignment of experimental vibronic absorption spectrum of gaseous oxalyl fluoride obtained. In particular, the systems of torsion energy levels for *trans*-oxalyl fluoride in the ground and lowest excited singlet and triplet electronic states were determined for the first time.

The one- and two-dimensional sections of the PES of the excited states along coordinates of internal rotation and symmetric non-planar distortion of the carbonyl fragments were constructed. It was shown that the internal rotation around C–C bond is accompanied by significant (up to 30°) non-planar distortion of both carbonyl fragments. The one-dimensional minimal energy paths corresponding to internal rotation have areas of ambiguity and are discontinuous. These facts are evidences of strong coupling of two internal large-amplite molecular motions in states of (*n*,π*) type. This effect is analogous to those found for other conjugated carbonyls acrolein [2] and oxalyl chloride [3] in excited (*n*, π*) states.

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[1] A.G. Császár, W.D. Allen, H.F.I. Schaefer III // J. Chem. Phys. 1998. 108. 9751.
[2] O.S. Bokareva, V.A. Bataev, V.I. Pupyshev, I.A. Godunov // Int. J. Quant. Chem. 2008. 108. 2719.
[3] S.I. Bokarev, V.I. Pupyshev, I.A. Godunov // J. Mol. Specrosc. JMS-09-54, in press.

Structure and Conformational Dynamics of Methyl Vinyl Ketone Molecule in the Ground and Lowest $^{1,3}(n,\pi^*)$ and $^{1,3}(\pi,\pi^*)$ Excited Electronic States

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The peculiarities of potential energy surfaces (PES) of methyl vinyl ketone molecule ($CH_2{=}CH{-}CO(CH_3)$) in the ground and $^{1,3}(n,\pi^*)$ and $^{1,3}(\pi,\pi^*)$ excited electronic states were investigated by means of *ab initio* quantum-chemical methods (MP2, DFT, QCISD, CCSD(T), CASSCF, CASPT2 with 6-311G(*d,p*), cc-pVTZ, and other AO basis sets).

The geometrical parameters and vibrational frequencies were determined. Relative energies of stationary points (minima on PES and transition states corresponding to the barriers of asymmetric (around central C-C bond) and symmetric (CH_3 group) rotations) were also calculated. Values of energy differences between *s-cis* and *s-trans* conformers and barriers to the symmetrical internal rotation (S_0) were determined more precisely using Valence Focal-Point Analysis technique, see e.g. [1]. To note is the good agreement of calculated and experimental structural data for the ground electronic state. Some reassignments of fundamentals were proposed.

The excitation of methyl vinyl ketone conformers in $^{1,3}(n,\pi^*)$ states led to the rotation of the CH_3 fragment by 60°, with the planar structure of molecule frame retained. The excitation in $^{3}(\pi,\pi^*)$ state led to the rotation of CH_2 fragment by about 90°, with the methyl top stayed unchanged. The structure of both conformers in $^{1}(\pi,\pi^*)$ state was more complicated.

In order to understand the peculiarities of the conformational *s-trans* — *s-cis* transition different sections of PES along the large-amplitude motion coordinates were constructed. It was found, that the asymmetric internal rotation in $^{1,3}(n,\pi^*)$ excited electronic states was accompanied both by the rotation of methyl rotor and the significant (more than 30°) non-planar distortion of carbonyl fragment. The minimal energy path consisted of two branches, had bifurcation points and areas of ambiguity. The asymmetric internal rotation in $^{3}(\pi,\pi^*)$ state was shown to be coupled with pyramidal distortion of vinyl fragment; the rotation around double C=C bond in $^{1,3}(\pi,\pi^*)$ states was accompanied by pyramidal distortion of methylene fragment. Such couplings were analogous to those found earlier for acrolein [2, 3].

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[1] A.G. Császár, W.D. Allen, H.F. Shaefer III, J. Chem. Phys. (1998) V. 108, P. 9751.

[2] O.S. Bokareva, V.A. Bataev, V.I. Pupyshev, I.A. Godunov, Int. J. Quant. Chem. (2008) V. 108, P. 2719.

[3] O.S. Bokareva, V.A. Bataev, V.I. Pupyshev, I.A. Godunov, Spectrochim. Acta A. (2009) accepted for publication.

Structure and Conformational Dynamics of the Dicyclopropyl Ketone Molecule in the Ground (S_0) and Lowest Excited (T_1 and S_1) Electronic States

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Using various *ab initio* methods we have studied structure and conformational dynamics of non-rigid dicyclopropyl ketone (DCPK) molecule with two similar cyclopropyl tops.

According to experimental data in the ground electronic state there are two conformers of DCPK: *cis-cis* and *cis-trans* [1]. From the temperature dependence of the lines in the IR-spectrum of DCPK, the conformer energy difference ΔE_1 was determined to be 530±27 cm^{-1} [2], *cis-cis* conformer is the most stable. Our RHF, MP2, B3LYP, CCSD, CCSD(T) calculations with Pople (up to 6-311++G(*d*,*p*) and 6-311+G(2*d*,2*p*)) and Dunning (up to cc-pV5Z) basis sets also show that the *cis-cis* and *cis-trans* conformations are the most stable ones (ΔE_1 = 530 cm^{-1} according to VFPA technique [3]). Barrier to internal rotation ΔV(*cis-cis* → *cis-trans*) = 2220 cm^{-1}. However the detailed analysis of the 2D torsion-torsion section of the PES of DCPK showed that there is another stable *gauche-gauche* conformation, but it is a sterically strained structure (the distance between the hydrogen atoms of the cyclopropyl rings is 2.2 Å) so the energy difference ΔE_2 between the *gauche-gauche* and *cis-cis* conformers is significant (2750 cm^{-1} according to VFPA). Thus DCPK molecule (three stable conformations) differs from the similar methylcyclopropyl ketone molecule with only two stable *cis-* and *near-trans* conformations [4].

Detailed analysis of the PES of the DCPK molecule was not performed earlier. Using MP2/6-311+G(2*d*,2*p*) method we calculated one (1D) and two-dimensional (2D) torsion sections of the PES for DCPK. On the PES there is a region where minima corresponding to *cis-cis* and *cis-trans* conformers are located, and a region of sterically strained structures, where *gauche-gauche* minimum is located. PES sections were used to calculate torsion transition energies in 1D and 2D approaches. Analysis of vibrational wave functions and PES shape demonstrated that due to the symmetry of the problem we observe the correlated rotation of cyclopropyl rings for *cis-cis* conformer and independent rotation of rings for *cis-trans* conformer.

CASPT2, CASPT3 calculations demonstrated that excitation of DCPK to the lowest T_1 and S_1 electronic states cause dramatic structural changes: pyramidalization of the carbonyl fragment (O out-of-plane angle is $\varphi_1 \approx 40°$) and rotation of cyclopropyl tops (rotation angle φ_1 = 60°, 190°, 320° (for $\varphi_1 > 0$) and 50°, 170°, 300° (for $\varphi_1 < 0$)). So on the torsion-inversion PES section there are six minima corresponding to the three pairs of enantiomers. For example, conformer energy difference in the T_1 electronic state (for the S_1 electronic state we observe similar picture) is considerably lower than in the S_0 electronic state (according to CASPT2/cc-pVTZ ΔE = 110 and 97 cm^{-1}, conformer $\varphi_1 \approx \pm 40°$ and φ_2 = 170, 190° is the most stable). On the torsion-torsion PES section as well as for the S_0 electronic state there is a region of sterically strained structures but the area of this region is smaller and the energies of the strained structures are lower than those for the S_0 electronic state. These differences may be observed because pyramidal structures are less sterically strained.

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[1] M. Traetteberg, P. Bakken, J. V. Quesada, V. S. Mastryukov, J. E. Boggs. J. Mol. Struct., **1999**, 485/486, 73-85.

[2] C. J. Wurrey, C. Zheng, G. A. Guirgis, J. R. Durig. Phys. Chem. Chem. Phys., **2004**, 6, 2125-2135.

[3] A.G. Császár, W.D. Allen, H.F. Schaefer III. J. Chem. Phys., **1998,** 108, 9751-9764.

[4] E.V. Rastoltseva, V.A. Bataev, I.A. Godunov. J. Mol. Struct. (THEOCHEM) (**2009**), doi: 10.1016/j.theochem.2009.03.016.

Performance of the 6-31G$^{\#\#}$ Basis Set for Calculations of ^{1}H Chemical Shifts of Hydrocarbons

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Accurate calculation of second-order molecular magnetic properties is still a challenging task for theoretical chemists. Previously we have tested performance of physically adapted 6-31G$^{\#\#}$ basis set for calculations of nuclear magnetic shielding constants [1, 2]. Procedure for construction of afore-mentioned basis set includes augmentation of standard 6-31G basis set by functions obtained from the solution of the nonhomogeneous Schrödinger equation for the model problem "one-electron atom in an external uniform magnetic field" using the closed representation of the Green's function [1, 2].

Since in the case of external magnetic field first-order correction functions generated by the perturbation operator for atom, located on the point of origin, equals zero, one can use for the nuclei of interest initial 6-31G basis set which could decrease the number of basis functions thus improving efficiency of used approach.

Here we report the results of GIAO-DFT calculations of the ^{1}H shielding constants for row of hydrocarbons with using of three basis sets (see legend of the Table). All calculations were done for geometries optimized at the same level of theory. Comparison of calculated values with experimental data confirms the correctness of using "unperturbed" 6-31G basis set for the nuclei of interest.

Table. Calculated and experimental absolute ^{1}H chemical shifts (ppm) for row of hydrocarbons relatively to CH_4, values of MAE and RMSE, and parameters of the linear regression equation $\delta_{expt} = A\delta_{calc} + B$

Functional	BP86			B3LYP			PBE1PBE			Exp.[3]
Basis set[a]	I	II	III	I	II	III	I	II	III	
C_2H_2	1.02	1.27	1.42	0.97	1.24	1.41	1.06	1.34	1.51	1.34
C_2H_4	5.63	5.41	5.54	5.52	5.32	5.46	5.64	5.45	5.61	5.18
C_2H_6	0.77	0.82	0.82	0.68	0.73	0.74	0.66	0.72	0.76	0.75
$CH_3C\underline{H}_2CH_3$	1.32	1.43	1.40	1.15	1.28	1.24	1.14	1.25	1.26	1.16
$C\underline{H}_3CH_2CH_3$	0.84	0.85	0.87	0.73	0.76	0.78	0.73	0.76	0.81	0.68
C_6H_6	7.47	7.21	7.40	7.37	7.20	7.41	7.51	7.32	7.55	7.13
c-C_6H_{12}	1.57	2.11	1.52	1.40	1.97	1.33	1.40	2.02	1.13	1.31
MAE	0.250	0.254	0.203	0.179	0.181	0.120	0.207	0.207	0.206	
RMSE	0.209	0.308	0.081	0.169	0.269	0.048	0.142	0.269	0.130	
A	0.938	0.998	0.973	0.933	0.989	0.959	0.914	0.970	0.934	
B	0.006	-0.228	-0.129	0.122	-0.119	-0.010	0.128	-0.118	0.022	
R	0.9972	0.9940	0.9996	0.9982	0.9954	0.9999	0.9987	0.9954	0.9989	

[a] I – 6-31G$^{\#\#}$ basis set used for all atoms, II – 6-31G basis set used for all Hydrogen atoms and 6-31G$^{\#\#}$ – for all Carbon atoms, III – 6-31G basis set used for one Hydrogen atom of interest and 6-31G$^{\#\#}$ – for the rest atoms

[1] 1. Rossikhin V.V., Kuz'menko V.V., Voronkov E.O., J. Phys. Chem., 1996, **100**, No 51,19801.

[2] 2. Rossikhin V.V., Okovytyy S.I., Kasyan L.I., Voronkov E.O., Umrikhina L.K., Leszczynski. J. J. Phys. Chem. A 2002,**106**, No 16, 4176.

[3] 3. W.Kutzelnigg, U.Fleischer, and M.Schindler.NMR Basic Principles and Progress, **23**,165-262, Springen-Ferlag, Berlin Heidelberg 1990.

π-Electron Coupled Cluster Calculations of Molecular Hyperpolarizabilities

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The calculations of nonlinear optic susceptibility of molecular systems can be rather difficult task when extensive systems (polymers, nanotubes) are considered. In such a case some kind of semiempirical theory can be applied. Different widespread all-valence approaches (AM1, PM3) demonstrated efficiency in calculations of compact systems but fails when longer systems investigated. Essential difficulty in description of quasy-one-dimensional systems connected with necessarity of accounting of the electron correlation effects.

In the present work the calculations of (hyper)polarizabilities have been done in a semiempirical framework within π-electron approximation for coupled cluster (CC) theory as well as for the second-order perturbation theory Møller-Pleset (MP2) and the Hartree-Fock (HF). The CC approach has been implemented in the general form [1] where all the necessary electron excitations accounted in the exact (connected) form. The wave function of such approach forms as:

$$|\Psi_{CC}\rangle = \exp\left(\sum_k T_k\right)|0\rangle, \tag{1}$$

where the T_k generates the superposition of k-fold excitations from the reference $|0\rangle$. Corresponding Schrödinger equation in presence of external field ($\mathbf{F}_\omega$) has the regular CC form:

$$\left\langle {}^{a_1..a_k}_{i_1...i_k}\right|\left(H + h(\mathbf{F}_\omega) - E_{CC}\right)\left|\Psi_{CC}\right\rangle = 0, \tag{2}$$

where **H** is Hamiltonian, operator $h(\mathbf{F}_\omega)$ is corresponding to contribution from the external electric field and $\left\langle {}^{a_1..a_k}_{i_1...i_k}\right|$ – k-fold excited determinant.

The calculations were performed for some π-electron systems (polyenes, polyynes, cyclic systems of aromatic series, etc). The calculations also include fragments of carbon nanotubes with different sizes and topologies (for such purpose we used the Local CCSD). For some smaller systems it was possible to make a comparison with the FCI results and with experimental data. In particular the effects of inclusion of high level electron correlations on the calculated values of (hyper)polarizabilities of the *betaine dye* were studied in details.

It was demonstrated that a correct description of (hyper)polarizabilities of polyenes can be already obtained at the CCSD level of theory, but for systems with triple bonds (poly-acetylenes) the correct description requires explicit inclusion of higher excitations in the CC wave function (CCSDTQ).

The effects of the medium surrounding the molecule also were investigated by using specific form of polarization-continuum model (PCM) [2]. In the PCM the CC equation transforms into the self-consistent reaction field form:

$$\left\langle {}^{a_1..a_k}_{i_1...i_k}\right|\left(H + h(\mathbf{F}_\omega) + V(\Psi_{CC}) - E_{CC}\right)\left|\Psi_{CC}\right\rangle = 0, \tag{3}$$

where the $V(\Psi_{CC})$ – reaction field contribution. As an example the hyperpolarizabilities of fullerene (C_{60}) were calculated in different medium. It was obtained that CCSD methanol/vacuum ratio for the second hyperpolarizability of C_{60} is equal to four.

[1] Lyakh D. I., Ivanov V. V., Adamowicz L., Journal of Chem. Phys., **122**, 024108, (2005).
[2] Luzanov A. V., Ivanov V. V., Ukrainian Physical Journal, **42**, 1187, (1997).

Influence of Nitro and Amino Groups on Aromaticity of Benzene Ring

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Influence of substituents on the properties of aromatic systems is one of the most significant issue under discussion in the organic chemistry. In spite of popularity of different rules for its qualitative estimation, e. g. ±*I* or ±*M* effects, there is some lack of its pure analysis, especially for polysubstituted molecules. Quantitative investigation of aromaticity of monosubstituted benzenes [1] revealed essential difference in the way and strength of that influence between donor and acceptor substituents.

Benzene rings with different number and arrangement of amino and nitro groups seem to be suitable model for analysis of effect of substituents on aromatic system and on each other, since they are strong π-donor and π-acceptor. Aromaticity of the number of such molecules was studied by using structural (Ia and HOMA), magnetic (NICS(1)zz), and structural-dynamic (kE) indices. All calculations performed using *ab initio* MP2/cc-pvTZ method, kE value obtained as minimum constant of the out-of-plane rigidity. All indices were found to correlate well (R_{corr} ~ 94 – 98%), so they can be discussed as integrated value.

Aromaticity changes a little with addition of nitro groups, but decreases much more with addition of amino group. Roughly, it depends on the number of amino groups. There is no appreciable effect of relative arrangement of substituents on aromaticity. Particularly, there is no supposed resonance effect between nitro and amino groups in the 1,2 and 1,4 positions, as compared to 1,3 arrangement. For molecules with a large number of substituents, it is observed direct interactions between them such as repulsion or hydrogen bonding. It complicates conformational dynamic of benzene ring so affects the value of kE index, though has no remarkable effect according to good correlation of kE and other indices.

[1] O.V.Shishkin, I.V.Omelchenko, M.V.Krasovska, R.I.Zubatyuk, L.Gorb, J.Leszczynski, J. Mol. Struc. 2006 (791) 158

The n-σ* Hyperconjugation *vs* the π-π Conjugation in Derivatives of Cyclohexene Containing Exocyclic Double Bond

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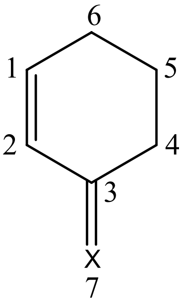
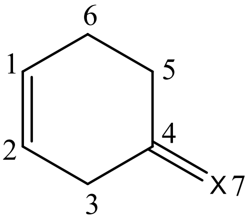
Derivatives of cyclohexene containing exocyclic double bond represent fundamental systems for stereochemistry of organic compounds. Their conformational characteristics are determined by interactions between unsaturated and saturated parts of molecule. Therefore it was performed systematic investigation of the equilibrium geometry and ring-inversion process for molecules **1-14** using MP2/6-311G(d,p) method. Detailed analysis of intramolecular interactions in molecules **1-7** demonstrates that geometrical parameters of molecules containing conjugated double bonds are determined by two opposite effects namely the π-π conjugation between double bonds and n→σ* hyperconjugation between lone pair of heteroatom of exocyclic double bond and σ-antibonding orbitals of neighboring endocyclic C-C bonds. The latter interactions are responsible for elongation of the C(sp^2)-C(sp^2) bond in oxygen and nitrogen-containing molecules, despite of stronger π-π interactions between two double bonds. Equilibrium conformations and ring inversion barriers of molecules **1-7** depend mainly on strength of the π-π interactions.



1 X=O
2 X=S
3 X=Se
4 X=NH
5 X=PH
6 X=AsH
7 X=CH_2



8 X=O
9 X=S
10 X=Se
11 X=NH
12 X=PH
13 X=AsH
14 X=CH_2

Geometrical parameters of tetrahydrocycles in molecules **8-14** where double bonds separated by methylene groups significantly depend on π→σ* hyperconjugation interactions between exocyclic double bond and neighboring methylene groups and the n→σ* interactions between lone pairs of heteroatom and σ-antibonding orbitals of the C(sp^2)-C(sp^3) bonds. A balance between these two interactions is responsible for variations in bond lengths, change of equilibrium conformation of ring and significant asymmetry of ring inversion profile.

DFT Modeling of ESR Parameters of Proximal ^{13}C nearby the NV Center in Nanodiamond for Quantum Processor

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Here we extend our previous density-functional analyses [1,2] of the structural, electronic and spin properties of hydrogen-terminated relaxed diamond nanoclusters with NV$^-$-centers. More specifically, the $C_{27}H_{36}$[NV]$^-$, $C_{33}H_{36}$[NV], $C_{36}H_{42}$[NV]$^-$, $C_{69}H_{84}$[NV]$^-$ $C_{84}H_{78}$[NV]$^-$ clusters have been studied to calculate, for a first time, both isotropic and anisotropic parts of the hyperfine interaction (*ihfi* and *ahfi*) and principal values of the hyperfine tensor (*pvht*) for various atoms in the clusters. The calculations performed for singly negatively charged clusters in the triplet ground state. Software packages GAMESS were used.
In Table we present our theoretical results for the *pvht* for cluster $C_{69}H_{84}$[NV]$^-$ along with the known experimental data [3] and theoretical results from supercell calculations [4].

Table. Principal values of the hyperfine tensor for NV--center in diamond: A11, A22, A33 – our calculated values (results of DFT calculations using the 3-21G basis set), A11[3], A22[3], A33[3] – experimental data [3], A11[4], A22[4], A33[4] – theoretical results from supercell calculations [10]. C1, C3 -1-th and 3-th neighbors with respect to vacancy. All values are in MHz.

Atom	*A*11	*A*22	*A*33	*A*11[3]	*A*22[3]	*A*33[3]	*A*33[4]	*A11*[4]	*A*33[4]
N	-1.47	-1.96	-1.96	±2.1	±2.1	±2.3	−1.7	−1.7	−1.7
C_1	125.8	126.	193.3	±123	±123	±205	109.5	110.2	185.4
C_3	8.3	8.5	13.0	±15.0	±15.0	±15.0	12.8	12.8	18.0

Respectively, the *ihfi* constants, and *pvht* have maximum values the three C atoms being the nearest to the vacancy, varying in ranges of 130-150 MHz for *ihfi*, 120-125 MHz for A11, A22 of *pvht* and ~193 - 210 MHz for A33 of *pvht* depending on the size and shape of the clusters. The calculated coupling constants for the C atoms belonging to the third coordination shells around the NV$^-$-center are about (±)4-12 MHz for *ihfi* , (±) 6-9 MHz for A11, A22 of *pvht* and 12- 13 MHz for A33 of *pvht* while those for the forth shell are ~ 0.9 MHz for *ihfi*.
The calculations confirmed that most part of the spin density is localized at the three carbon atoms being the nearest to the vacancy. Moreover, noticeable part of spin density is also localized on third neighbor to the vacancy carbon atoms. These findings are in good agreement with the experimental data of [4,5] and show that rather distant ^{13}C nuclear spins around NV$^-$-center can be used to implement quantum register with optical access.

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[1] V.A. Pushkarchuk, S.Ya. Kilin, A.P. Nizovtsev, A.L. Pushkarchuk, A.B. Filonov, V.E. Borisenko, *Opt. Spectrosc.* **99**, 245 (2005).

[2] V.A. Pushkarchuk, S.Ya. Kilin, A.P. Nizovtsev, A.L. Pushkarchuk, A.B. Filonov, V.E. Borisenko, *J. Appl. Spectrosc.* **74,** 101 (2007).

[3] L. Childress *et al.*, *Science* **314,** 281 (2006).

[4] A. Gali *et al.*, *Phys. Rev.* **B77**, 155206 (2008).

Spin Correlations in Simple Aromatic Biradicals and Polyradicals

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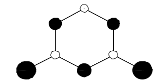
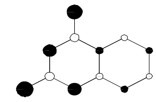
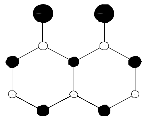
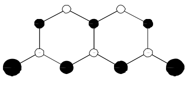
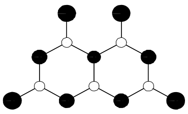
While chemistry of organic polyradicals has developed to maturity in the past 10-15 years [1], theoretical studies in the field are somewhat more sporadic, especially for very high-spin polyradical structures. Here we report our preliminary results for the electronic structure of some typical biradicals such as meta-xylylene and more complex systems, and one tetraradical (see Table below). We applied the full configuration interaction (FCI) model for π-shells by using the standard PPP hamiltonian. To check the validity of the π-scheme used, *ab initio* computations on the same systems are performed within CASSCF/6-31G**. In the table all structures are presented so that π-FCI spin densities on carbon atoms are displayed by black and white circuses (for positive and negative values respectively). The most important is energy gap $-\Delta E$ between high-spin and low-spin states: $\Delta E = E[S_0] - E[S_0 - 1]$ where S_0 is the ground state spin. Fine spin correlations are reflected via the so-called zero-field splitting parameter $\mathcal{D}$ which we computed only within π-FCI by a π-technique familiar in the triplet excited states theory [2].

High spin system	$\mathcal{D}$ in cm^{-1}	ΔE in kcal/mol	
	π-FCI	π-FCI	CASSCF
	0.019	-9.8	-12.8
	0.018	-11.0	-12.4
	0.027	-6.3	-7.3
	0.008	-5.7	-8.6
	-	-6.4	-8.9

From the table we see that ΔE shows a similar behavior at both, π-FCI and CASSCF, levels of description. Some interesting details are revealed by the analysis of leading atom-atom contributions to the parameter $\mathcal{D}$**.** This topics and more general many-electron spin correlation matrices are considered in the report as well.

[1] J. A. Crayston, J. N. Devine and J. C. Walton, Tetrahedron 56 (2000) 7829; A. Rajca, Adv. Phys.Org. Chem. 40 (2005) 153.

[2] A. V. Luzanov, V. N. Poltavets, J. Struct. Chem. 15 (1974) 457.

Mobility of Solitonic Charge and Geometrical Waves in Linear Conjugated Systems in Electric Field

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Linear conjugated systems **1** are excellently important for numerous applications in materials

$[R_1 — (CH)_m — R_2]^z \quad z = 0, \pm 1$ **1**

because of their specific electronic, linear and non-linear optical, opto-optical properties and molecular wires [1]; also, they are favourite model molecules to verify the new theoretical approach and to study of the dependence of the electron structure in the ground and excited states as well as the nature of the electron transition on an extension of the conjugated chain, symmetry, total charge, topology of terminal groups, etc.

According to the current views [1], the charge (electron or hole) injected to the highly-polarized collective system of π-electrons is not delocalized uniformly over the whole π-system, but is self-localized in the form of a charge wave, i.e. as a kink or soliton. The quantum-chemical calculations have shown that the charge wave is of a finite length, approximately, 15-17 carbon atoms. Simultaneously with a charge wave, there is a generation of a solitonic-like wave of the alternated bond lengths, so called, geometrical or topological soliton. The shapes and the locations of the charge and bond length waves are mutually connected. When the length of the conjugated chain exceeds the dimension of the solitonic wave, the soliton becomes mobile.

The applied electric field causes the solitonic waves to move along the electric field vector.

The velocity of moving of the geometrical soliton was shown to be equal ~ 1 km/s.

In the present work the results of quantum-chemical investigation of the dependence of mobility of solitonic waves on length of conjugated system **1** (m), nature of the terminal groups R_1 and R_2 ,(CH_2 , NH_2, SH), the occupancy of the electron shell (neutral molecule, cation, anion) and value of electric field strength E_{ef}.

The quantum –chemical simulation has shown that solitonic wave moves as whole object untill E_{ef} = 0.05a.u. (Fig. 1); the further increasing of electric field strength leads to distortion of solitonic waves and even to destruction of the molecular wire.

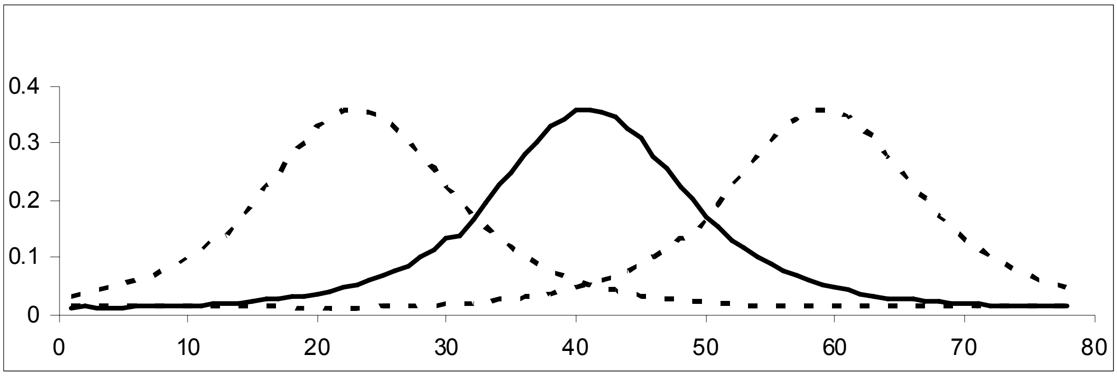

Fig.1 The moving of soliton in the system **1** upon m=40, z=1, R_1=R_2=CH_2

[1] Bredas J.L., Street G.B. Polaron, bipolaron and solitons in conductiong polymers. Acc.Chem.Res. 1985, **18**, 309-315.

Quantum-Chemical Modelling of Hydration of the Functional Groups In Ion Exchangers

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The new approach to ion hydration in ion exchangers considers it as the totality of all phenomena occurring in the process adding water molecules to a polyelectrolyte fragment [1]. A non-empirical quantum chemical method SCF MO LCAO in approximation of molecular fragments was used to compute coordination of all atoms in the systems at states corresponding to their energy minima. This allowed determination and visualizing the positions and orientations of all participants in the hydration process (fixed and counter-ions, water molecules) at different stage of hydration. The numbers of water molecules bound only to the counter-ion or fixed ion simultaneously to the both of them and bound only to the other water molecules have been computed. An explicit difference in the nature of hydration of ion exchangers with different functional groups and counter-ions has been observed. Structures of hydration systems in the most spread types of ion exchangers (with $-SO_3^-Kt^+$, $-CH_2N(CH_3)_3^+An^-$, $-COOO^-Kt^+$,) have been described. Alkali and halogenide ions were taken as counterions. For calculations of local interionic and intermolecular interactions the program GAMESS [2] was used. For large multiatomic systems the best results gave non-empirical calculations with minimal basis set Huzinaga MINI [3]. Some properties of sorption complexes are calculated with using of HF/6-31G(d) and B3LYP/6-31G(d) level of the theory. Below we give a brief outlook of the results of calculations for hydration structures of functional group in the most widespread types of ion exchangers.

Sulfonic Type Ion Exchangers.

In the anhydrous ion exchanger all ions of alkali metals coordinate two oxygen atoms of sulfonic groups. For Li^+ and Na^+, addition of ten water molecules causes complete dissociation of the ionic pairs. In the case of K^+, Rb^+ and Cs^+, the one of Me - O bonds remains unchanged at the further hydration. The total number of water molecules involved in the formation of hydration complex is little dependent on the type of ion and is equal to7-9 water molecules per ionic pair counterion – fixed ion. Stepwise hydration occurs differently for different counterions. Previously we noted a marked difference in selectivity of ion exchange I^+-H^+ of the structure forming ions (with “positive” hydration, Li^+ and Na^+) and structure breaking ions (with “negative” hydration, K^+, Rb^+, Cs^+). Quantum Chemical calculations explain the nature of this effect. In fully hydrated ion exchangers Li^+ and Na^+ are not fixed at the sulfonic group while K^+, Rb^+ and Cs^+ remain bound to one of its oxygen atoms.

Benzyltrimethylamine Functional Groups.

In anhydrous state F^-, Cl^-, Br^- and I^- are situated in the distances from N-atom of the functional group much shorter than those in the crystals of relative salts of trimethylammonium. Hydration of the functional groups in all cases leads to removal of anions from the cation at distances greatly exceeding their ionic radii. The idea of merging of two hydrophobic ions ($RN(CH_3)_3^+$ and An^-, $An^- = Cl^-, Br^-, I^-$) as a reason for high selectivity of anion exchange contradicts to the results of quantum chemical calculations. We observed that the hydrophobic effect reveals in formation cavities in water structure around large anions seen as increased distance between the large anions and the nearest water molecule.

This work was partially supported by Belorussian Republican Foundation for Fundamental Research (project X09-091)

[1] 1. Soldatov V.S., Zelenkovskii V.M., Bezyazychnaya T.V. In Ion Exchange Technology for Today and Tomorrow (Proc. IEX’04) Ed. M. Cox. SCI, London. 2004. P. 365.

[2] 2. Schmidt M.W., Baldridge K.K, Boatz. J.A// J. Comput. Chem.- 1993. -V. 14. - P.1347.

[3] 3. Huzinaga S., Andzelm J., Klobukowski M. // Gaussian Basis Sets for molecular calculations: Elsevier. Amsterdam. 1984. 426 p.

The Way Proteins of Replicative Complexes Tecognize the Watson-Crick Nucleotide Pairs: A Simple Physical Model

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The *in vivo* replication processes of DNA have extremely high precision – on an average 10^{-9} mistakes per one nucleotide [1]. However, elementary physical mechanisms of these processes remain vague.

Nowadays, it is theoretically [2] and experimentally [3,4] established on models that *in vitro* DNA polymerases recognize Watson-Crick nucleotide through (H) bonds between amino acid residues of active centre, on the one hand, and so-called invariant atomic groups of nucleotide bases and sugar-phosphate residues of nucleotides, on the other hand. We believe that such conception is mistaken because it ignores the role that proteins play in replicative complexe which function *in vivo* together with DNA polymerase and in such a way highten at fidelity of replication on 3-4 degree in comparison with the similar value that received in the model experiments without these proteins *in vitro* [5,6].

We suggest and prove the simple physical model of additional recognition of the Watson-Crick base pairs by the proteins of replicative complex from the side of major groove of DNA using non-empirical quantum-chemical methods in this work. The lateral radical of asparagin or glutamin, which invariant co-operates (taking into account the turn of this group on 180°) forming two H-bonds NH..O4/6 and C=O..HN6/4 with each of four Watson-Crick base pairs is shown to be the most appropriate.

At the same time such model virtually eliminates the mistakes of biosynthesis of DNA related to the creation of false pairs AC/CA and GT/TG through the instrumentality of bases in the canonic (basic) form, and highlight the benefit of tautomeric mechanism of point spontaneous mutations according to Watson and Crick [7]. It is proved that the suggested mechanism of recognition inhibit the formation of pairs of G*T/GT* better than pairs AC*/A*C at the biosynthesis of DNA (asterisk markes so-called “rare” (mutational) tautomers of nucleic bases). Those pairs are recognized in the active center of DNA polymerase as correct pairs [8].

[1] *Drake J.W.* Spontaneous Mutation: Comparative Rates of Spontaneous Mutation//Nature.-1969.-Vol.**221**,№5186.-P.1132.

[2] *Bruskov V.I., Poltev V.I.* The recognition of complementary pairs of nitrous bases by enzymes and strengthening of specificity of co-operations in the processes of matrix synthesis// Lectures of Academy of Sciences.-1974.-Vol.**219**,№1.-P.231-233.

[3] *Ahn J., Werneburg B.*G., *Tsai M.-D.* DNA polymerase β:structure-friendly relationship from pre-steady-state kinetic analyses of all possible correct and incorrect base pairs for wild type and R283A mutant // Biochemistry. - 1997. - Vol. **36**. – P.1100-1107.

[4] *Morales J.C., Kool E.T.* Functional hydrogen-bonding map of the minor groove binding tracks of six DNA polymerases // Biochemistry. – 2000. – Vol.**39**. – P.12979-12988.

[5] *Trautner T.A., Swartz M.N, and Kornberg Arthur* Enzymatic synthesis of deoxyribonucleic acid, X.influence of bromuracil substitutions on replication//PNAS.-1962.-Vol48,№3.-P.449-455.

[6] *Hall Z. W., Lehman I. R.* An *in vitro* transversion by a mutationally altered T4-induced DNA polymerase//J.Mol.Biol.-1968.-Vol.**36**, №3.-P.321-333.

[7] *Watson J.D., Crick F.H.C.* The structure of DNA//Cold Spring Harbor Symp. on Quant. Biol.- 1953 .-Vol.**18**.-P. 123-131.

[8] *Kool E.T.* Hydrogen bonding, base stacking, and steric effects in DNA replication // Ann.Rev.Biophys.Biomol.Struct.-2001.-Vol.**30**.-P.1-22.

DNA B–Z Transition Basic Physical Mechanism: an *Ab initio* Quantum Chemistry Study

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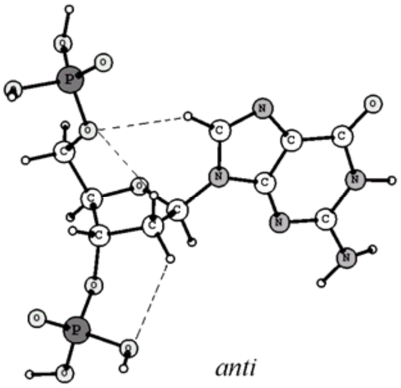
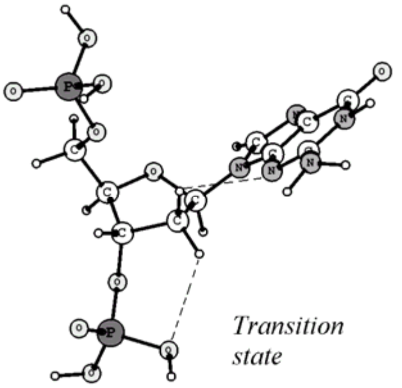
It is well established that DNA in Z-form has a significant biological meaning. At the same time, the 'driving forces' of B to Z DNA transition process remain unclear.

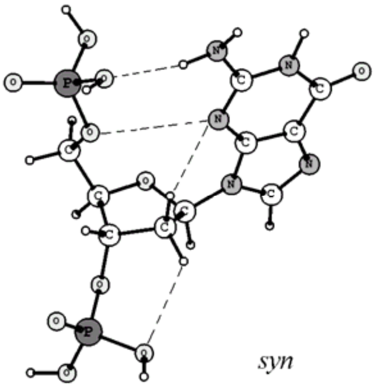
In this study we present an *ab initio* quantum chemistry investigation of *syn*/*anti* transition in model deoxyguanosine nucleotide with electro-neutral phosphate groups in 3' and 5' ends. This compound can, to our opinion, serve as a representative model of a nucleotide in course of B to Z transition.

We used *anti*-conformation nucleotide optimized geometry (a B-form model) with torsion angles values similar to those of crystal DNA. The *syn*-conformation (a Z-form model) was obtained from *anti*- one by changing glycoside torsion angle for 180° and subsequent geometry optimization. Based on these two conformers of deoxyguanosine nucleotide the *syn*/*anti* transition state was found using QST2 algorithm.

All geometry optimization were carried out on DFT b3lyp/6-31G(d,p) theory level in Gaussian 03w, and the electronic density analysis was performed in AIM2000.







The main result is that the *syn*-conformer energy is little bit lower than *anti*- one, and the transition state energy is 4.6 kcal/mol higher than one of *anti*-conformer. It is an energetic preference of *syn*-conformation which can serve as a 'driving force' of B to Z transition. To determine its origin the hydrogen bond energy analysis [1] was performed. The following H-Bonds were found: N_2-H…$O_{1P5'}$ (the bond energy, kcal/mol, is 4.0), $C_{2'}$-H…N_3 (2.4), $C_{2'}$-H…$O_{5'}$ (1.5) and $O_{5'}$…N_3 (van der Waals contact, 0.8) in *syn*-conformer; C_8-H…$O_{5'}$ (1.1), $C_{2'}$-H…$O_{5'}$ (1.9) and $C_{2'}$-H…$O_{5'}$ (1.5) in *anti*-conformer and $C_{2'}$-H…N_3 (2.3) and $C_{2'}$-H…$O_{5'}$ (1.5) in transition state.

We believe that the existence of N_2-H…$O_{1P5'}$ hydrogen bond in *syn*-orientated conformer is the key to understanding the *syn*- versus *anti*- energetic preference and so far – the nature of B to Z transition of DNA.

[1] *Espinosa E., Molins E., Lecomte C.* Hydrogen bond strengths revealed by topological analyses of experimentally observed electron densities // Chemical Physics Letters. – 1998. – Vol. **285**, p. 170 – 173.

Model Considerations on the Nucleotide Bases' Tautomerism Concerned with Protein-Nucleic Acid Contacts. Spectroscopic and Quantum Chemistry Data

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Tautomerism of nucleic acid bases is one of the most intriguing features. Up to now the nucleotide bases tautomerism concerned mainly the problem of the DNA spontaneous mutations. The question of the bases' tautomerism arose in the course of spectroscopic study of specific interactions between protein and nucleic acids in model point contacts of the bases with deprotonated carboxylic group (carboxylate ion) of aspartic and glutamic (amino) acids' residues, modelled in dimethylsulfoxide (DMSO) by sodium acetate (NaAc, CH_3COO^-: Na^+). In a number of cases the interpretation of UV, IR and ^1H NMR data turns out to be impossible without the assumption of the bases' tautomeric transformations in model complexes of protein-nucleic acid recognition.

Previous quantum chemical calculations of the adenine, isoguanine, purine and xanthine tautomer complexes with CH_3COO^- in vacuum confirmed transitions from the ground-state to high-energy rare tautomeric forms, which allowed consistent interpretation of experimental data.

This work deals with tautomeric transformations of uracil (Ura) and thymine (Thy) in their model complexes with deprotonated carboxylic group of amino acids. Essential changes in the bases' UV spectra on their interaction with NaAc, vanishing signals of both imino protons in ^1H NMR spectra and perceptible decrease in intensity of both IR bands, related to the carbonyl groups' stretching vibrations ν(C=O), imply enolic tautomers involvement. Results of quantum chemical calculations of the tautomers' double complexes with CH_3COO^- at the MP2/6-311++G(2df,pd)//B3LYP/ 6-311++G(d,p) level of theory proved to be incompatible with the spectral features: the ground-state diketo tautomers of Ura and Thy form the most stable complexes. Despite the enolic tautomers' complexes are much closer in energy to the diketo ones as compared to isolated tautomers, the energy gap between them is such, that in tautomeric equilibrium dominate diketo forms.

To take into account influence of ion Na^+, triple complexes of the type $CH3COO^-$:Ura(Thy) tautomer: Na^+ were calculated, as a consequence of which for both bases three triple complexes formed by enolic tautomers appeared more stable, than by diketo ones. This makes understandable the UV and ^1H NMR data, but rather high residual intensity of the ν(C=O) bands in the IR spectra remains unclear. Therefore the DMSO effect was evaluated, applying the CPCM solvation model to triple complexes of the Ura tautomers. It turned out, that in DMSO triple complex of the ground-state diketo tautomer becomes the most stable again. However, the enolic ones only slightly exceed it in energy and under physiological temperatures coexist with the most stable triple complex. In all the complexes proton transfer occurs along H-bonds and imino protons are very liable: they transit from nitrogen to oxygen atoms under enolic tautomers' formation and then are transferred to carboxylate ion. As in the course of such transformations the bases pass a number of intermediate states, their imino protons' signals cannot be detected in ^1H NMR spectra. Moderate, comparing to effects in UV and ^1H NMR spectra, decrease in the IR ν(C=O) bands' intensities is determined by those carbonyl groups, which became enolic ones. The two ν(C=O) bands of the ground-state triple complex and the rest one from each enolic complex are responsible for rather high residual IR absorption of carbonyl groups. Since it is known that in most of enzymes environment of active sites is much less polar (dielectric constant ε equals only a few units), than in DMSO solution (ε=48), and much closer to vacuum (ε=1), the conclusion could be made, that *in vivo* diketo ↔ enolic equilibrium in Ura (Thy) may be more shifted to the right as compared to our model system. So, results of this work pointed out to possible important role of the nucleotide bases' high-energy tautomers in the processes of protein-nucleic acid recognition.

Conformational Properties of Deoxynucleoside-3’,5’-Diphosphates

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Studies of conformational, dynamical, and energetic properties of components of nucleic acids are important for understanding of structural features of polynucleotides. The deoxyribonucleoside-3’5’-diphosphates (DNDPs) were used in present studies as a model system to investigate conformational properties of the DNA backbone.

The conformational space of DNDPs as studied by molecular dynamics (MD) simulations shows the same ranges of backbone dihedral angles as in known double-helical forms of DNA. High variability of conformations in DNDPs is mainly provided by flexibility of dihedrals α, ζ, ε and also χ in purines. Only limited number of these conformations can be observed in polynucleotides due to restrictions imposed by the double-helical structure. The simulations also show, that population of the north conformations of sugar ring in DNDPs is significantly lower as compared to nucleosides and nucleotides due to repulsion between charged phosphates, in agreement with experimental data. The comparisons of calculated AMBER parm99, bsc0 and MP2/6-311+G(d,p) energies, as well as populations of common conformers in simulations and in DNA crystal structures, show some disbalance in parametrisation of γ and χ torsion angles in Cornell et al force field.

Effect of solvent and cations on conformational space of DNDP was studied by carrying out MD simulations of DNDPs in gas phase, implicit and explicit solvent. The *ab initio* geometry and energy of selected conformers was also compared in gas phase and using COSMO solvent model. Inclusion of solvent and cations results in change of comparative energies and populations of conformers.

Molecular Mechanics Simulation of Interaction of Oxyethylated Glycerol Derivatives with Alkali Metal Ions and Amino Acid Proline

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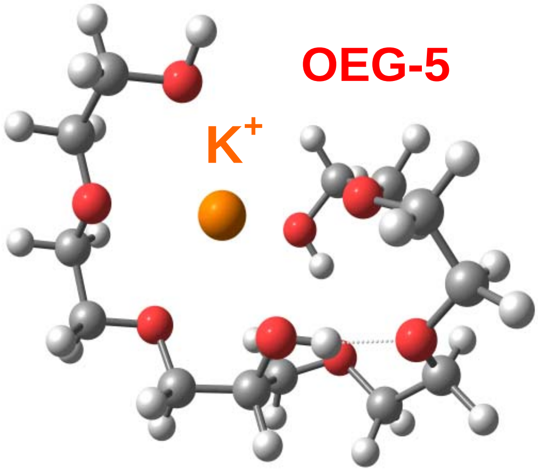
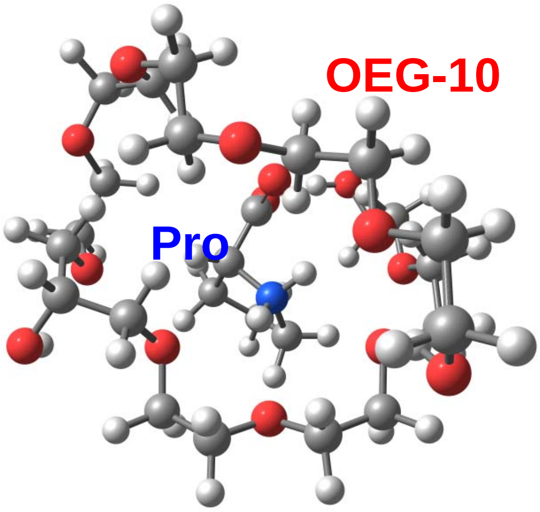
Polyatomic alcohols and polyethers find many useful applications, one of which is cryoprotection. A function of cryoprotectors, along with prevention of phase separation, is in preservation of the solvate shell of biomolecules and other components of biological fluids on temperature decrease. In the present work molecular mechanics simulation with CHARMM force field was applied to modelling of the structure of the complexes formed by amino acid proline and alkali metal ions with oligomers of a new cryoprotector synthesized at the Institute for Problems of Cryobiology and Cryomedicine of NAS of Ukraine (Kharkov, Ukraine), based on oxyethylated glycerol derivatives OEG-5: $HO\text{-}(CH_2\text{-}CH_2\text{-}O)_x\text{-}CH_2\text{-}CHOH\text{-}CH_2\text{-}(O\text{-}CH_2\text{-}CH_2)_y\text{-}OH$ (where x+y=n, mean n value is 5 and polydispersity index is 1.05).

Stable complexes of Na^+, K^+ and protonated proline with OEG-5 oligomers were detected in mass spectrometric experiments. There are literature data showing that stabilization of complexes of polyethers with alkali metal ions is due to wrapping of the polymer chain around the monoatomic ion [1]. We have suggested a possibility of wrapping of the OEG-5 chains around small biomolecules, such as proline amino acid.

The starting conformations for molecular mechanics simulation were constructed using the most extended OEG-n conformation and ions location at the center of the chain. In the course of the system evolution the OEG-n chains bend and tend to wrap the ion. The bending of the chain leads to formation of a crown ether-like structure with the ether oxygens oriented to the metal cation.





Oligomers of OEG with a long enough chain wrap around the proline molecule being in zwitterionic form. The complex is stabilized by 4 hydrogen bonds formed by COO^- and NH_3^+ groups of proline with terminal OH groups and ether chain oxygens of OEG oligomer.

Wrapping of OEG-5 polymer chains over the alkali metal ions and small biomolecules present in biological fluids provides stabilization of such supramolecular structures and, obviously, facilitate preservation of solvation shell of biomolecules on cryoconservation of biological materials.

[1] T. Wyttenbach, G. von Helden, M.T. Bowers, Conformations of Alkali Ion Cationized Polyethers in the Gas Phase: Polyethylene Glycol and Bis[(benzo-15-crown-5)-15-ylmethyl] Pimelate // Int. J. Mass Spectrom. Ion Proc. **165/166** (1997) 377-390.

Interaction of Single Nucleic Acid Bases and Watson-Crick Base Pairs with Carbon Surfaces. MP2 and DFT Study

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In this work we have used quantum chemical methods (MP2 and DFT) to study the interactions between nucleic acid bases (NABs) and single-walled carbon nanotubes (SWCNT). Calculations of the interaction energies between the NABs and a fragment of the zigzag(10,0) carbon nanotube performed at the MP2/6-31++G(d,p)[NABs atoms]|6-31G(d)[nanotube atoms] level of theory with accounting for the BSSE during geometry optimization allowed us to order the NABs according to the increasing interaction energy value. The order is: Guanine (-67.1 kJ/mol) > Adenine (-59.0 kJ/mol) > Cytosine(-50.3 kJ/mol) ≈ Thymine (-50.2 kJ/mol) > Uracil (-44.2 kJ/mol). The MP2 equilibrium structures and the interaction energies were used as reference points in the evaluation of the ability of various functionals in the DFT method to predict those structures and energies. We showed that the M05, MPWB1K, and MPW1B95 density functionals are capable of correctly predicting the SWCNT-NAB geometries but not the interaction energies, while the M05-2X functional is capable of correctly predicting both the geometries and the interaction energies.

Also in the present work we studied the interactions between nucleic acid base pairs and carbon surfaces and planar graphene using the M05-2X and MPWB1K density functionals and the MP2 method. We found that A-T and G-C Watson-Crick base pairs have very similar interaction energy both with curved and planar carbon surfaces. Interaction energies calculated at the M05-2X level of theory are -89.6 and -88.4 kcal/mol for the AT-nanotube and GC-nanotube complexes, respectively while the interactions of the base pairs with planar graphene are stronger: -110.2 and -109.9 kJ/mol for the AT-graphene and GC-graphene complexes, respectively. Interaction with carbon surfaces does not change the energies of the H-bonds in the base pairs. On other hand the interactions between base pairs and the carbon surfaces are 7-9% lower than combined interaction energies of the single bases. This study demonstrates that the M05-2X and MP2//M05-2X approaches are very effective and accurate computational tools which may be used to study the stacked complexes formed by organic molecules with the carbon surfaces.

1.4-DHP-lipid forms a tubular micellae

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The cationic amphiphilic lipid tipe compound 1,1'-{[3,5-bis(dodecyloxycarbonyl)-4-phenyl-1,4-dihydropyridin-2,6-diyl]dimethylene} bispyridinium dibromide (1,4-DHP lipid) is a gene transfection agent [1, 2]. The electronic structure of 1,4-DHP lipid molecule was calculated with *ab initio* quantum mechanics to obtain the charges for molecular dynamics (MD) with AMBER 8.0 force field. 1,4-DHP-lipid molecules were subjected to MD from the initial structure of a periodic lipid bilayer-water box, with a small amount of excessive water on the lipid edges to ensure the mobility of lipid molecules. After 14 ns of MD simulation the lipid molecules with the fatty acid tails started to squeeze from one bilayer layer to another one. After 35 ns few lipid molecules turned with their charged heads to the side of the lipid bilayer and after 100 ns a profound tubular micelle structure began to form. The tubular micelle structure becomes more perfect during the course of simulation of 300 ns (Fig).

Conclusion is that one of the gene transfection agent 1,4-DHP lipid structures is a tubular micellae, and we could expect that such the micellaes are capable to form lipoplex for the DNA transfection.

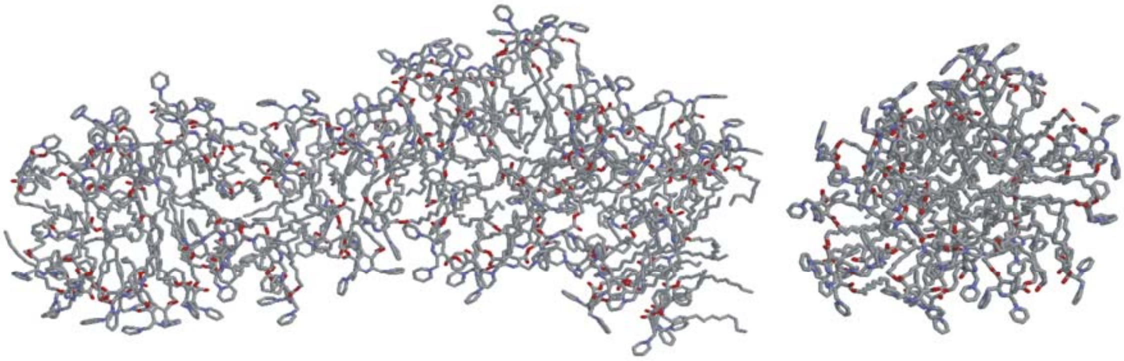

Fig. 1,4-DHP lipid tubomicellae side view and top view.

This work was supported by Stipend of Finland Academy of Sciences for IL, and by Latvian Science Council Grant 05.1768. Calculations were performed on computers of the Gdansk Academic Computer Center TASK.

[1] Z.Hyvonen, A.Plotniece, I.Reine, B.Chekavichus, G.Duburs, A.Urtti Novel cationic amphiphilic 1,4-dihydropyridine derivatives for DNA delivery. Biochim. Biophys. Acta, (2000) 1509, 451 – 466.

[2] Z.Hyvonen, S. Ronkko, M.-R. Toppinen, I. Jaaskelainen, A.Plotniece, A.Urtti . Dioleoyl phosphatidylethanolamine and PEG-lipid conjugates modify DNA delivery mediated by 1,4-dihydropyridine amphiphiles. Journal of Controlled Release, (2004) 99, 177-190.

Molecular Dynamics Simulation of Nitroreductase in Three States

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Nitroreductase is a member of a group of enzymes that reduce a broad range of nitroaromatic compounds and has potential uses in bioremediation and chemotherapy. These enzymes facilitate NADH-driven nitroreduction reaction, which is the quintessential first step in the catabolism of a variety of NACs. Although the major processes affecting the biodegradation of NACs have been investigated qualitatively, many issues regarding a reaction mechanism and enzymatic selectivity remain unsolved.

To understand better the influence of inhibitors and NACs substrate on geometrical and time dependent properties of the enzyme we performed series of molecular dynamics (MD) simulations. The structure and dynamics of the nitroreductase enzyme from *Enterobacter cloacae* has been calculated for the oxidized form, in separate complex with benzoate inhibitor and for the two-electron reduced form. Statistical averages were sampled from 50 ns NPT classical MD simulation in the explicit water environment using AMBER force field.

In the oxidized enzyme, the FMN flavin ring system adopts a slightly bent conformation, which is also consistent with X-Ray crystallography data. This bend increases even further in the reduced form of the enzyme. The induced bend in the oxidized enzyme may favor reduction, and it may also account for the characteristic inability of the enzyme to stabilize the one electron-reduced semiquinone flavin, which is also planar. Simulation the inhibited enzyme shows increased flexibility of H6 helix. These motions may represent a mechanism for accommodating varied substrates. Other obtained results were also interpreted in terms of electrostatic interaction between components of the studied systems and principal component analysis (PCA).

About Using Quantum Fidelity Measures for Quantifing Molecular Similarity

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The quantum information theory can provide additional ways for undestanding molecular similarity problem. In this report we apply the standard Uhlmann-Jozősa fidelity measure [1] in a modified form using the conventional reduced density matrices (RDMs). To be specific, let us consider a system A in a pure state which is determined by a many-electron state vector. The second system B is assumed to be in a mixed state which is specified by the associated RDM. Then the quantum fidelity measure $F[A,B]$ is determined by the RDM expectation over the wave function considered (for some niceties see Ref. [1], p. 410). This automatically leads to quantifying molecular similarity at the many-electron level.

Here our main concern is the comparison between A and B for the case in which B structurally corresponds to the related subsystem in A. For instance, consider the conjugated π-system containing a benzene ring. Then treating the benzene molecule as A and the main molecule as B (after reducing it to an iso-π-electronic and "iso-basis" problem), we can identify $F[A,B]$ with a local benzenoid character index. The computations are quite simple (they are equivalent to obtaining coefficients in the characteristic polynomial for a product of idempotent density matrices of the A and B systems). Some π-calculations in the PPP scheme demonstrate the capabilities of the introduced index $\varsigma_{\text{benz}} = F[\text{benzene, system}]$ for the relative ranking of a benzene-likeness:

π-System	ς_{benz}	π-System	ς_{benz}	π-System	ς_{benz}
Naphthalene	0.852	Hexabenzo-coronene	0.863; 0.600; 0.733	C_{60} (Fullerene)	0.702
Antracene	0.811; 0.771	Indacene	0.661	C_{60} (15-Cyclacene)	0.697
Phenantrene	0.889; 0.710	Kekulene	0.671; 0.814	Graphene	≈ 0.64

The index can be applied as a measure of local aromaticity (with the usual restrictions caused by the π-approximation used here). The comparison with the Polanski aromaticity index and related approaches (e. g., see [2] and references therein) are also presented.

In this vein, a general consideration can be proposed for interatomic similatity measures and related quantities up to chirality degrees. We complement this analysis by including, as an additional characteristics, the collectivity numbers which are previously introduced and generalized in the context of "multi-configurationality" and complexity of quantum states [3].

[1] M. A. Nielsen, I. L. Chuang, Quantum Computation and Quantum Information. Cambridge, 2000.

[2] P. Bultinck , R. Ponec, and R. Carbo-Dorca, J. Comput. Chem. 28 (2007) 152.

[3] A. V. Luzanov, Russ. Chem. Rev. 49 (1980) 1033; A. V. Luzanov and O. A. Zhikol, Int. J. Quant. Chem. 104 (2005) 167; A. V. Luzanov and O. V. Prezhdo, Mol. Phys. 105 (2007) 2879; A. V. Luzanov, J. Chem. Phys. 129 (2008) 094103.

The Estimation of Nonequivalence of Molecular Graph Vertexes on the Basis of the Topological Model of an Informational Field

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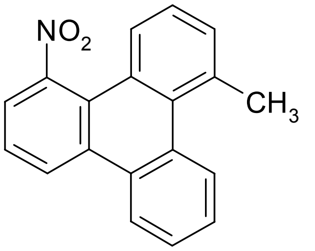
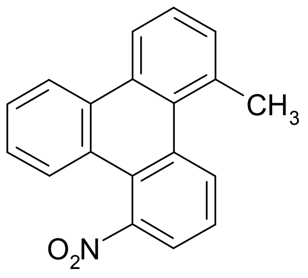
In this work the conception of the informational field (IF) [1] is used in the framework of the topological model of a molecule for the estimation of equivalence/nonequivalence of atoms and molecular fragments. The decision of such task can be claimed, for example, for determination of canonical numeration in a molecular graph, interpretations of different spectrums, different nomenclatural problems, etc. Such investigations are most actual for structurally homogeneous molecules, for example, for fullerenes, nanotubes, etc.

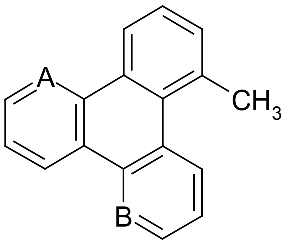
Three algorithms of the informational field are offered within the framework of topological model: taking into account a minimum path between couples of vertexes, taking into account all paths of information distribution on the ribs of graph and taking into account the attenuation coefficient.

Realizations of topological model of IF are most effective when taking into account not only the paths of minimum length between the couples of vertexes but also other paths of information distribution on the ribs of the molecular graphs.

For the analysis of efficiency of given approaches a test problem was decided. As a model example the derivates of triphenylene were used:







Early the estimation of nonequivalence of molecular graph vertexes A and B was decided by the method of potentials of graph [2]. Authors noted that topological nonequivalence vertexes A and B are isospectral, and given vertexes are not distinguished by such methods of classification of graph vertexes, as extended associativity and its vector generalizations, characteristic polynomial, maximal own vector. The offered method of potentials in work [2] allows to distinguish vertexes A and B. However, taking into account the use of numerous operations of arrays in the method of potentials of graph, it is possible to assume that the use of such approach can cause considerable calculable difficulties for large structurally homogeneous systems such, as fullerenes, nanotubes, etc.

The test task was decided also by the developed algorithms of the informational field. Realization of such algorithms is considerably more simple and can be applied for an analysis of large structurally homogeneous molecular systems.

Possibilities of the developed approaches were investigated also for the estimation of nonequivalence of atoms more difficult structurally homogeneous molecular systems. Fullerenes C32, C76 and C78 were considered as research objects.

[1] Kuz'min V.E., Ognichenko L.N., Artemenko A.G. // J. Mol. Model. - 2001. - N 7. - 278.
[2] Gitlina L.S., Golender V.E., Drboglav V.V. and other Methods of presentation and treatment of structural information for the analysis of structure - activity relationship. - Riga, 1981.

Computer-Aided Design of Novel Anti-Coxsackievirus Agents

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Coxsackieviruses (CVB) can cause severe diseases of the heart, liver, eyes and pancreas, as well as acute infections of the central nervous system. Battling CVB represents an important health care task that requires design and development of new drugs. Application of modern computer technologies shortens the development time and reduces costs of antiviral drug research.

The goal of the present study is design of novel selective antiviral agents by the means of QSAR analysis of antiviral activity of various chemicals against pleconaril-resistant CVB3 Nancy strain.

The modeling dataset included 93 structurally diverse compounds, mainly N,N'-(bis-5-nitropyrimidyl)dispirotripiperazine, [(biphenyloxy)propyl]isoxazole and 4H-pyrazolo[1,5-a]pyrimidin-7-one derivatives as well as several well-known antivirals including pleconaril, spirobromine, etc. Thorough investigation of the relationship between antiviral activity against the pleconaril-resistant clinical CVB3 isolate Nancy (IC_{50}, μM), selectivity index (ratio of CC_{50} to IC_{50}) and the structure of investigated compounds was carried out using HiT QSAR. Cytotoxicity on HeLa cells (CC_{50}, μM) was predicted by the HiT QSAR HeLa Virtual Screening Tool.

Hierarchical QSAR Technology (HiT QSAR) is based on Simplex representation of molecular structure (SiRMS). In the SiRMS approach, a molecule is represented as a system of different simplex descriptors (tetratomic fragments with fixed composition, structure, chirality and symmetry). The level of simplex descriptors increases consecutively from 1D to 4D representation of molecular structure. At the stage of simplex descriptor generation different atom characteristics can be used, such as: 1) atom type; 2) partial atom charge 3) lipophilicity 4) atomic refraction 5) donor/acceptor of hydrogen in the potential H-bond; etc. The key feature of the SiRMS approach is the use of diverse variants of differentiation of simplex vertexes (atoms). Rigorous QSAR models ($R^2_{ext} = 0.78$) were developed based on 2D level of simplex descriptors using partial least squares (PLS) statistical approach. Predictions for external datasets and designed/screened compounds were made using consensus scheme, i.e., by averaging predictions generated with multiple validated training set models. Y-scrambling test was used to prove that models do not reflect a chance correlation ($Q^2_{YS} = 0.38$) and 5-fold external cross validation was used for assessing the predictivity of consensus models. Ellipsoid, Tree (local) and leverage approaches were used for estimation of the domain of applicability (DA) of developed models. Successful models were explored to determine molecular fragments promoting or interfering with the target property as well as the degree of their influence. This information was used for subsequent computer-aided design of novel antiviral compounds.

Conclusions:

SiRMS based HiT QSAR approach allows us to successfully analyze antiviral action of various compounds using a 2D level of molecular structure representation.

The molecular fragments promoting or interfering with investigated activities were determined. Removal of one methyl group from the central benzene ring of pleconaril strongly increases activity.

A high impact of atom's type (~40%), electrostatics (~25%) and hydrophobicity (~25%) on variation of antiviral activity was found. Two novel anti-CVB3 agents with high activity against CVB3 97-927 and CVB3 Nancy were designed and validated experimentally.

Prediction of Selectivity and Activity Spectrum of Nuclear Receptors Ligands by Analysis of Virtual Interactions

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The main aim of this work is the development of the predictive models of xenobiotics interaction with different nuclear receptors. The nuclear receptors is a big group of transcription factors that have vary conservative domain structure and play an important role in the controlling of the development, homeostasis, and metabolism of the organism. The human, mouse and rat genomes have been analyzed. The database of sequences of ligand-binding domains was produced using data on 48 annotated nuclear receptor genes as well as their putative homologues. The subset of 14 quality resolved three-dimensional structures of ligand-binding domains were selected from Protein Data Bank for further modeling of virtual complexes. The comprehensive database of nuclear receptor effectors has been assembled. It contains the data about 2661 chemicals and their biological activity (146 types), including 58 types of nuclear receptor-related biological activities. The full database consists of 5730 entries. We have carried out the optimization of molecular docking procedure and followed estimation of protein-ligand interaction virtual affinity values. The set of utility programs and macros was created for easing the calculations for any chemical compound. We have chosen the MM-PBSA method for analyzing various parameters of virtual complexes. Virtual complexes were modeled for 14 known receptor effectors using the 2661 chemicals as potential ligands. In 60% cases it was possible to produce the virtual complex. The most time-expensive calculations were performed at this stage and the resulting data will be useful for further analysis. However, the simple models of linear regressions were not successful for analysis of correlations between MM-PBSA integral values and known complexes affinities (R square values = 0.4 and 0.48 for progesterone receptor and estrogen receptor respectively). So the development of more complex mathematical models is became the goal of our further studies.

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The QSPR analysis of tyrosinase substrates reactivity

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The development of new technologies with usage of oxidative-reductive enzyme, tyrosinase (EC 1.14.18.1) – is a prospective route of waste waters dephenolization, due to tyrosinase selectivity, possibility of usage in the wide range of pH, temperatures, concentrations of pollutants, and formation of less toxic products. However, its application is restricted by the high cost of commercial preparations, so, it is desirable to obtain the partially purified enzyme.

The partially purified mushroom *Agaricus bisporus* tyrosinase preparation was isolated with protein yield of 0,67 mg/g of mushrooms, copper content 0,19 %, specific activity 500 U/mg protein min (for tyrosine). The E. Cohen's method of isolation was modified by polycaproamide addition, which couples the polyphenols oxidation products – tyrosinase inhibitors, what allowed 3-fold increasing the preparation's activity. The 90 % of total protein possesses phenoloxidase activity, as it was shown by the native PAGE-electrophoresis.

In the developed conditions (pH 6.5, t 25 °C, τ 15 min) the partially purified TYR-preparation had catalyzed oxidation of the wide range of phenolic compounds with different degree of bioconversion (from 0% to 100%), depending on their structures.

For quantitative analysis of "structure-degree of bioconversion" relationship statistical Random Forest (RF) method has been used. Earlier it was shown that RF method could be very effective in solution of QSAR tasks. RF methodology seems to be very helpful in solution of current task due to it naturally produces consensus non-linear models. Moreover RF has the following important advantages: i) RF models can't be overfitted; ii) there is no need in rather complicated and time-consuming process of variable selection; iii) compounds with various mechanism of action could be studied within the same (single) training set. Last two advantages are related to decision tree algorithm which is the base of RF approach.

All investigated compounds (25 structures) have been divided onto two classes depending to its degree of bioconversion: high ($\geq$80%), low (<80%). Different whole-molecule molecular descriptors (2D and 3D) have been used for molecular structure description: moments of inertia and their ratios), E_{HOMO}, E_{LUMO}, dipole moment, polarizability and lipophilicity (LogP).

The quite good RF consensus model (containing 200 trees) with high statistic characteristics has been obtained: risk of estimate for work set is 0%, risk of estimate for out-of-bag set is 16%. The model has been used for qualitative prediction of bioconversion degree for ten compounds described in literature (external test set). The model also demonstrate high predictive ability: risk of estimate for external test set is 20%. The analysis of variable importance shows that the most important factor in the process of bioconversion is the shape of molecule (50-70%) estimated by ellipsoid of inertia descriptors. The dipole moment, lipophilicity and polarizability of molecule also have important role (15-30%, 5-10% and 5-10% respectively).

QSAR Analysis of the Antiherpetic Activity of Macroheterocyclic Compounds and Its Structural Analogs

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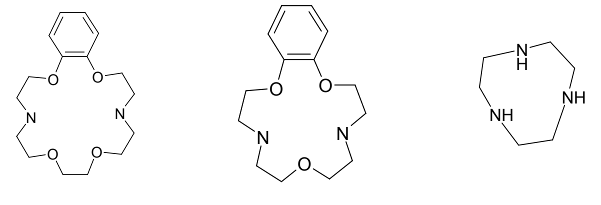
Today despite an abundance of antiherpetic drugs at pharmaceutical market, virus family Herpes viridae remains practically uncontrollable infection. It is characterized both by genetic feature of a virus agent and prolonged persistence of these viruses in a human body, together with appearance of virus strains which resist well-known antiherpetic drugs. The important step in the solving of the problem of new medical products search is QSAR-analysis. In the present work the direct design of new highly active compounds is carried out based on QSAR-analysis of macroheterocyclic compounds with antiherpetic activity. The set consists of 17 compounds for which antiherpetic activity had been researched with the help of cytomorphological method. These compounds have been used for QSAR models construction.

QSAR methods based on simplex representation of molecular structure (SiRMS) and circular models (CM) have been used for description of molecular structure. In the SiRMS any molecule can be represented as the system of different simplexes (tetratomic fragments of fixed structure, chirality and symmetry). In CM any molecule is represented in unified pseudo-cycle, due to which its spectra of physicochemical characteristics are formed. The descriptors are the values of amplitudes of different harmonic components of analysis of this spectrum.

QSAR models have been obtained using partial least squares (PLS) method. The statistic characteristics for PLS models are quite satisfactory ($R^2 = 0.90 - 0.93$; $Q^2 = 0.7 - 0.8$; $R^2_{test} = 0.54 - 0.55$).

On the basis of these models influences of different molecular fragments on antiherpetic activity was calculated. The analysis of contributions of fragments has shown that accumulation of nitrogen-containing fragments leads to increasing of antiherpetic activity. The essential factor for activity manifestation is presence of phenyl in a macrocycle. Replacement of atoms of oxygen by nitrogen in macroheterocycle leads to increasing antiherpetic activity. On the basis of the obtained information 3 novel compounds with high predicted activity was designed. After synthesis of these compounds high predicted activity values have been confirmed experimentally.



Designed highly active compounds

It is important to mark that all investigated benzo-azacrown ethers is highly active antiherpetic agents. Therefore, it would be expedient to perform further researches of antiherpetic drugs among different benzo-crown ethers and their nitrogenous analogues.

Computational and QSAR Study of the Alkylnaphthyl Ketones Adsorption on Silver-Ion Stationary Phase

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Complexation of transition metals with organic ligands have attracted considerable attention within the last decades, since the interactions metal cation – π-system are of great importance in biology, and material chemistry as well as in molecular recognition and guest-host chemistry.[1] Over the years many studies were focused on complexation of various metal cations (Cu^+, Ag^+, Au^+, *etc*) with benzene. In contrast the complexations of metal cations (especially, Ag^+) with aromatic π-systems different from benzene have been investigated only little. Thus, taking into consideration the importance of the studies on the metal-π interactions and absence of the data for the competitive complexation of Ag(I) with alkylnaphthyl ketones, we now present the combined DFT/MP2 and QSRR study on this problem.

Based on the experimentally obtained [2] retention times of aryl alkylketones the QSRR-model for constant and variable concentration of modifier (isopropanol) is developed. The relative error in prediction through developed equations does not exceed 5% – 8%. The retention times of alkylnaphthyl ketones on silver-containing stationary phase are influenced by dipole moment, length of the alkyl substituent as well as by the concentration of the modifier in the mobile phase.

The B3PW91/DZVP and MP2/DZVP computations favour formation of Ag(I) complexes via the carbonyl oxygen and agree well with each other. Despite the fact that MP2 describes the weak interaction better than DFT, this less expensive method still valid for the QSRR modelling. From the QSRR/DFT/MP2 studies we suggest that the interactions of alkylnaphthyl ketones with silver-containing stationary phases proceed via the complexation through the oxygen atom of the carbonyl group both with and without modifier. [3]

[1] Ma JC, Dougherty DA. Chem Rev 1997; 97:1303.
[2] Yarho YG. Kiev: Cand. Sci. Thesis. National Technical University of Ukraine "KPI", 1997: 197.
[3] Levandovskiy IA, Shubina TE, Fokin AA, *submitted.*

QSRR Studies of Methylbenzenes Adsorption on Silver-Ion Stationary Phase

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For the purpose of the interpretation of chromatographic experiments we developed the thermodynamic model of sorption - desolvation in connection with two-component mobile phase [1]. In accordance with this model the dependence of the capacity factor on the experimental condition takes the form:

$$\ln k' = \ln\frac{V_{SP}\rho_S A_L^{\infty}}{V_{MP}} - \frac{\Delta G_I^0}{RT} - N_I\left[\frac{1}{A_L^{\infty}}\cdot\frac{\Delta G_{SI}^0}{RT} + \ln K_L x_L\right], \qquad (1)$$

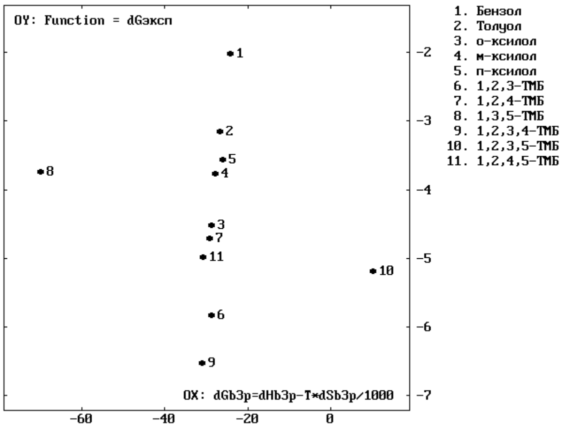
In connection with the quantum-chemical calculations of the adsorption process equation (1) is possible to rewrite in the approximation form:

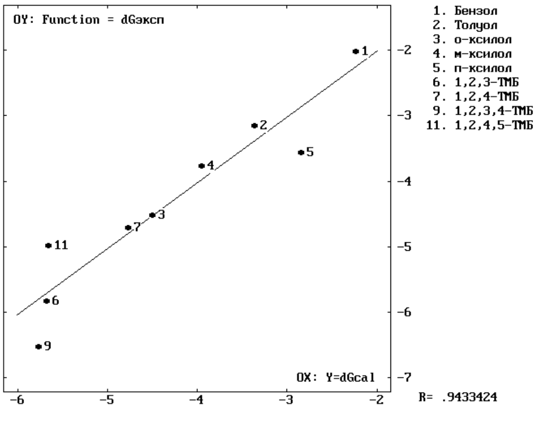
$$\Delta G_{exp} = a_0 + a_1\Delta G + a_2 N + a_3 z, \qquad (2)$$

ΔG - the result of the quantum-chemical calculation of the equilibrium adsorption;

It was proposed that upon adsorption of homologues the adsorption energy does not change significantly, only the energy of solvation. To verify this assumption we have performed quantum-chemical (B3PW91/DZVP) calculations of polymethylbenzenes and their complexes with silver ion. The complexation energies of methylbenzenes were computed according to the following scheme:

$$\text{Alk–Ar} + \text{Ag}^+ \rightarrow \text{Alk-Ar–Ag}^+$$





The ΔG_{exp} *vs* ΔG_{DFT} relationship showed good agreement (R=0.94, eq. 2) and proved existence of homologues series and confirmed results of chromatographical experiments[2].

$$\Delta G_{\exp} = a_0 + a_1\cdot\Delta G_{DFT} + a_2\cdot N \qquad (3)$$

ΔG_{exp} – chromatographically determined energy of adsorption; ΔG_{DFT} - the result of the quantum-chemical calculation of the equilibrium adsorption; N – experimental degree of desolvation

[1] V.N. Rodionov, B.V. Chernyaev, I.A. Levandovskiy, T.E. Shubina, et al. (2005). Naukovi Visti – National Technical University of Ukraine “KPI", 3, 143-152.

[2] Yarho YG. Kiev: Cand. Sci. Thesis. National Technical University of Ukraine "KPI", 1997: 197.

QSRR Studies of Adsorption of Methylnaphthalenes on Silver-Ion Stationary Phase

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For the purpose of the interpretation of chromatographic experiments we developed the thermodynamic model of sorption - desolvation in connection with two-component mobile phase [1]. In accordance with this model the dependence of the capacity factor on the experimental condition takes the form:

$$\ln k' = \ln \frac{V_{SP} \rho_S A_L^{\infty}}{V_{MP}} - \frac{\Delta G_I^0}{RT} - N_I \left[\frac{1}{A_L^{\infty}} \cdot \frac{\Delta G_{SI}^0}{RT} + \ln K_L x_L \right], \quad (1)$$

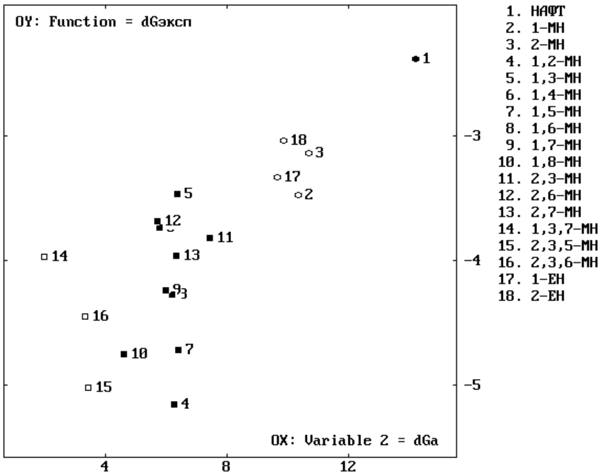
In connection with the quantum-chemical calculations of the adsorption process equation (1) is possible to rewrite in the approximation form:

$$\Delta G_{\exp} = a_0 + a_1 \Delta G + a_2 N + a_3 z, \quad (2)$$

ΔG – the result of the quantum-chemical calculation of the equilibrium adsorption;

It was proposed that upon adsorption of structurally related compounds, the homologous series of adsorption exist – namely, during the adsorption of homologues the adsorption energy does not change significantly, only the energy of solvation. To verify this assumption we have performed quantum-chemical (B3PW91/DZVP) calculations of methylnaphthalenes and their radical-cations. The formation energy of radical-cations was computed according to the following scheme:

$$\mathrm{Ar} + \mathrm{Ag}^{+} \rightarrow \mathrm{Ar}^{+\bullet} + \mathrm{Ag}$$



The plot ΔG_{exp} *vs* ΔG_{DFT} showed existence of four groups:

a) naphtalene (•)
b) 1-, 2- methylnaphthalene and 1-, 2- ethylnaphtalene (monoalkylnaphthalene) (○)
c) dimethylnaphthalene (▪)
d) trimethylnaphthalene (□)

and their relationship proved existence of homologues series and confirm results of chromatographical experiments[2].

We also have developed QSRR equations with R = 0.92 – 0.95, depending on the modifier (isopropanol (0.92) or methanol (0.95)).

[1] V.N. Rodionov, B.V. Chernyaev, I.A. Levandovskiy, T.E. Shubina, et al. (2005). Naukovi Visti – National Technical University of Ukraine “KPI", 3, 143-152.

[2] Y.G. Yarho Kiev: Cand. Sci. Thesis. National Technical University of Ukraine "KPI", 1997, 197.

QSAR Study of Pharmacokinetic Characteristics of Drugs

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The therapeutic action of a drug is usually correlated with the delivery of the active substance to the site or more accurately, sites, of pharmacological action. Thus, the bioavailability is typically defined as a fraction of an administered dose of unchanged drug that reaches the systemic circulation. The bioavailability of a drug is an important attribute that is investigated early in drug development and used throughout development. In many cases, it is the deciding factor as to whether or not a drug candidate is selected for further development.

Thus, the aim of the present work is QSAR analysis of bioavailability and other important pharmacokinetic properties of various drugs, such as semi-elimination period, clearance, and volume of distribution in the organism. The modeling dataset included about 600 structurally diverse drugs, e.g. ozeltamivir, valacyclovir, amprenavir, paracetamol, diazepam, furosemide, salycilic acid, etc.

For solution of QSAR tasks the Hierarchical QSAR Technology (HiT QSAR) based on Simplex representation of molecular structure (SiRMS) was used. In the SiRMS approach a molecule is represented as a system of different simplex descriptors (tetratomic fragments with fixed composition, structure, chirality and symmetry). The key feature of the SiRMS approach is the use of sundry variants of differentiation of simplex vertexes (atoms) at the stage of simplex descriptor generation, such as: 1) atom type; 2) partial atom charge 3) lipophilicity; 4) atomic refraction 5) donor/acceptor of hydrogen in the potential H-bond; etc.

In this study, QSAR models were developed based on 2D level of simplex descriptors using partial least squares (PLS) and Random Forest (RF) statistical approaches. In the both methods predictions for external datasets and designed/screened compounds were made using consensus scheme, i.e., by averaging predictions generated with multiple validated training set models. Successful PLS models were explored to determine molecular fragments promoting or interfering with the target property as well as the degree of their influence. Statistically significant models with $R^2 > 0.8$ and $Q^2 > 0.6$ were used for consensus prediction. The predictivity of consensus HiT QSAR model has been additionally validated by applying it to an additional external test set of antiviral compounds, and the results were satisfactory ($R^2_{test} > 0.5$).

Role of Crystal Stucture on Thrombin Paradox

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Thrombin is a serine protease and remains the primary target for the development of novel anticoagulants because of its position at the end of the blood clotting cascade. Thrombin plays both procoagulant (fast) and anticoagulant (slow) roles in the blood coagulation cascade so plays a key role in hemostasis. The switch from anticoagulant (slow) to procoagulant (fast) form of thrombin known as the thrombin paradox (Griffin, 1995) and has a great interest.Although there are some X-ray and experimental studies in the literature, these studies aren't sufficient to explain the structural and conformational changes of thrombin. Since the first structure of thrombin was published over 500 thrombin structures deposited in the Protein Databank. It is possible to obtain X-ray crystal structures or NMR (nuclear magnetic resonans) structures from the RCSB Protein Databank. For MD simulations starting structures are important and usually they are obtained from Protein Databank. These crystallized structures have ligands and water molecules.In this study we used 1PPB pdb code that refined with the smallest resolution value (1.9 Å) of full length chain thrombin structures. We performed three MD simulations, 40 ns each, with the different starting structures and energy minimization steps in order to understand the role of crystal water in defining the nature of conformational changes and to address issues of binding site flexibility and motion of thrombin .We compared results of simulations and defined the most stable one. Then we observed the conformational changes and flexible residues located in the specificity sites and some inserting loops. Obtained results may lead to innovative strategies for control of thrombin functions in vivo.

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This work was carried out under the HPC-EUROPA project(RH3-CT-2003-50607), with the support of the European Community's Research Infrastructures action of the European Research Area Programme.

[1] Griffin, J. H. ,1995, Blood coagulation: The thrombin paradox, Nature, 378, 337–338

Computational Screening in Analysis of Low-Molecular Inhibitors of C1q – IgG Interaction

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We made computational screening of nearly 100 of low-molecular compounds to their predicted binding site on the globular head of C1q complement protein. On the base of this screening, we estimated their inhibition activity (IC50) for C1q—IgG interaction.

Local decrease of immune response can be used in treatment of such diseases as heart stroke, asthma, Alzheimer's disease, immune conflicts in transplantation, etc. The classical pathway of the complement system activation is triggered by binding of the globular head of C1q, a subcomponent of first component of complement system, to IgG or IgM antibodies. This interaction can be inhibited by a range of negatively-charged low-molecular organic compounds that bind to C1q and can be used in medicines for diseases listed before. To find a good method to search for more powerful inhibitors, one should know the mechanism of this inhibition, which is unknown.

In our previous work, we used blind molecular docking method to find a number of possible binding sites for these compounds at the globular head of C1q. The site at the apex of C1q globular head that showed the strongest correlation between computed free energies and the experimental inhibitory activity was considered to be responsible for the inhibition process. This correlation was further used to predict IC50 for another set of ligands.

Our docking results are now being refined by using docking of flexible ligands to C1q with flexible amino acid side chains at the binding site instead of the rigid receptor model used before.

Quantum chemical and molecular dynamical studies of oxygen interaction with Pt_nX_m and Pd_nX_m (X–first row transition metals) binary nanoclusters

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At present bimetallic nanoclusters Pt_nX_m and Pd_nX_m (X – transition metals Cr, Fe, Co, Ni) are widely used as nanocatalysts in low temperature fuel cells. Such materials posses better catalytic activity, compared with pure metal nanoparticles, in oxygen reduction reactions. Theoretical studies by means of quantum chemistry and molecular dynamics are intensively used to explain behaviors of the nanosystems and to forecast their reactivity.

The aim of this work was a computer study of regularities of electron density changes in the most active reaction site for the series of binary stable nanoclusters $Pt_{37}X_{18}$ and $Pd_{37}X_{18}$ (X – metals Cr, Fe, Co, Ni) and molecular oxygen adsorption at the nanoclusters surface (111). We used a density functional theory (DFT) method in the generalized gradient approximation with exchange correlation functional B88-LYP and double zeta valence polarization basis set. The studies were carried out by the program StoBe 2008 [1].

Thermodynamically stability of different configurations nanoclusters Pt_nX_m and Pd_nX_m was examined in water boxes with 181 molecules by means of standard molecular dynamics with force field interatomic potentials. Nanoclusters with icosaedral structures were found to be the most stable in the time frames 0–50 ps and more.

DFT results showed that maximum of electron densities in the adsorption sites of molecular oxygen on the surface (111) are observed in the following sequence $Pt_{37}Co_{18} > Pt_{37}Ni_{18} > Pt_{37}Fe_{18} > Pt_{37}Cr_{18}$ and $Pd_{37}Fe_{18} > Pd_{37}Cr_{18} > Pd_{37}Co_{18} > Pd_{37}Ni_{18}$. The calculated binary nanoclusters should confirm the growth of adsorption energies for molecular oxygen in the range of 15-30% as compared with corresponding nanoclusters of platinum and palladium.

Adsorption heats and activation energies were calculated for all possible processes at the surface (111) of binary nanoclusters of platinum and palladium – molecular oxygen adsorption, electron transfer to the molecule with the formation of single charged anion, dissociation of the anion to oxygen atom and anion and final reduction of the anion to double charged anion as the slowest phase of whole reduction process. It was shown that in the proposed consequence nanoclusters $Pt_{37}Co_{18}$ and $Pd_{37}Fe_{18}$ posses the lowest activation energies and the highest adsorption heats in three-fold sites of the surface (111). We founded that besides the nature of binary nanoclusters, geometry of reaction center positions has a determinative influence on the rate of oxygen reduction reaction. The three-fold position should be formed by three surface atoms of noble metal with the position of second component atom of the first sublayer exactly below the center of the surface triangle.

Our molecular dynamics simulation in combination with DFT calculation showed satisfactory agreement with experiments and more accurate calculations. The results obtained may be used in theoretical choice of effective catalysts for oxygen reduction in low temperature fuel cells.

[1] Hermann, K.; Pettersson, L. G. M.; Casida, M. E. et al. StoBe2008, Version 3.0; 3.0 ed., 2008.

Ab initio Study of the Iron(III)Hydroperoxide Intermediate in Alkanes Oxidations Catalyzed by Nonheme Iron Center

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Oxidation is the most important tool to introduce functionality in very unreactive molecules like alkanes. Ideally these oxidation reactions should be carried out using molecular oxygen or its reduced form hydrogen peroxide. However, in order to be able to perform these reactions a catalyst is required. A good starting point for the design of new catalysts is to look at nature, which has developed highly reactive and selective oxidation enzymes. Many of these enzymes rely on one or two iron atoms in their active site. A good example of this class is iron bleomycin (FeBLM), a metalloglycopeptide that is clinically used in cancer treatment owing to the ability to oxidatively cleave DNA. This mononuclear iron system is also capable of oxidising a wide range of organic substrates using molecular oxygen or hydrogen peroxide. Spectroscopic studies of activated bleomycin support its formulation as a low-spin hydroperoxidoiron(III) species. Earlier [1] a model for activated BLM has been synthesized that mimics its reactivity and gives rise to the same optical and EPR spectra. This model is based on iron(II) complex of a new pentadentate ligand N4Py,(N4Py =N,N-bis(2-pyridylmethyl)-N-bis(2-pyridyl)methylamine). It reacts with H_2O_2 to generate a transient purple species which is characterized as a low-spin hydroperoxoiron(III) complex [(N4Py)FeOOH](2+) (Fig. 1). This intermediate is able to oxidize alkanes. There are several puzzles associated with [(N4Py)FeOOH](2+) chemistry, which still remain unexplained. In our effort to understand the factor affecting the homolysis of the O-O bond of this hydroperoxide intermediate to give two radical type oxidants (Fe(IV)O and OH) and to elucidate the mechanism of N4PyFe(2+) catalysed oxidations of alkanes in presence of H2O2, we have investigated using quantum chemical methods all intermediates which are involved in this process: N4Py, Fe(II)N4Py, Fe(III)N4Py, [Fe(N4Py)OOH](2+),[(N4Py)FeO$_2$], (N4Py)Fe(IV)=O, (N4Py)Fe(V)=O , OOH, OH, HO(-), Fe(2+), Fe(3+), H_2O_2, and O_2. Calculations have been carried out at the DFT and MP2 levels using 3-21G* and 6-31G* basis sets. Solvent effects have been included by means of polarizable continuum model. Our results indicate two possible reaction catalityc mechanisms for alkane oxidation using ([(N4Py)Fe](2+) + H_2O_2) system.

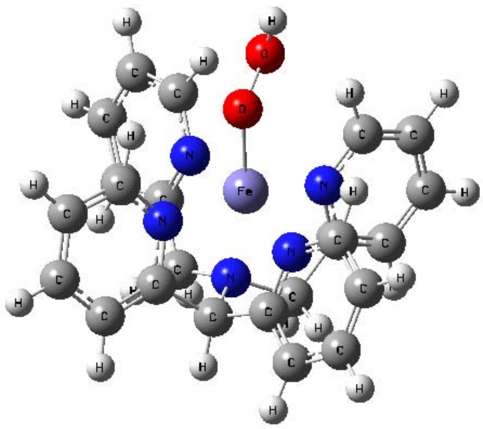

Fig. 1. Optimized structure of complex [(N4Py)FeOOH](2+) at DFT/B3LYP/6-31G(d) level

This work was supported by the Program of the Department of Chemistry and Material Sciences of the Russian Academy of Sciences, “Theoretical and experimental study of nature of chemical bonds and of most important chemical reactions and processes”.

[1] M. Lubben, A. Meetsma, E.C. Wilkinson, B. Feringa, and L. Que, Jr. Angew.Chem. Int.Ed. Engl. 1995, 34, 1512.

Quantum-Chemical Research of the Flame Inhibition Processes

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Any burning is first of all a chemical reaction of the combustible mixture components accompanied by heat emitting and creating of disperse kind mass-transfer process in gas. That is why all the phenomena of burning and fire-extinguishing are closely connected with ideas and rules of chemical kinetics and first of all with the concept of the rate of chemical reaction running under non-isothermal conditions. Then the heat evaluated due to reaction accelerates the latter, in according to the Arrenius rule. The availability of such a correlation is a high degree characteristic of the most of burning phenomena.

There are considerable differences in the conformities to natural laws of the flame suppression that are conditioned by differences in the chain carrier types reacting with the inhibitor. The effect of extinguishing consists in the deactivation of the flame active sites $Y^\bullet$ ($O^\bullet$, $H^\bullet$, $OH^\bullet$ and so on) at the surface of fire extinguishing powder particle that is in the flame torch or in the gas phase including the thermal decomposition products of inhibiting agent [1].

There are widely used phosphorus organic compounds among various chemical additives to fire-extinguishing powders. Thus, trimethyl phosphate (TMP) has been shown [2] to be an effective burning inhibitor. Firstly the reaction mechanism of phosphorus oxides with radicals – flame active sites was studied by Twarowski [2] who examined a catalytic effect of phosphorus oxides on the $H^\bullet$ and $OH^\bullet$ recombination reaction. It was shown in the same work by an experiment that on addition of TMP into flame the $HPO_2^\bullet$, $PO_2^\bullet$ and $PO^\bullet$ particles (formed due to thermal decomposition of TMP) are the most active inhibiting ones.

The quantum-chemical calculations have been carried to clarify the particularity of inhibiting mechanism. The research has shown that besides elemental stages in the inhibition cycle, suggested in [2] the important reaction is also: $PO^\bullet + O^\bullet = PO_2^\bullet$. The results of calculation have presented in the table.

Table

№	The elemental stages	The interaction energy E, kcal/mol
1	$PO^\bullet + O^\bullet = PO_2^\bullet$	25,1
2	$PO^\bullet + OH^\bullet = HOPO$	50,2
3	$PO^\bullet + H^\bullet = HPO^\bullet$	37,6
4	$PO_2^\bullet + OH^\bullet = HOPO_2$	18,8
5	$PO_2^\bullet + H^\bullet = HOPO$	81,5
6	$HOPO + H^\bullet = PO_2^\bullet + H_2$	6,3
7	$HOPO + OH^\bullet = PO_2^\bullet + H_2O$	6,5

As we can see from the table the reactions 1, 3, 4, 6, 7 are the most probable. The particles $PO^\bullet$, $PO_2^\bullet$, HOPO – active scavenging components of reaction mixture, that coincides with experiments [2]. Thus, at the application phosphorus containing fire suppressants these radical play cruel role in the inhibition processes.

[1] Krasnyanskiy M.G., Fire-Extinguishing and Explosion-Suppressing Powders. Donetsk: Donbass, 1990. – 11 p. (In Russian).

[2] Twarowski A. The Influence of phosphorus oxides and acids on rate of H + OH recombination // Combust. Flame. – 1994. – V.94. – P. 91-107

The Quantum-Chemical Investigation of Chlorophosphates Aminolysis

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Phosphorylation reactions involving phosphate mono- and diesters represent a group of essential chemical and biochemical processes varying from simple organic synthesis to enzyme catalyzed replication of DNA molecules. Therefore a deep understanding through careful theoretical research of the nucleophilic substitution mechanism near the tetracoordinated Phosphorus atom is significant.

In this work we have investigated the potential energy surface of model phosphorylation reaction of methylamine by dimethylchlorophosphate at the MP2/6-31G(d) and MP2/6-311+G(d,p) levels of theory in acetonitrile solution (ε=36,64, CPCM-model). In consideration of our previous results, that show the preference of non-classic front-side nucleophilic attack under classic back-side in case of Sulfur derivatives, we have considered those two possible pathways: (**I**) – back-side and (**II**) – front-side for the model reaction. Calculated values of geometric and activation parameters are given in Table.

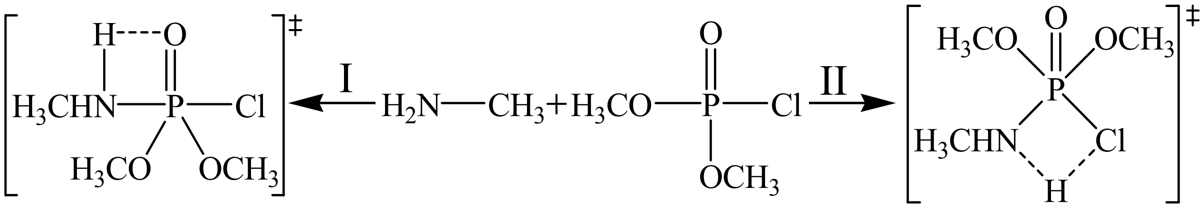

Table. – Calculated geometric parameters of transition states (I) and (II) and activation barriers of model reaction relatively to the sum of isolated reagents

Method/basis	Bond lengths, Å				Valent angles $\angle NPCl$, ^{0}		ΔE^{ACT}, kJ/mol	
	P–N		P–Cl					
	I	**II**	**I**	**II**	**I**	**II**	**I**	**II**
MP2/6-31G(d)	1,840	1,926	2,214	2,674	171,4	71,4	122,2	75,8
MP2/6-311+G(d,p)	1,840	1,916	2,233	2,686	171,4	70,9	122,9	88,2

According to the results of calculation the non-classic front-side approach of amino-group has activation barrier 40,0 kJ/mol lower then classic back-side attack, and thus is dominant.

Located transition state of preferable front-side nucleophilic attack has later character. Calculated Wyberg indexes of P–N and P–Cl bonds in structure (**II**) equal 0,42 and 0,28 respectively. In order to explain obtained results Natural Bond Orbital analysis of transition state (**II**) at B3LYP/6-31G(d) level of theory has been performed. The obtained data describe bond and antibond P–N in equations:

$$\sigma_{P\text{–}N} = 0{,}364(sp^{4,10}d^{1,94})P + 0{,}932(sp^{4,27})N$$
$$\sigma_{P\text{–}N}{*} = 0{,}364(sp^{4,10}d^{1,94})P - 0{,}932(sp^{4,27})N$$

where 0,364 and 0,932 are the correspondent polarization coefficients; a hybrid label is showing the $sp^{4,10}d^{1,94}$-hybridization of Phosphorus atom. Specific reactivity of Phosphorus derivatives is stipulated by the presence of vacant 3d-orbitals in Phosphorus atom which make significant contribution (~28 %) in P–N bond's molecular orbitals in transition state (**II**).

Theoretical Study of Aziridine Ring Opening Process

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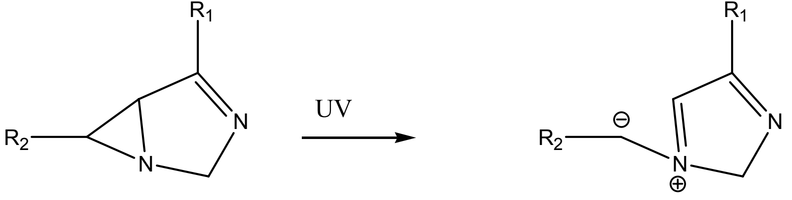
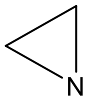
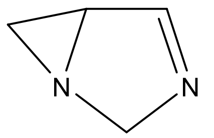
Bicyclic aziridines represent a very interesting class of organic compounds, possessing unique photochromic properties. It was demonstrated that these compounds form deeply colored, fairly stable materials under UV radiation. This property is associated with opening of aziridine ring leading to formation of corresponding ylides.





1



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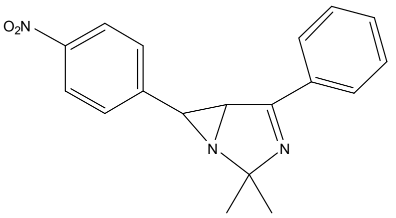

3

Quantum-chemical study of ring opening process in aziridine 1 by MP2, DFT and CISD methods demonstrates only possibility of breakage of the C-C bond. It was found that transition state of this process possesses clearly biradical character in agreement with MCSCF data. This indicates homolytic character of bond breakage with further fast redistribution of charge and spin density in final ylide. It should be noted that among DFT methods only BH&H and M05-2X functionals reproduce the character of the transition state.

Activation barrier of ring opening depends significantly on state of molecule and presence of substituents or fused rings. The highest barrier (about 50 kcal/mol) was found for ground state of unsubstituted aziridine 1. Transition of molecule to singlet (S_1) or triplet (T_1) excited state results in considerable decrease of barrier up to 7 kcal/mol. Presence of fused five-membered ring in bicyclic aziridine 2 and substituents in 3 results in further decrease of barrier in all states. The lowest barrier is observed for triplet state of molecule 3 (about 5 kcal/mol).

Results of calculations agree well with experimental data for compound 3. In particular this concerns existence of radicals under UV radiation. This allows to suggest that ring opening process in photochromic aziridines occurs in triplet excited state.

Ab initio Study of Reactivity of *c*-Amino-1,2,4-Triazoles

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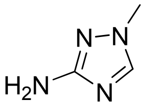
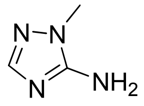
Amino-1,2,4-triazoles are key reagents in the synthesis of substituted 1,2,4-triazoles and condensed heterocycles [1]. It is known from the literature [2-4] that reactivity of isomeric 1-substituted 3-amino-1,2,4-triazoles and 5-amino-1,2,4-triazoles towards electrophiles is considerably different.



1



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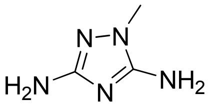

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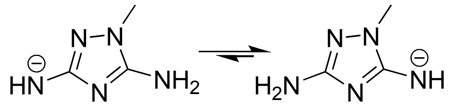

4A **4B**

We found that 1-substituted 3,5-diamino-1,2,4-triazole possesses topological parameters very close to the both 3-amino- and 5-amino-1,2,4-triazoles **1-2** (Table 1) and can be convenient model for the experimental and theoretical studying of the reactivity of C-amino-1,2,4-triazoles.

Table 1. The geometrical parameters, electron charge density, *ρ(r)*, its $\nabla^2\rho(r)$ and Ellipticity, *ε*, of structures 1, 2, 3 for the different bond (3,-1) critical points at the MP2/aug-cc-pVDZ level.

Compound	Bond	Bond Length, Å	$\rho(r)$, e/au^3	$\nabla^2\rho(r)$, e/au^5	ε	Bond Length, Å	$\rho(r)$, e/au^3	$\nabla^2\rho(r)$, e/au^5	ε
		vacuum				water			
1	C(3)-NH_2	1.395	0.303	-0.524	0.154	1.394	0.305	-0.522	0.153
3	C(3)-NH_2	1.397	0.302	-0.527	0.153	1.396	0.304	-0.526	0.150
	C(5)-NH_2	1.405	0.298	-0.560	0.132	1.391	0.307	-0.552	0.151
2	C(5)-NH_2	1.404	0.298	-0.558	0.131	1.391	0.307	-0.548	0.150

Table 2. The reactivity of compound 3 towards electrophiles: local charge (*q*), Fukui function (f_N^-) and local softness (s_N^-).

	vacuum				**water**			
	q_{NPA}	q_{AIM}	f_N^-	s_N^-, 1/au	q_{NPA}	q_{AIM}	f_N^-	s_N^-, 1/au
N2	-0.39	-0.69	-0.13	-0.73	-0.44	-0.74	-0.13	-0.71
3-NH_2	**-0.87**	**-1.21**	**-0.16**	**-0.92**	**-0.91**	**-1.25**	**-0.17**	**-0.94**
N4	-0.60	-1.11	-0.03	-0.19	-0.67	-1.16	-0.05	-0.26
5-NH_2	**-0.88**	**-1.19**	**-0.12**	**-0.67**	**-0.90**	**-1.24**	**-0.13**	**-0.73**

The second-order Møller-Plesset (MP2) calculations of nucleophilic Fukui functions (f_N^-) and condensed local softnesses (s_N^-) (obtained form natural population analysis) has shown that 3-NH_2 should be more nucleophilic than 5-NH_2 (Table 2). However, the inversion of reactivity will occur in the presence of strong bases owing to the deprotonation of 5-NH_2 and formation of more nucleophilic anion **4B,** which is thermodynamically more stable than **4A**. Our calculations are in good agreement with experimental data [2-4].

[1] Curtis A.D.M., Jennings N. 1,2,4-Triazoles. *Comprehensive Heterocyclic Chemistry III.* Vol. 5, P. 160-209, Elsevier, **2008**.

[2] V. M. Chernyshev, V. A. Rakitov, V. A. Taranushich, V. V. Blinov. *Chem. Heterocycl. Comp.* **2005**, *41*, 1139-1146.

[3] V. M. Chernyshev, V. A. Rakitov, A. V. Astakhov, A. N. Sokolov, V. A. Taranushich. *Russ. J. Appl. Chem.* **2006**, *79*, 624-630.

[4] V. M. Chernyshev, A. E. Kosov, E. S. Gladkov, S. V. Shishkina, V. A. Taranushich, S. M. Desenko, O. V. Shishkin *Russ. Chem. Bull.* **2006**, *55*, 338-344

Computation Studying of Reactivity of Some Fluorine-Containing Imines in Reactions of Electrochemical Carboxylation

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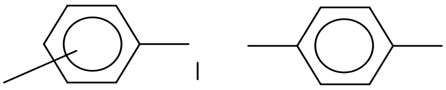
Ukrainian Academy of Technological Cybernetics Sciences, Poltava Department

Fluorocontaining amino acids and their derivatives already found widespread application in medicine, pharmacology, etc. However, now, fluorine-containing N-phenylphenylglycine derivatives are still practically unexplored due to the synthetic difficulties. One of ways of their producing is the process of electrochemical carboxylation of corresponding imines with the fluorine atom or fluorine-containing group [1]. The intermediate particles, the imines anion radicals (AR), can undergo different conversions, in particular, they can interact between themselves to produce dimers that, as the result, decrease amino acids yield.

In this work the quantum-chemical calculations of energy formations of anion-radicals, spin conditions of investigated imines were undertaken with the purpose of studying of reactivity of fluorine-containing imines. The calculations were carried out in the approaches of AM1 with the Unrestricted Hartree-Fock Method.



As the objects for investigations we used the following imines (**1**: R^1=*para*-F, R^2=H; **2**: R^1=*meta*-F, R^2=H; **3**: R^1=*ortho*-F, R^2=H; **4**: R^1= *para*-F, R^2=OCH_3; **5**: R^1= *para*-F, R^2=CH_3; **6**: R^1= *para*-F, R^2=F; **7**: R^1= *para*-F, R^2=Cl; **8**: R^1=*para*-F, R^2=Br; **9**: R^1=*para*-F, R^2=CF_3; **10**: R^1= *para*-F, R^2=COOEt). They contain the fluorine atoms at different positions in the benzylidene fragment (1-3), and imines with fluorine atom in the para-position of the benzylidene fragment and electron-donor (4,5) or electron-acceptor (6-10) substituents in the aniline fragment.

The correlation between the amino acids yields and the stability of anion-radical was obtained on the base of value of the AR energy formation. If the energy formation of AP is high (40-90 eV), the corresponding amino acids are formed at higher yields (>44%) and amino acids with low yields (39-15%) are formed from less stable AR (14-20 eV).

It was of interest to elucidate the influence of the nature of different substituents in the imines benzylidene and aniline fragments on the yields of corresponding amino acids. We examined the distribution of π-electron density on the carbon and nitrogen atoms of >C=N- fragment in the imines containing electron-acceptor substituents in an aniline fragment. As follows from calculated data, the amino acid yields are critically dependent on the electron structure of the imines. In general, there can be discerned a trend for increasing in efficiency of amino acid yield with decreasing of electron density on nitrogen atom.

We also investigated the energy of higher occupied molecular orbital (HOMO), the distribution of π-electron density on >C=N- fragment in the imines molecules, and also the distribution of π-electron density and spin density on this bond in AR. In AR imines, which have HOMO of π-type the electronic density is concentrated on nitrogen atom in all AR, except for V. The spin population in all AR is shifted to carbon atom. The total spin population $\Sigma\ \sigma(C)+\sigma(N)$ of the studying fragment in all AR is more than 40%, that well correlates with the value of efficiency of amino acids yield.

[1] V.G. Koshechko, V.E. Titov, V.N. Bondarenko, V.D. Pokhodenko//Journal of Fluorine Chemistry 129 (2008) 701-706.

Theoretical Study of Mechanism of 4-Phenyl-1,3-dihydro-1,5-benzodiazepin-2-one Acylation by Acetic Anhydride

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J. Leszczynski[b]

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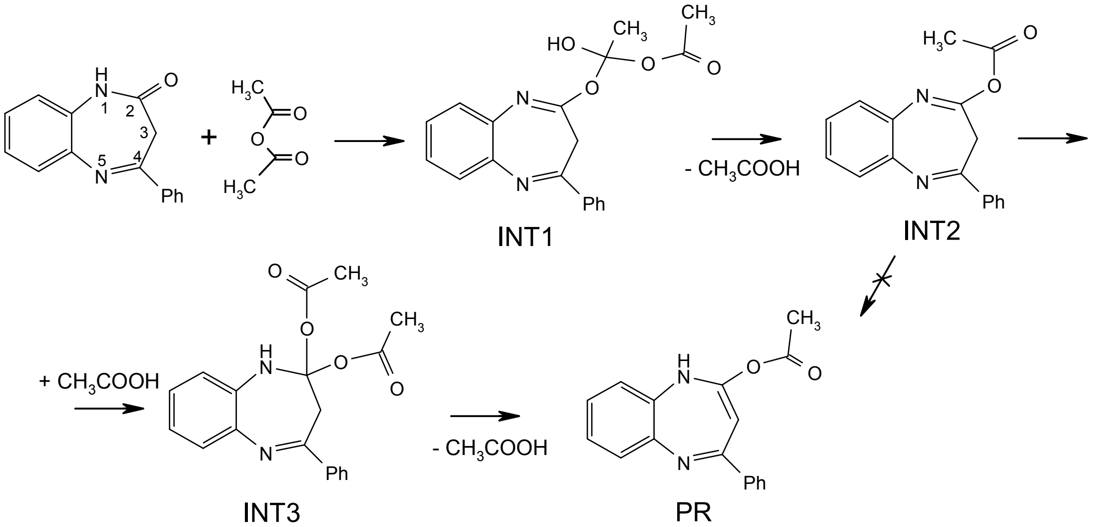
The increasing interest in the chemistry of 1,5-benzodiazepin-2-ones is caused by their well established biological activity. The acylation products of benzodiazepinones are potential agents for application in biochemistry research and in medicinal chemistry. To obtain the mechanistic details of their formation the mechanism for the acylation reaction of 4-phenyl-1,3-dihydro-1,5-benzodiazepin-2-one (**1**) with acetic anhydride was investigated at the MP2/6-311+G**//B3LYP/6-31G* level of theory. Solvent effects were considered via polarizable continuum model.



The obtained results show that in the investigating mechanism the first step consists of the acetic anhydride molecule addition to the oxygen atom of the 4-phenyl-2,3-dihydro-1,5-benzodiazepin-2-one with formation of the INT1. Further elimination of acetic acid occurs. The acetic acid addition to the $N_1=C_2$ bond of INT2 yields INT3. And, finally, removal of acetic acid molecule leads to *O*-acyl-4-phenyl-2,3-dihydro-1,5-benzodiazepin-2-one as a main product that is in agreement with the experimental observation. The direct imine-enamine tautomerization INT2→PR is characterized by very high free energy barrier and, therefore, does not take place. The first step is a rate-determining step of this reaction.

DFT Study on Reaction of Glycidyl Phenyl Ether and N-phenyl-N-sulfophenylglycidyl Amide with Bicyclo[2.2.1]hept-5-en-endo-2-ylmetylamine

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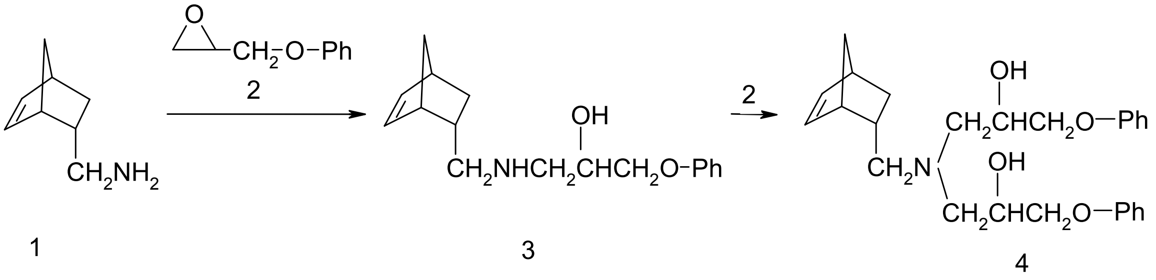
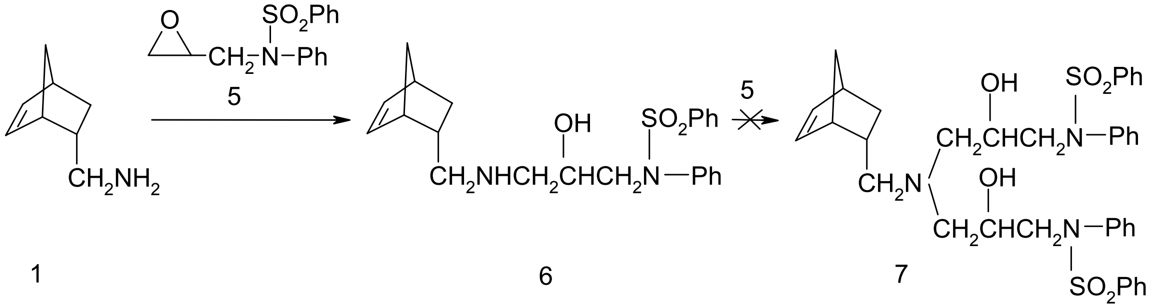
[b] *Interdisciplinary Nanotoxicity Center, Department of Chemistry, Jackson State University, Jackson, Mississippi 39217, USA*

[c] *Kirovograd State Pedagogical University, Kirovograd, 25006, Ukraine*

Glycidyl ethers are known during many decades and presently are actively studied and widely used in organic chemistry. In the recent years different types of biological action are revealed for actively studied products of aminolysis of glycidyl ethers; among them hypothensive, antiviral, antibacterial and antitubercular agents and β-blocators are found.

In the present study reactions of aminolysis of glycidyl phenyl ether (2) and N-phenyl-N-sulfophenylglycidyl amide (5) by bicyclo[2.2.1]hept-5-en-endo-2-ylmetylamine (1) were theoretically investigated.





In order to take into account all possible conformations of reagents and different ways for their approaching the following procedure for localization of transition states has been used in the study:

1) Full conformational analysis of the primary products of aminolysys using MMX approach
2) Selecting among localized structures those with values of NCCO torsion angle equals or close to 180^0 which corresponds to transition state for transoid opening of epoxy cycle and reoptimization at PM6 level.
3) Setting up for the selected structures C-O and C-N bond lengths equal to 1.8 Å and optimization of the corresponding transition states and calculations of activation barriers at PM6 level.
4) Additional optimization of the most stable transition states at the B3LYP/6-31G* level of theory.

The obtained results show that interaction of bicyclo[2.2.1]hept-5-en-endo-2-ylmetylamine with glycidyl ether may occur in ratio 1:1 and 1:2 leading to products 3 and 4, respectively. While interaction of amine (1) with amide (5) takes place only in ratio 1:1 because of steric hindrance in during sylfonamide attack of compound 6.

DFT Calculations of Substituent and Solvent Effects on the Electrode Potentials of Imidazole and its Derivatives

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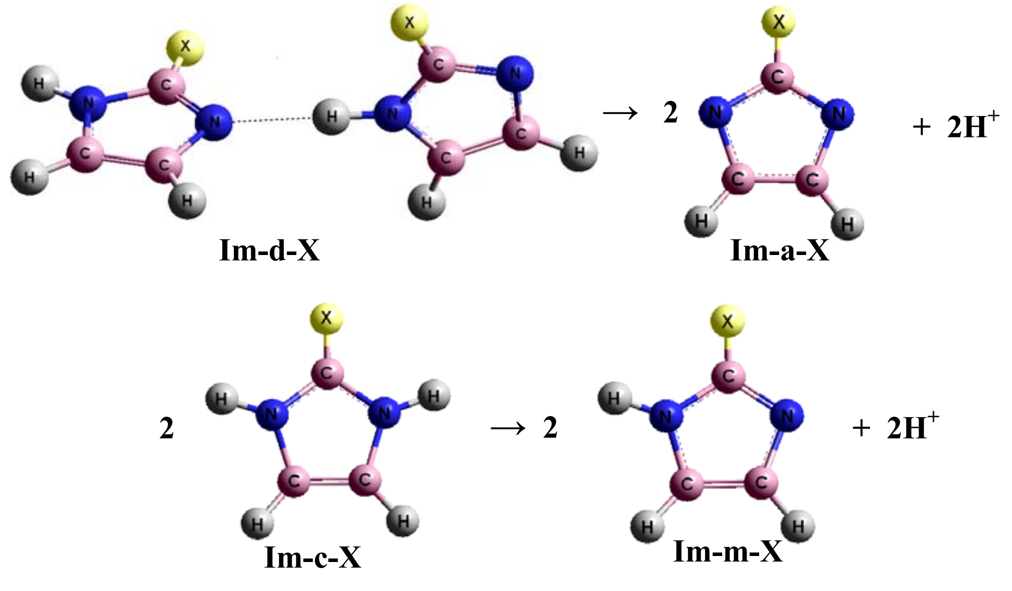
Imidazole structure which contains a proton donor N-H and proton acceptor N atom have been studied as a model system both experimentally and theoretically [1]. In this study, we have calculated standard electrode potentials (E^o) of half reactions of imidazole and its derivatives from thermochemical values by using B3LYP/6-31+G(d) method. For imidazole derivatives, calculations have been done by binding electron donating -CH_3, -NH_2, -OCH_3 and electron withdrawing -NO_2, -Cl, -F and Br functional groups to the second numbered carbon atom of imidazole molecule. Standard electrode potentials (E^o) of half reaction for dimer and protonated structures of molecules have been calculated versus normal hydrogen electrode (NHE) (Scheme 1) by using the calculated standard Gibbs Free Energies (ΔG^o). Calculations have been done in two different solution phases as protic (water) and aprotic (acetonitrile) medium. The Polarisable Continuum Model (PCM) has been used to describe the solution phase calculations.



X = H, NO_2, NH_2, CH_3, F, Cl, Br

Scheme 1

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[1] (a) W. W. Bachovchin, Biochemistry 25, 7751, 1986, (b) T. Noguchi, Y. Inoue, and X. S. Tang, Biochemistry 38, 399, 1999, (c) M. Sorlie, J. Christiansen, B. J. Lemon, J. W. Peters, D. R. Dean, and B. J. Hales, Biochemistry 40, 1540, 2001, (d) Bender, M. L.; Bergeron, R. J.; Komiyama, M. Wiley-Interscience: New York, 1984; p 312, (e) Stewart, R. Academic Press: Orlando, FL, 1985; Vol. 46, p 313, (f) D.M. Blow, Acc. Chem. Res. 9, 1976, 145, (g) R.K. McMullan, J. Epstein, J.R. Ruble, B.M. Craven, Acta Crystallogr. B35, 1979, 688, (h) B.M. Craven, R.K. McMullan, J.D. Bell, H.C. Freeman, Acta Crystallogr. B33, 1977, 2585, (i) J.L Brédas, M.P. Poskin, J. Delhalle, J.M. André, J. Phys. Chem. 1984, 88, 5882-5887, (j) M. Tafazzoli, S.K. Amini, Chemical Physics Letters 431, 2006, 421–427, (k) S. Scheiner, M. Yi, J.Phys.Chem. 1996, 100, 9235-9241, (l) N.O.Pekmez, Muzaffer Can, Attila Yildiz, Acta Chim. Slov, 2007, 54, 131.

Calculation of Raman Spectra of Benzophenone and Deuterated Benzophenone

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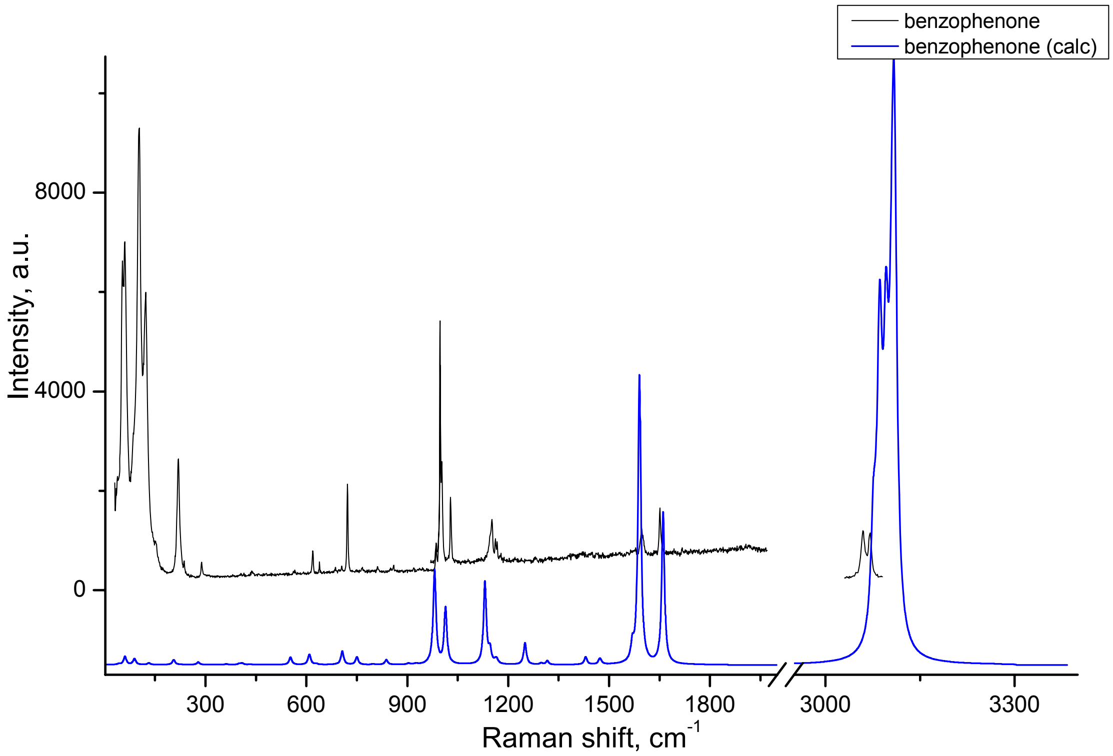
Benzophenone is widely used in organic photochemistry. Raman spectra of benzophenone and its deuterated analog were measured experimentally and computed using Gaussian 03 package. Computations were executed using DFT/b3lyp functional in 6-31+g(d,p) basis set. Calculation were performed for free molecules. Calculated spectra matches with experimental quite good. Average dilatation from experiment is 28 cm^{-1}. Comparing experimental and computed results “scaling” coefficient were calculated. It is equal 0.96. This value concurs with data presented in literature. After scaling average dilatation becomes 8 cm^{-1}. Relative shifts of spectral lines after deuteration agree with experimental with high accuracy (about 1 cm^{-1}).



To elucidate possible connection between deuteration of intramolecular H-bonds and abnormal Raman shift under duteration of organic molecules with cyclic fragments Raman spectra of 2,2′-dihydroxybenzophenone and deuterated 2,2′-dihydroxybenzophenone were computed. This derivative of benzophenone contains two adjacent OH groups that substitute two hydrogen atoms. In deuterated 2,2′-dihydroxybenzophenone groups OH were replaced with OD. After deuteration some lines (for example 1060-cm^{-1} peak) experienced blue shift. In Raman spectrum of deuterated benzophenone no shifts to higher frequencies were observed.

Does Exist Transition Metal-Proton Adducts in High-Silica Zeolite ZSM-5?

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Metal/zeolite catalysts offer challenging perspectives for catalysis. In numerous catalysts at least one of the zeolite-supported elements is completely reduced to the zerovalent state. As a result, small nano-clusters or even isolated atoms of the transition metal are formed. Coproducts of such reduction are protons, which act as strong acid site. The material thus exposes two types of catalytically active centers: transition metal atoms and protons. In 1973 Dalla Betta and Boudart reported an unusually high hydrogenation activity of small Pt particles in Y zeolite. They ascribed this to an electron transfer from the Pt clusters to the zeolite. Later studies (W. M. H. Sachtler, 1991) with zeolite-supported Pt, Pd, and Rh showed that the electron deficiency is related to the proton concentration of the zeolite. The results suggest that transition metal clusters in zeolites interact with zeolite protons and form metal-proton adducts. Since protons in metal-proton adducts are bridging between metal atoms and oxygen ions of the zeolite wall, they also act as chemical anchors.

We present herein a density functional study (B3LYP functional) of the interaction of H-form of ZSM-5 with different embedded clusters which contain four metal atoms (M_4) namely: Co_4, Rh_4, Pd_4, and Pt_4. The Bronsted sites in ZSM-5 are represented by a model cluster 20T-ring (T denoted tetrahedral Al and Si atoms), where there are single framework Al atom in ring containing ten T atoms, one of which is Al atom. This 20T-cluster is picked out from the main channel of the ZSM-5 zeolite. The Si atom of the central tetrahedral site (T-12 site) is substituted with an Al atom and the terminal dangling bonds are satisfied by the H atoms. For practical purpose, we employed a larger basis set CEP-31G only for the metal cluster, the 3-21G(d) basis set for Si, Al atoms, and the 3-21G basis set for oxygen and hydrogen atoms. The wall-bound M_4 embedded clusters are each in the singlet state. The geometry optimization of the studied M_4-20T-clusters has been performed only for active site including M_4- moiety. The natural bond orbital (NBO) charges on the M_4 cluster were calculated for the structures obtained by optimization calculations.

One important result of our calculation is that during structure optimization the bridged proton which compensates the negative charge of an $AlO_4(-)$ tetrahedron in a zeolite framework moves to M_4 embedded cluster. In accordance with DFT calculations this proton is bound to M_4 embedded cluster in 20T-cluster. A comparison of calculated NBO charges for Co_4, Rh_4, Pd_4, and Pt_4 clusters embedded in large 20T-cluster indicates that the negative charge transfer occurs from zeolite framework to protonated M_4 embedded cluster (the values of this transfer decrease the summary positive charge on M_4 from +1 to 0.59-0.65 au).

One should note that such barrier-less proton transfer from zeolitic Bronsted sites to the embedded Co_4, Rh_4, Pd_4, and Pt_4 clusters has never been previously reported for ZSM-5 zeolite. The intriguing question we have been attempting to address in our research is the following: does exist transition metal-proton adduct in high-silica zeolite ZSM-5. Our modeling calculations at DFT/B3LYP level show clearly that transition metal-proton adduct in high-silica zeolite ZSM-5 are stable and bearing the high positive charge.

Post Hartree-Fock Study on Decomposition of Nitrous Oxide on Ga–ZSM-5

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Nitrous oxide (N_2O) is a potent greenhouse gas and contributes to ozone layer depletion [1]. This has prompted the development of several abatement technologies based mainly on the catalytic decomposition. The reaction mechanism for nitrous oxide decomposition has been studied on gallium site in Ga-ZSM-5 using the MP2/6-31+G(d) method. The active centers were taken to be mononuclear $[Ga]^+$, $[Ga=O]^+$, and $[GaO_2]^+$ and the surrounding portion of the zeolite was represented by a 3T cluster, namely $[AlSi_2O_4H_8]^-$. The first elementary step of N_2O decomposition involves the formation of $[GaO]^+$ and the release of N_2. The metal-oxo species produced in this step then reacts with N_2O again, to release N_2 and form $[GaO_2]^+$. The calculated activation energies at MP2 level for N_2O dissociation on Ga-ZSM-5 and GaO-ZSM-5 are 15.7 and 26.5 kcal/mol at 298 K, respectively. The third elementary step of N_2O decomposition on GaO_2-ZSM-5 involves the formation of $[GaO_3]^+$ and the release of N_2. The calculated activation energy at MP2 level for N_2O dissociation on GaO_2-ZSM-5 is 43.7 kcal/mol. Four-order perturbation theory (MP4//MP2) predicts that the activation barriers for nitrous oxide dissociation at 298 K on Ga-ZSM-5, GaO-ZSM-5, and GaO_2-ZSM-5 are 13.9, 13.0, and 34.4 kcal/mol, respectively. The calculated energy for desorption of singlet O_2 from the $3T^-[Ga(O)_3]^+$ cluster at MP2 level is 33.4 kcal/mol. When one takes into account the entropy gained upon desorption of singlet O_2, the contribution of entropy to the free energy of desorption is $T\Delta S$ =12.3 kcal/mol at 298 K. The calculated energy of the singlet oxygen desorption from $3T^-[OGaO_2]^+$ cluster ΔH (298 K)=+43.57 kcal/mol and ΔG(298 K)=30.13 kcal/mol is significantly higher than the barriers of the singlet molecular oxygen desorption from $3T^-[Ga(O)_3]^+$ cluster [2].

This work was supported by the RFBR (project 05-03-33103).

[1] Prather, M. J. *Science.* **1998**, *279,* pp. 1339-1341.
[2] Solkan, V. N., Zhidomirov. *International Journal of Quantum Chemistry.* 2008. Vol. 108, Iss. 14. pp. 2732-2743.

Surface Layer Structure of Mesoporous Silicas Containing Amino and Thiol Groups

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Mesoporous silicas with complexing groups in the surface layer obtained by sol-gel or template synthesis find progressively wider range of applications in sorption technologies, catalysis, chromatography, chemo- and biosensor design. Properties of such materials are determined first of all by composition and structure of their surface layer. However, unlike modified silica, there is still no comprehensive understanding of structure and behaviour of a functional layer of these compounds. Even in the simplest case of mesoporous silica with 3-aminopropyl groups there is still no agreement on whether the group is in protonized molecular form or forming a hydrogen bond with other groups of the layer. Moreover, in case of hydrogen bond formation, the mechanism of the bond may vary in the presence of water molecules of silanol (or other groups) in the surface layer. The goal of current study is to examine surface clusters of amino- and thiolcontaining mesoporous silica using quantum-chemical calculations [DFT/B3LYP/6-31G(d,p)] to determine the most energetically favorable configuration of hydrogen bond when it is formed, conditions of protonization of those groups, and the most likely changes in the surface layer when water presence is reduced or eliminated.

The surface of amino- and thiolcontaining mesoporous silica was modelled with $(HO)_2Si(OH)[(CH_2)_3NH_2]$ and $Si_6O_9(OH)_4[(CH_2)_3NH_2][(CH_2)_3SH]$ or $Si_6O_9(OH)_4[(CH_2)_3NH_2]_2$ clusters representing T^2 and T^3 structure units respectively.

Based on the results of analysis of quantum-chemical calculations, we arrived to the following conclusions:

1) In the presence of a single molecule water there is no protonization of amino groups. However, it becomes possible with the increasing number of water molecules in the surface layer.
2) The most energetically favorable H-bond formation is achieved when water molecules form a bridge between 3-aminopropyl and silanol groups. The hydrogen atoms of amino-groups are not utilized.
3) When water is completely removed from the surface layer, H-bond formation between amino-groups becomes possible.
4) In the absence of water, the H-bond between amino and silanol groups is stronger then between amino and thiol groups. Reintroducing water molecules results in the bridge formation described in 2.

The above conclusions are in agreement with experimental studies of functionalized mesoporous silicas, namely IR spectroscopy of thermo-vacuumed samples and solid state multinucleus NMR spectroscopy.

Atomic Structure of Near-Surface Region of Nano - Si Doped by H and O Atoms: A PM3 and DFT Modelling

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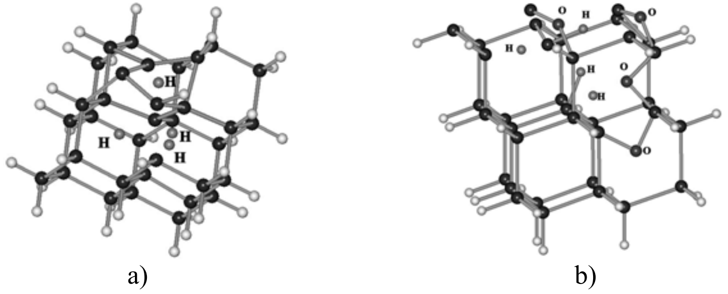
Earlier [1] we have demonstrated experimentally that the hydrogen ion-beam treatment of standard Cz Si wafers even at 300 K leaded to the formation of a thin insulating oxygen-containing layer on the treated surface. To understand the origin of this effect we have carried out the systematic theoretical studies of atomic configurations of various silicon nanoclusters with interstitial H and O atoms as impurities, obtained by semiempirical (PM3) and DFT quantum-chemical methods.

The aim of this simulating research is to study the influence of H- and O-atoms incorporation into near-surface region of Si on changes of atomic structure of Si-H and Si-O complexes with different number of impurity atoms.

A set of clusters $Si_XH_Y[H_LO_M]$ was used in order to reproduce local atomic structure of nano-Si (111) and (100) surface and H- or O-containing nanodimensional complexes with different number of impurity atoms for the appropriate near-surface region of Si. Here X - number of Si atoms, Y - number of H atoms saturating dangling bonds in a cluster, on *border* atoms in the *cluster*, L - number of H atoms creating hydrogen-containing defects, M - number of O atoms incorporated in hydrogen-containing defects. The PM3 and DFT levels quantum chemical theory for geometry structure optimisation of all clusters was used.

In Figure below we present mainly the results for $Si_{35}H_{30}[H_4]$ and $Si_{35}H_{30}[H_4O_4]$ clusters as a representative examples.



a) b)

Fig. Clusters after geometry structure optimization using PM3 level theory: (*a*) cluster $Si_{35}H_{30}[H_4]$ with four H atoms incorporated in near-surface region; (*b*) cluster $Si_{35}H_{30}[H_4O_4]$ with four H and O atoms incorporated in near-surface region . Black circles represent Si atoms, white - H atoms saturating dangling bonds, hydrogen and oxygen atoms incorporated in near-surface region are denoted as H andO.

For clusters containing nanodimensional Si-H complexes, hydrogen atoms, initially located at the near-surface atomic layers are diffused to the surface, forming covalent chemical bonds with some surface Si atoms and stabilizing them in the surface layers. Residuary surface atoms are relaxed to the bulk of the cluster. Hydrogen atoms which are in deeper atomic layers are located in the interstitial positions of silicon lattice. Furthermore the initial stage of amorphization of silicon layers subjected to hydrogenation is observed.

For clusters containing nanodimensional Si-H and Si-O complexes, we observe, just as in the previous case, localization of hydrogen atoms with the formation of initial *amorphization* stages of silicon layers. At the same time, oxygen atoms carry out a role of the stabilizing factor stimulating the formation of the initial precursors of silicon oxide from the *amorphized* silicon layer.

This work was supported by the project № 6.08 of the "Nanomaterials and Nanotechnology" Program.

[1] O. Zinchuk, A. Saad, N. Drozdov, A. Fedotov, S. Kobeleva, A. Mazanik, A. Patryn, V. Pilipenko, A. Pushkarchuk, *J. Mat. Sci: Mat. El.* **19**, 273 (2008).

Ab initio Modeling of Methylene Blue Dimers and Its Interactions with Nanoforms of Carbon

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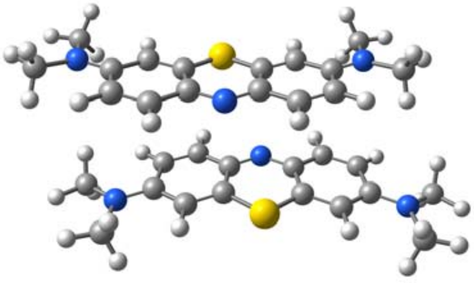
Both cationic dye methylene blue (MB) and nanoforms of carbon are utilized in design of modern nanodevices, which necessitates detailed knowledge on their structure and electronic properties. Present calculations were imitated for interpretation of two experimental facts, revealed during mass spectrometric studies of the above objects. Firstly, relatively stable dimers of MB cations were observed to exist in the gas phase. Secondly, ultrasound sonication of the mixture of carbon nanotubes (CNT) with MB in water resulted in temporary stabilization of the aqueous suspension. Parameters of the laser desorption mass spectra of such samples indicated monomolecular adsorption of MB cation on CNT surface.

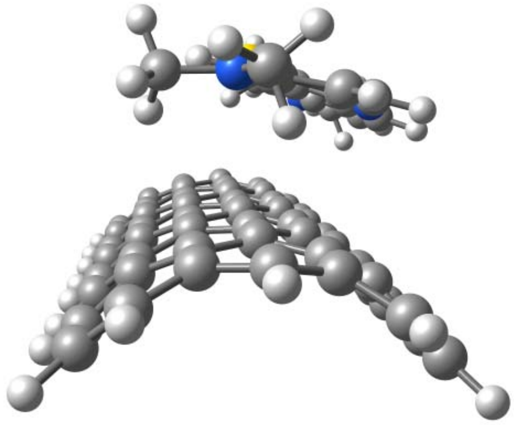


Optimized geometry
of methylene blue dimer

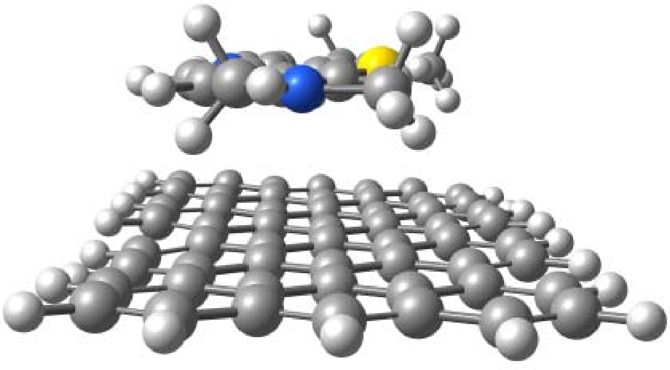
Ab initio quantum mechanical calculations of the above objects observed in the mass spectrometric experiments were performed by DFT M05-2X method with 6-31++G(d, p) basis set.

It was established that, although the energy of interactions in the optimized structure of the dimer formed by MB cations is positive (repulsive) 121,1 kJ/mol, there is a local minimum at 3,4 A separation of the monomers followed by a barrier of 20,3 kJ/mol, which permits existence of such a dime in the gas phase.

The energy of interaction of MB cation with the surface of a CNT fragment and a graphene sheet appeared to be relatively high, comprising -159.0 kJ/mol and -176.0 kJ/mol correspondingly.



MB cation with the surface of a CNT fragment



MB cation with the graphene sheet

Frontier orbitals analysis has shown localization of the orbitals on both the MB cation and CNT permitting electron transfer in the system, which is essential for its functioning in nanodevices.

This work was partially supported by STCU grant #4918.

Coexistence of Molecular and Ion Associates in Hydrated Complexes of Methylphosphonic Acid

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The current state-of-the-art of silica supported living organisms for medical use faces a fundamental problem, the lack of an adequate understanding of the mechanism of interaction between separate cells or microorganisms and silica nanoparticles. Both silica nanoparticles and cells of live organisms, particularly the erythrocytes, are known to have a negative charge on their surfaces as a result of the electrolytic dissociation of silica surface silanols of OH groups of cell membrane phosphonic acids. In aqueous suspensions of animal reproductive cells silica nanoparticles are known to be adsorbed on cell membranes. However no similar interaction is found in non-aqueous media. It therefore becomes evident that an important role in this interaction must be played by hydrated protons and centers of negative charge remaining on the lipid layer molecules and hydrated protons.

The elucidation of the structure of hydrated complexes of phosphonic acids would be of both practical and theoretical importance. While a detailed and direct experimental study might be plagued by technical problems, the development of theoretical quantum chemistry models seems amenable and could provide a useful insight into the nature of these systems.

Despite the advances made by modern ab initio quantum chemistry methods, writing a model that takes into account all the details of the simplest lipidic membranes or their aggregates is still impossible. Therefore the most simple organophosphorous acid – methylphosphonic acid $CH_3PO(OH)_2$ could be used in order to study some general trends. This choice is justified by the relatively simple structure of most phosphonic acid molecules which have identical polar heads and contain a non-dissociated $PO(OH)_2$ group.

The electronic structure and the equilibrium geometry of the hydrated complexes of methylphosphonic acids were investigated by the Density Functional Theory Method (B3LYP functional with 6-31G** basis set). Molecular structures were found to coexist with their ion associates. The interconversion between the two forms involves the simultaneous transfer of two protons, a process with a low energy barrier.

Ab initio Modeling of Potassium Aspartate in Vacuum and Aqueous Media

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The information concerning molecular structure of amino acids derivatives is important for detection of mechanisms of medicinal action of the appropriate medicines, and for the development of more effective methods of synthesis and procedures of application of the relative drugs. In continuation to our previous papers [1-4] we present here the results of *ab initio*/MINI quantum-chemical studies of structure and stability of potassium aspartate ($(Asp^{-})\,K^{+}$) in vacuum and water solutions and potassium aspartate crystallohydrates ($(Asp^{-})\,K^{+}\cdot 0.5H_2O$).

The $(Asp^{-})\,K^{+}$ is one of the active components of potassium - magnesium aspartates, a medical product which is known as Asparcam (Belarus, Ukraine, Russia), Panangin® (Gedeon Richter, Hungary), Pamaton® (PHARMACIA AD).

The most stable conformers of $(Asp^{-})_{\alpha}K^{+}$and $(Asp^{-})_{\beta}K^{+}$ complexes in gas phase, obtained by using the DFT B3LYP/6-311++G(d,p)-optimizing [5] have been selected as an initial geometry. The comparison of our *ab initio* / MINI level theory and [5] results for geometry structure are represented in Fig. below.

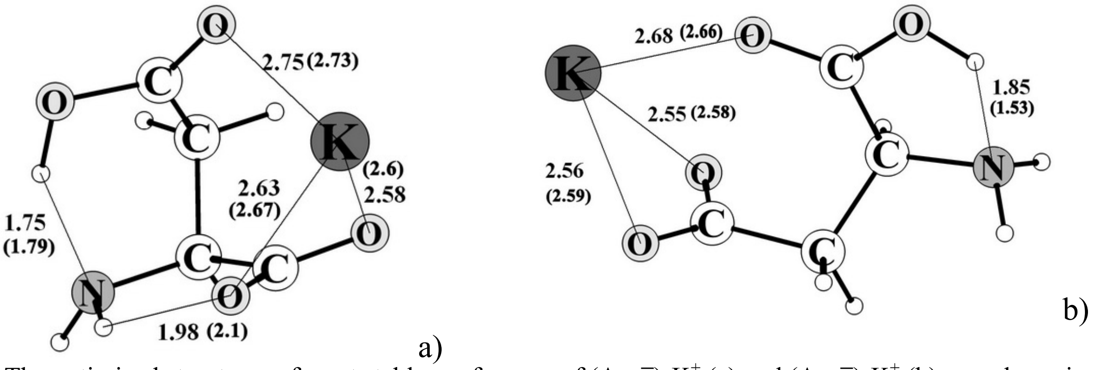

Figure. The optimized structures of most stable conformers of $(Asp^{-})_{\alpha}K^{+}$ (a) and $(Asp^{-})_{\beta}K^{+}$ (b) complexes in gas phase. Numbers by the bonds indicates distance, between the atoms received by our *ab initio* / MINI and of DFT B3LYP/6-311++G(d,p)-optimization [5] (in parenthesis).

As shown from the figure the method using ab initio/MINI level theory is in a good agreement with the DFT B3LYP/6-311++G(d,p) level theory. For this reason we have used our approach for the other structures in our studies. From our calculations we observed that the $(Asp^{-})_{\alpha}K^{+}$ conformer in vacuum and the $(Asp^{-})_{\beta}K^{+}$ conformer in aqueous medium are the most stable.

The calculated structure of crystallohydrate appeared independent of the structure of initial $(Asp^{-})\,K^{+}$ (α or β) as well of their number.

[1] Soldatov V.S., Pushkarchuk A.L., Kuvaeva Z.I. MACC-1 Book of abstracts ; Kharkiv, 30June- 1 Jule 2005, p. 71

[2] Soldatov V.S., Pushkarchuk A.L., Kuvaeva Z.I. MACC-2 Book of abstracts ; Kyiv, Ukraine, 2 - 4 July 2007, p. 75

[3] Soldatov V.S., Pushkarchuk A.L., Kuvaeva Z.I. 12th International Workshop on New Approaches to High-Tech:Nano-Design, Technology, Computer Simulations (NDTCS-2008) June 23-27, 2008, Minsk, Belarus pp. 73-77

[4] Soldatov V.S., Pushkarchuk A.L., Kuvaeva Z.I. Book of Abstracts of XII International Conference on Quantum Optics and Quantum Information, September 20-23, 2008, Vilnius, Lithuania. – 2008. – P. 56-57.

[5] Wichien Sang-Aroon, Vithaya Ruangpornvisuti. J. of Molecular Graphics and Modelling 2008 **26** P. 982–990

Quantum-Chemical Description of the Thermodynamics of Clusterization of Substituted Alkanes at Air/Water Interface in the Frameworks of PM3 Method

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Spontaneous clusterization of substituted alkanes at air/water interface starts with the certain length of the hydrocarbon radical. We have developed quantum-chemical model of thermodynamic characteristics of clusterization which correctly describes this phenomenon. There are two assumptions on the basis of the offered model: firstly, interactions between molecules of substituted alkanes are caused by formation of hydrogen-hydrogen interactions between their hydrocarbon radicals (see fig.1) and, secondly, their contributions are additive. So after calculation of thermodynamic parameters of clusters with the limited number of molecules we can determine thermodynamic characteristics of clusterization of big associates, and also infinite 2D-films.

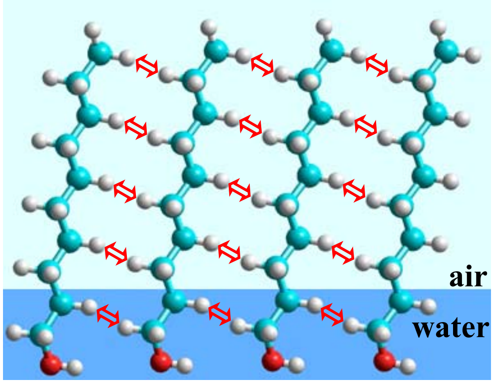

Fig.1 Orientation of molecules of substituted alkanes at air/water interface

Thermodynamic parameters (entalpy, entropy and Gibbs energy) of clusterization of the saturated alcohols [1], thioalcohols [2], amines [3], carbon acids [4], and also *cis*-monoenic carbon acids [5] have been calculated. All calculations were held within the frameworks of quantum-chemical program complex Mopac2000 with a help of semiempirical method PM3 because this method considers hydrogen-hydrogen interaction between hydrocarbon radicals of substituted alkanes. PM3 method is parameterized on heats of formation so it reproduces thermodynamic parameters correctly. For all investigated systems correlation dependences of their thermodynamic parameters of clusterization on the number of intermolecular H-H interactions have been constructed. We have determined energetic contributions of these interactions and calculated thermodynamic parameters of clusterization of infinite films. Contributions of H-H interactions for different classes substituted alkanes are identical, so this interactions have similar nature. Results of calculations shown, that spontaneous clusterization alcohols starts with the length of hydrocarbon radical of 10-11 carbon atoms, thioalcohols-14-15 atoms, amines-18-19 atoms, carbonic acids-14-15. This agrees well with experimental data. For *cis*-monoenic carbonic acids clusterization starts with the radical length of 17-19 carbon atoms, because of presence in their structure one unsaturated *cis*-bond. So clusterization process becomes energetically favourable when there are 5-9 intermolecular H-H interactions in the chain. It is connected with an influence of intermolecular interactions between functional groups which are different in the different systems. We have found some types of regular orientation of functional groups in cluster.

[1] Yu.B. Vysotsky, V.S. Bryantsev, V.B. Fainerman, D. Vollhardt, J. Phys. Chem.B 106 (2002) 11285.
[2] Yu.B. Vysotsky, E.A. Belyaeva, V.B. Fainerman, D. Vollhardt, R. Miller, J. Phys.Chem. 111 (2007) 5374.
[3] Yu.B. Vysotsky, E.A. Belyaeva, V.B. Fainerman, D. Vollhardt, R. Miller, J. Phys.Chem. 111 (2007) 15342.
[4] Yu.B. Vysotsky, D.V. Muratov, F.L. Boldyreva, V.B. Fainerman, D. Vollhardt,R. Miller, J. Phys. Chem. B 110 (2006) 4717.
[5] Yu. B. Vysotsky, E. A. Belyaeva, V. B. Fainerman, D. Vollhardt, E. V. Aksenenko, R. Miller. J. Phys. Chem. In print.

Structure of Crystalline Two-Dimensional Clusters of α-Amino Acids at Water/Air Interface in PM3 Method

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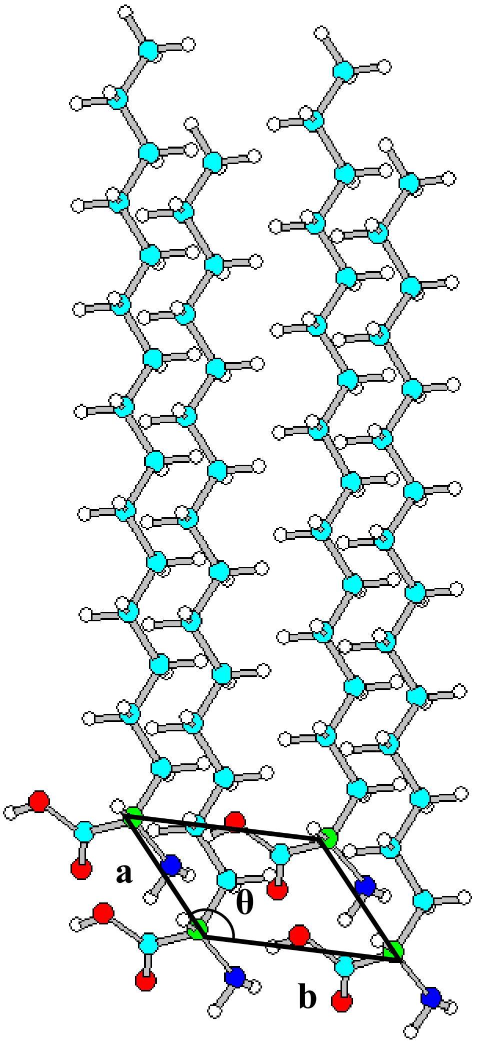

Fig.1. Scheme of the infinite 2D-cluster unit cell of α-amino acid

The two dimensional crystalline packing arrangement of S-enantiomericaly pure α-amino acids $C_nH_{2n+1}CHNH_2COOH$ (n=5–15) monolayers at water/air interface was investigated in the frameworks of PM3 method. The rectangle tetramers (Fig.1), built on the base of six the most energy-profitable conformations of monomers, were investigated as the unit cells of 2D-clusters of α-amino acids. The structure of monomers was defined with help of two dihedral angles (α and β) of functional groups –COOH and $-NH_2$ relative to hydrocarbon chain. These angles for monomers correspond to the next: -81° and -55°, -107° and 48°, 88° and -53°, 67° and 64°, -160° and 160°, 34° and 160°. Here the first angle defines the position of carboxyl group and the second angle defines the position of amine group.

Table 1. The unit cell parameters of infinite 2D-clusters of α-amino acids

Conformer	Structural parameters of monomers		The unit cell parameters of infinite 2D-clusters			
	α	β	*a*, Å	*b*, Å	*θ*, °	*t*, °
Tetramer 1	-81°	-55°	4,71	5,71	103	30
Tetramer 2	-107°	48°	4,84	5,81	94	30
Tetramer 3	88°	-53°	4,84	5,42	104	30
Tetramer 4	67°	64°	5,51	5,90	105	30
Tetramer 5	-160°	160°	4,49	5,86	103	30
Tetramer 6	34°	160°	4,66	5,73	102	30

Calculated values of structural parameters of unit cell well agree with experimental data [1] determined by synchrotron grazing incidence X-ray diffraction. These measurements yielded an oblique cell of dimensions a=4,91Å, b=5,25 Å, θ=112°. The tilt angle t between the molecular axis and the normal to the water surface was obtained ~36°, with the chains lying in planes close to the normal to the a axis.

[1] Weissbuch I., Berfeld M., Bouwman W., Kjaer K., Als-Nielsen J., Lahav M., Lieserowitz L. Separation of enantiomers and racemate formation in two-dimensional crystals at the water surface from racemic α-amino acid amphiphiles: design and structure. // J. Am. Chem. Soc., 1997. - Vol. 119 (5) – P. 933 – 942.

Quantum-Chemical Treatment of Possibility of Binuclear Aqua-Complex Formation in Water Solutions of a Sulfuric Acid

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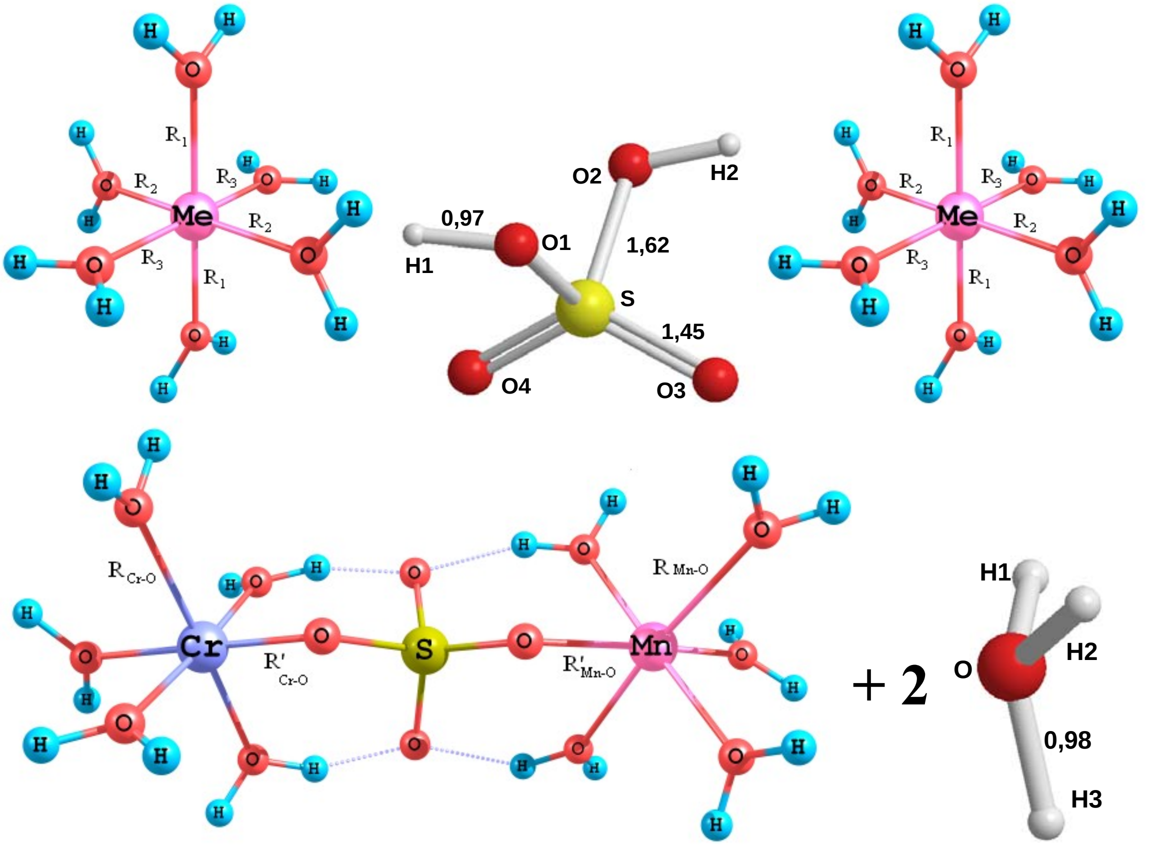
The molecular and electronic structures of mononuclear and binuclear aqua-complexes of chrome (III) and manganese (II) were investigated by means of quantum chemical method DFT/B3LYP with the effective core potential and double-ζ basis sets LANL2DZ for atoms of transition elements and basis sets 6-31G ** for other atoms. Model reaction of formation of mixed binuclear aqua-complex with sulfate-bridged ligand is considered:

$$Cr^{3+}(H_2O)_6 + H_2SO_4 + Mn^{2+}(H_2O)_6 \rightarrow [(H_2O)_5Cr–SO_4–Mn(H_2O)_5]^{3+} + 2(H_3O^+).$$



The calculated vibration spectrum of binuclear aqua-complex (without imaginary frequency) characterizes a stationary state of a complex. The calculated reduction of Gibbs Free Energy for model reaction ($\Delta_rG^o_{298}$ = -501 kJ) characterizes the possibility of spontaneous formation of binuclear aqua-complex $[(H_2O)_5Cr–SO_4–Mn(H_2O)_5]^{3+}$. On the basis of these received results it is assumed [1], that such binuclear aqua-complex may play a role of the catalyst in liquid phase oxidation of organic and inorganic compounds in water solutions of a sulfuric acid.

Computational time from the Ukrainian-American Laboratory of Computational Chemistry SSI «Institute for Single Crystals» NAS of Ukraine is gratefully acknowledged.

[1] V.V. Bondar, O.I. Zakharova, Yu.B. Vysotsky, N.F. Tyupalo. J. Mol. Struct.(Theochem)-2009 (in press).

Experimental and Theoretical Study of Charge Density Distribution in 3,4-Diamino-1,2,4-Triazole

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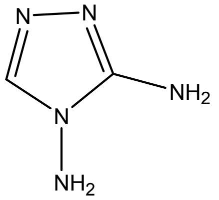
Heterocyclic 1,2-diamines are widely used reagents in organic synthesis due to their ability to form cyclic fragments. Their crystal structure is also interesting from viewpoint of character of intermolecular interactions. Therefore we performed experimental and theoretical analysis of electron density distribution in crystals of 3,4-diamino-1,2,4-triazole (DAT) using X-ray diffraction and ab anitio quantum chemistry (MP2/aug-cc-pvdz) methods.



DAT

The topological analysis of charge density distribution obtained from X-ray diffraction data showed that in the molecule of DAT both amino groups have pyramidal configuration. The amino group at the carbon atom has small degree of the pyramidality what indicate the considerable conjugation between π-systems of the triazole ring and the nitrogen atom lone pair. Lone pair of the nitrogen atom of second amino group has almost orthogonal orientation with respect to π-system of the heterocycle causing absence of n-π conjugation. This agrees well with characteristics of the bond critical point (BCP) of the N-N(H_2) bond. It is interesting that very close characteristics of BCP are observed for the N-N bond of triazole ring. This allows to assume violation of conjugation within aromatic ring.

The topological analysis of charge density distribution in the field of the intermolecular interactions in the crystal of DAT demonstrates existence of BCP for classic N-H…N and as well as for non-classic N-H…N, N-H…π and C-H…N hydrogen bonds and stacking interaction. Characteristics of bond critical points allow to classify these interactions as weak intermolecular hydrogen bonds and stacking interactions. Energies of these interactions derived from experimental charge density distribution and theoretical calculations agree very well except stacking interaction.

Quantum-Chemical Study of Structural Forms of "Osmium (VI) – 3-Methyl-2,6-dimercapto-1,4-thiopirone" Complexes

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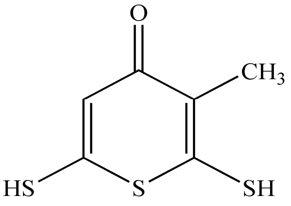
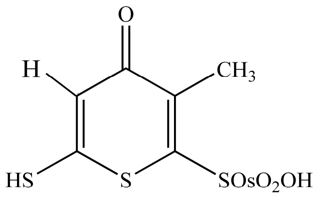
Metal derivatives of 2,6-dimercapto-1,4-thiopirone are used as analytical forms for determinftion of chalcogenophilic metals, including precious metals. Recently we have synthesized complexes of Osmium (VI) with 3-methyl-2,6-dimercapto-1,4- thiopirone (H_2M), some of them were used as analytical forms for the concentration and quantification of osmium in various ways, while the others - as ion exchange membranes of osmium-selective electrodes. Composition of these complexes has been determined by experimental methods, but data on their structure in the literature is still absent.

In this research we present the results of quantum-chemical studies of structures and energical characteristics of the synthesized complexes of Os (VI) with H_2M. Calculations were carried out PBE/TZP//PBE/TZVPP level of theory with full geometry optimization without constraints on symmetry.

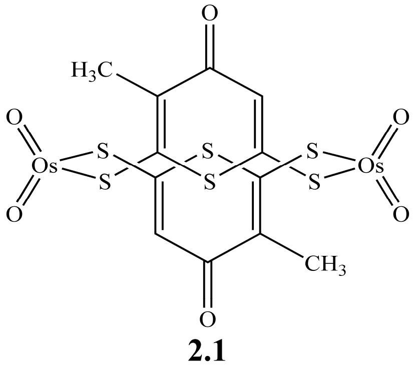
According to the calculation of all possible complexes formed between the different chemical forms of Os (VI) and H_2M in solution at pH 2-4, the most stable structure includes coordination of the metal to the sulfur atom of one of dimercaptogroup. There is no coordination of osmium with endocyclic sulfur atom in the complexes (see, for example, structure **1**).



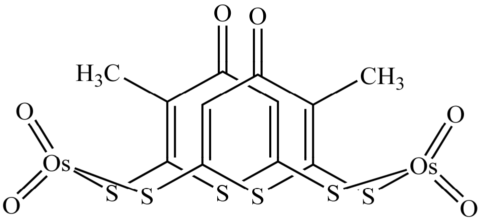
H_2M



1



2.1



2.2

In neutral and alkalescent environments the most stable complexes corresponds to the molar ratio of Os (VI) to organic ligand equal to 2:2. Structure of binuclear chelate $[-OsO_2-M-]_2$, in which both mercapto groups participate in the complexation have virtually the same energy for two different conformer - superphane (2.1) and crossbones (2.2).

In the framework of the theory of Atoms in Molecules it has been shown that Os-S bonds could be assigned to an intermediate type of interatomic interaction. They represent the interaction of a dense inner core electronic density of osmium atoms with a looser and more polarisable area of the electron density of sulphur atom, which is dominated by its compression in the direction of lines.

DFT Modeling of Structural, Electronic and Spin Properties of Eu@C_{60}, Eu@C_{82} and N@C_{60} as Candidates for Qubits

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A.P. Nizovtsev[c], V.A. Pushkarchuk[d], I.V. Bondarev[e]

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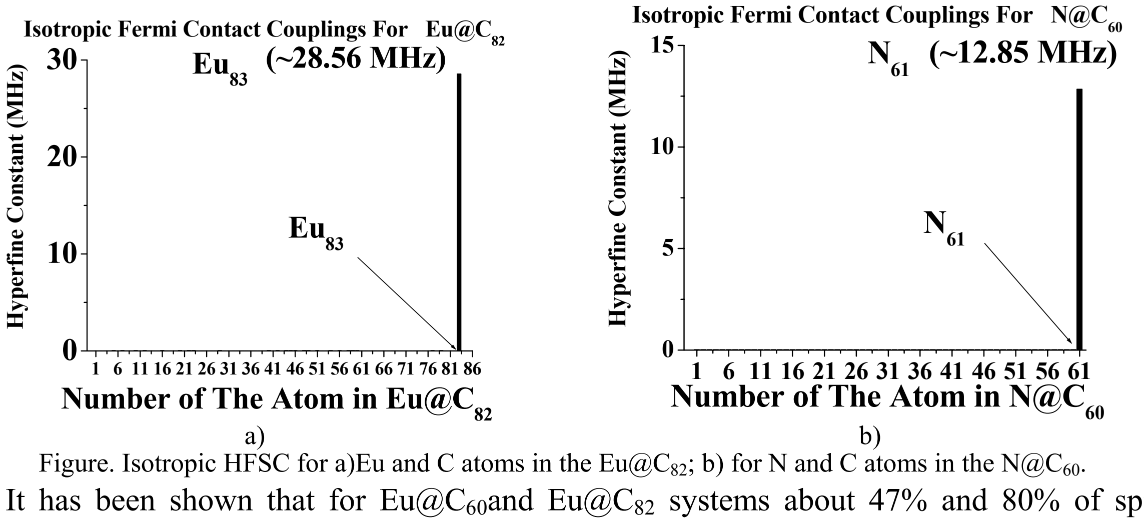
Doping carbon nanostructures with atomic or molecular complexes allows expanding the sphere of their application, in particular, construction of systems on their basis capable to be in coherent quantum states within a rather long time. Such conditions, as a rule, are realized on spin systems. It is supposed that such systems can be used for creation of devices for quantum processing of information.

Here we present the density functional theory (DFT) analyses of structural, electronic and spin properties of possibility to create coherent quantum conditions in a complexes Eu atom + fullerene and N atom + fullerene. Structures Eu@C_{60}, Eu@C_{82} and N@C_{60} containing endohedral Eu and N atoms inside the corresponding fullerene were considered. Calculations were carried out for the system in its ground spin state S=7/2 for Eu@C_{60}, Eu@C_{82} and S=3/2 for N@C_{60} within ROHF and UHF level theory with full optimization of geometrical structure. The calculations were performed using B3LYP1 functional and MINI, 3-21G and cep-4g basis functions. After optimization of geometry structure Eu atom has appeared to be shifted from the fullerene center. Its distance to carbon atoms varies in limits from 3.61Å to 3.64Å for Eu@C_{60} and from 3.0Å to 5.6Å for Eu@C_{82} complexes. For N@C_{60} atom N is located in the center of the fullerene.

The spin density, isotropic and anisotropic hyperfine splitting constants (HFSC) of ^{14}N , ^{153}Eu and ^{13}C in endohedral structures were calculated.

In Figure below we present the example of calculated isotropic HFSC for ^{14}N, ^{153}Eu and ^{13}C for Eu@C_{82} and N@C_{60}.



a) b)

Figure. Isotropic HFSC for a)Eu and C atoms in the Eu@C_{82}; b) for N and C atoms in the N@C_{60}.

It has been shown that for Eu@$C_{60}$and Eu@C_{82} systems about 47% and 80% of spin density respectively is located on the Eu nucleus and for N@C_{60} system about 99% of spin density respectively is located on the N nucleus. In all cases the spin density and HFSC located on the endohedral nucleus two order exceeds the one distributed over the carbon shell. Therefore, both complexes have obviously expressed localization of spin density on Eu and N nucleus, that is one of the basic necessary requirements to candidates for qubits.

This work was supported by the project №1.05.2 of the "Nanomaterials and Nanotechnology" of Republic of Belarus Program.

Intramolecular Self-Inclusion of Aromatic Ring of Substituent into Calix[4]arene Cavity

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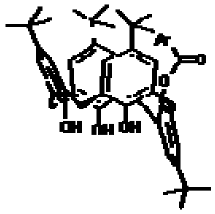
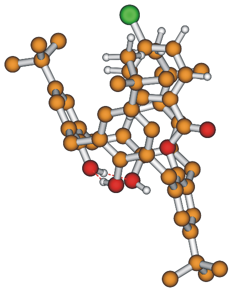
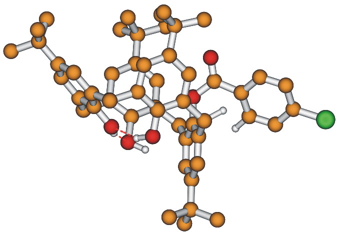
Calixarenes represent perspective class of organic compounds for the modeling of the molecular identification processes and for the investigation of molecular and ionic transfer through cellular membrane processes etc.

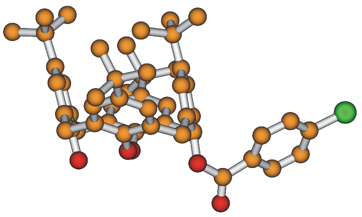




1a



1b



1c

The X-ray diffraction study of the compound **1a** demonstrates that it has a *partial cone* conformation of macrocyclic skeleton and chlorophenylacylic group is located in a cavity of the macrocycle in crystal phase. The quantum-chemical calculations of relative stability of **1a** and its conformers (**1b** and **1c**) using M05-2X/cc-pvdz method shows that **1a** has the lowest energy in vacuum. The difference in energy between conformers with different orientation of the chlorophenyl substituent is considerably greater (14.4 kcal/mol) as compared with difference in energy between conformers with different conformation of the macrocyclic skeleton (1.1 kcal/mol). Analysis of the distribution of the electron density in **1a** using "Atoms in Molecule" theory allows to conclude that the formation of the C-H...π intramolecular interactions in the case of the self-inclusion of the aromatic ring of chlorophenylacylic substituent into calix[4]arene cavity is responsible for stabilization of a *partial cone* conformation.

Berberine Raman Spectra: Experiment and Quantum-Mechanical Interpretation by the DFT method

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[b]Institute of Molecular Biology and Genetics, Kyiv, Ukraine

Berberine is a plant isoquinoline alkaloid with diverse biological and pharmacological activity. The drugs of berberine have bactericidal, anti-inflammatory and anticancer activity. For understanding of mechanisms of its therapeutic action it is necessary to have information about its complexation with DNA. We observed the manifestations in Raman spectra of the resonant interaction between the DNA and berberine molecular vibrations in the range where their spectra overlap (1000-1800 cm^{-1}). A considerable growth of the intensity was found for lines that corresponded to vibrations of both DNA and berberine in the berberine+DNA mixture. For explanation of this and others manifestations of interaction we have studied the experimental and calculated Raman spectra of berberine.

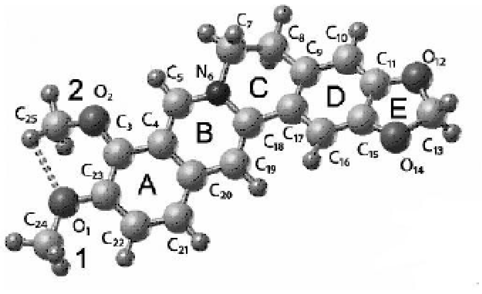

Fig.1. Structure of berberine cation.

Raman spectra of microcrystalline berberine chloride at laser excitation wavelength 6328Å have been obtained at room temperature. About two tens vibrational modes are registered in a region of 1000-1700 cm^{-1}.

The geometric structure of the cation of berberine has been obtained by the DFT B3LYP/6-311++G(d,p) method without any structural limitation. It was found that the berberine molecule is almost flat, a deviation from planarity is observed for the partly saturated ring C (see Fig.1). The intramolecular hydrogen bond CH…O between methoxy groups of OCH_3 of berberine has been detected for the first time. The existence of a bond have been determined on availability of the critical point of the (3,-1) type in the electronic density distribution. This analysis was accomplished by AIM-2000 program.

At this theory levels in a harmonic approximation the berberine Raman spectra has been calculated. The spectrum consists of 123 undegenerate vibrations, 48 of them lie in actual range 1000-1700 cm^{-1}. These modes are mostly in-plane vibrations of the rings and connected groups CH_2, OCH_3. For adjustment of experimental and calculated frequencies the scaling factor 0.985 was applied because the DFT method gives overvalued frequencies. It was shown the experimental and calculated spectra of molecular vibrations are in good agreement in the actual region of 1000-1700 cm^{-1}. Intensities of vibrations in the range of <1000 cm^{-1} (mostly out-of-plane ring vibrations) and 3000-3300 cm^{-1} (vibrations of the C-H bonds) are small (less by 2-4 orders) both in experimental and calculated spectra.

Summarizing, the DFT method at this theory level can be applied with a good reliability for calculation of the vibration spectra of others isoquinoline alkaloids, the experimental Raman spectra of which are inaccessible for one reason or another.

DFT Study of the Infrared Spectra of Steroid Hormones

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Steroid hormones are involved in cell membranes regulating their permeability, assist in RNA syntheses, etc. Biological activity of these hormones depends on their geometrical and electronic structure [1]. Molecular geometry and vibration frequencies of the typical steroid hormones, 17β-estradiol and estriol, are calculated by density functional theory with the B3LYP/6-31G** approximation [2]. Intensities of infrared absorption and Raman spectra for estradiol are in a moderate agreement with experiment. On the ground of quantum chemical calculations of frequencies and normal modes the assignments of all vibrational bands in the spectra of these hormones are presented. The analysis of the infrared spectra of both hormones indicates some nontrivial structure-spectra correlations. A series of specific vibrations are predicted in the low-frequency region of the IR spectra; their roles in hormone-receptor interaction and in energy transfer processes are discussed in connection with therapeutic effects. For these purposes it is strongly desirable to have comprehensive information about electronic structures of these hormones, and about their connection with infrared (IR), ultraviolet and NMR spectra [3–5] which finally help to establish more profound structure-activity relationship. In recent time the role of IR methods is greatly increased in biomedical analysis of hormones. Fourier transform infrared and near-infrared spectroscopy, the use of IR imaging play increasing role in study of the structureactivity relationship for hormones. The structure of estrogen receptors and their interaction with 17β-estradiol and estriol are of particular interest today because the treatment of breast cancer and the cause of the disease are intricately linked to the activity of the estrogen receptor and the normal blood serum level of these hormones. In this talk we present for the first time quantum chemical calculation of the force field and all vibrational modes in the typical steroid hormones, 17β-estradiol and estriol, by the density functional theory (DFT). Geometry of these molecules is optimized by DFT method with the combined B3LYP functional using the split-valence basis set 6-31G**. The vibrational assignments given in previous studies still leave many bands unassigned in the IR spectra of hormones and our DFT calculation improve the situation. Our results can be used in developments of new analytic IR technique useful for diagnostic purposes and the drag delivery control.

[1] Devlin T. M. Textbook of Biochemistry with Clinical Correlations. 4th Ed. – New York: Willey-Liss, 1997. – 896 p.
[2] Frisch M. J. et. al., *Gaussian 03*, revision C.02, Gaussian Inc., Wallingford, CT, 2004.
[3] Smith W. B. // Magn. Reson. Chem. – 1999. – 37. – № 2. – P. 103-106.
[4] http://www/aist.go.jp/RIODB/SDBS/ (National Institute of Advanced Industrial Science and Technology, date of acces)
[5] Barnett S. B., Butler I. S., Top S., Jaouen G. // Vibration. Spectroscopy. – 1995. – 8. – № 2. – P. 263-277.

Theoretical Study of Vibrational Spectra of the Sensibilizing Dye for the TiO_2 Nanocrystalline Solar Cells

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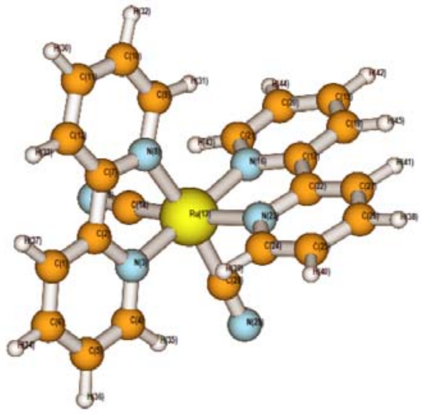

Fig.1. Optimized structure of $[Ru(bpy)_2(CN)_2]$ complex

Harvesting energy directly from sunlight using photovoltaic technology is an essential component of the future global energy production programs. A simple $[Ru(bpy)_2(CN)_2]$ (bpy = 2,2′-bipyridine) complex is studied by DFT method with optimized structure and vibrational analysis in order to predict the role of vibronic perturbations in the spectra and in the interface electron transfer rate. The density functional theory (DFT) method with the hybrid B3LYP functional and the Lanl2DZ basis set [1] is used for geometry optimization of the $[Ru(bpy)_2(CN)_2]$ complex (Fig. 1) and its vibrational spectra (Fig. 2) calculations. We use a scaling factor of 0.9756 for fitting the calculated vibrational frequencies to the available experimental data on the 2,2'-bipyridine and bpy complexes with metals.

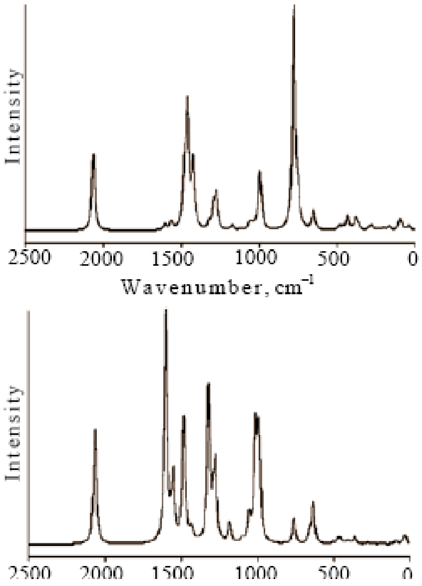

Fig 2. The calculated infrared (above) and Raman spectrum of the $[Ru(bpy)_2(CN)_2]$ complex

Valence vibrations of the C=C bonds with small admixture of the C–C links occur in the narrow region near 1600 cm^{-1} (Fig. 1). They are very active in Raman scattering, but have low IR intensity. In the SERRS spectrum of the similar $[Fe(bpy)_2(CN)_2]$ complex this mode is found at 1604 cm^{-1} [2] in a good fit with our result. Valence vibrations of the CN ligands at 2066 cm^{-1} are active in both IR and Raman spectra; this modes of the in-phase and out-of-phase types are characteristic. Valence vibrations of the C–C links are very important with respect to electron transfer upon light absorption, though they have not gained much attention from experimentalists. They provide a narrow IR band at about 1480 cm^{-1} (Fig. 2). The most intense IR band occurs at 777 cm^{-1}. This is out-of-plane CH vibration.

Stretching vibrations of the CN ligands split into 2066 and 2059 cm^{-1} (in-phase and out-of-phase) are very active in the Raman spectrum. One can expect that they would be enhanced upon the dye-surface interaction and participate in electron-transfer process. The most intense Raman band at 1598 cm^{-1} is determined by C=C stretching vibrations of the bpy rings with small contributions of the C–C links. In the SERRS spectra of the $[Fe(bpy)_2(CN)_2]$ dye the C=C band is observed at 1604 cm^{-1} [3]. Our DFT calculation indicates that vibrations of the C–C inter-rings link are very intense in the Raman spectrum, especially in the triplet excited state. The main intense band in this region has been observed at 1489 cm^{-1}.

[1] Frisch M. J. et. al., *Gaussian 03*, revision C.02, Gaussian Inc., Wallingford, CT, 2004.
[2] M. Muniz-Miranda, J. Raman Spectrosc. 31, 637, 2000.
[3] T. J. Dines, R. D. Peacock, J. Chem. Soc. Faraday Trans. 1, 84, 3445, 1988.

Tautomerism and Resonance-Assisted Hydrogen Bonding in Substituted Heterocyclic Systems

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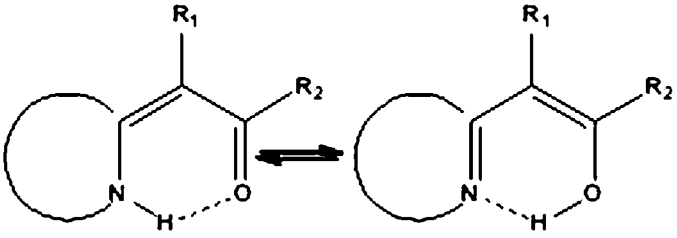
Tautomerism and hydrogen bonding significantly influence on the structure, properties and reactivity of various organic compounds. Formation of hydrogen bonds very often is responsible for stabilization of particular conformers and tautomers of heterocyclic systems. Strong H-bonds are often observed along with significant molecule polarization. This creates possibility for intramolecular proton transfer leading to tautomeric transitions.



NH OH

It was demonstrated [1-2] that in heterocyclic systems shown at the Scheme relative stability of tautomers depends by aromaticity of heterocycle, which is in general different in NH and OH forms. However, analysis of Cambridge Structural Database reveals that all of the structures containing the fragment shown at the Scheme exist in NH tautomeric form, regardless the type of heterocycle. Quantum-chemical calculations at the MP2 and DFT levels of theory demonstrate that the relative stability and properties of intramolecular resonance-assisted hydrogen bonds are controlled by several factors: relative inherent proton affinity of heteroatoms involved into hydrogen bond, the difference of heterocycle aromaticity in NH and OH tautomers, nature of substituent present. It was found that in crystals formally less aromatic tautomers are stabilized due to significant polarization which provides increase of heterocycle aromaticity. Such polarization is supported by the substituent effects and intermolecular resonance-assisted hydrogen bonding.

[1] Zubatyuk, R.I., Volovenko, Y.M., Shishkin, O.V., Gorb, L., Leszczynski, J., *J. Org. Chem*, **2007**, *72*, 725

[2] Zubatyuk, R.I., Shishkin, O.V., Gorb, L., Leszczynski, J., *J. Phys. Chem. A*, **2009**, *113*, 2943

Probing the Nature of Chelate Hydrogen Bonds Forming 7-Membered Conjugated Rings in Negatively Charged Systems

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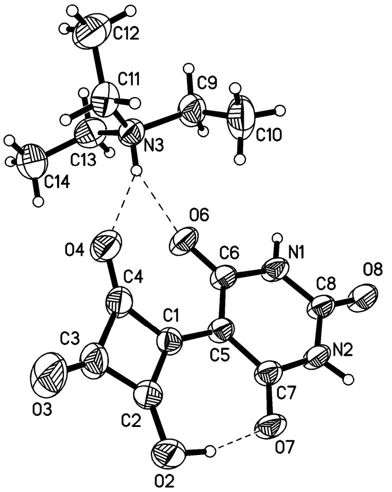
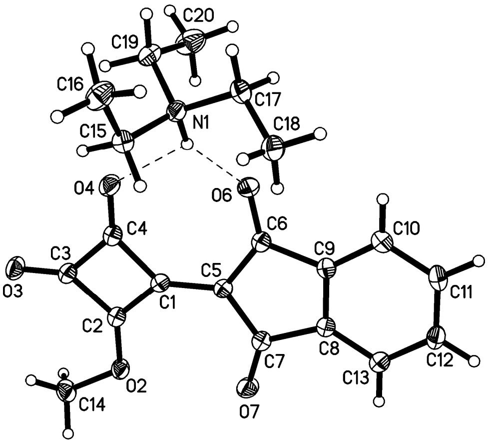
Positive synergism between hydrogen bond strength and delocalization within the spacer in enols of ***β***-diketones is well-known as effect of resonance-assisted hydrogen bonding RAHB. The concept of RAHB implies even number of alternating single and double bonds in the spacer because it makes prerequisites for interchanging of single and double bonds positions and thus for strong resonance within the spacer. It is clear that in molecules containing odd number of bonds in the spacer resonance possible in the case of presence of surplus charge.



1



2

In the anions of squarine derivatives which are shown at the Figure bond length equialization within the spacer occures regardless the formation of H-bond, as established by X-Ray diffraction study. Quantum-chemical calculations of the anions and some model molecules performed at the MP2 and DFT levels of theory demonstrate that the intramolecular H-bond in the molecule 1 could not be considered as resonance-assisted, but rather charge-assisted. In such systems resonace leads to negative charge delocalization over the spacer and thus weaks electrostatic interactions between proton donor and proton acceptor atoms. Therefore, chelate H-bonds forming 7-membered rings in conjugated negatively charged systems could be considered as resonance-weakened H-bonds.

Bond Energy Estimation via XRD: from H-EH Interactions to Metal-Ligand Bonds

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Intermolecular Interactions of DNA Bases and the Bases with Water Molecules: Mass Spectrometric Studies

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Computer-Assisted Search for New Types of Organic Reactions: An Application of the ARGENT-1 Program

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The main purpose of the reaction design tools consists in the systematical search for new types of organic reactions. Several old programs of this sort, as well as possibilities provided by our new software system, called ARGENT-1, are briefly considered in the report. This system is shown to be a flexible and efficient tool that allows to search for interconversions of neutral molecules, ions, radicals, and even ion-radicals. Mathematical models of its 3 generation stages (associated with orbits of power groups acting on the sets of mappings from one finite set to another one) and some unique features of its program interface (such as navigation possibility in the ocean of obtained results or unusual models of input/output) are theoretically well-founded. The powerful selection criteria in ARGENT-1 make it possible to easily take into account required, allowed, and forbidden types of bond changes, valence states and charges of atoms, number of components, cycles, specific fragments, symmetry and degeneracy characteristics, and some chemically useful heuristics and user's preferences as well.

Several results obtained by ARGENT-1 (new possible allodesmic interconversions, several perspective multistep reactions, and unusual types of degenerate processes) are explicitly commented in the report. Some mathematically significant details (such as rigorous formulation of the problem, analytical enumeration formulas and new original generation algorithms) as well as the most attractive features of the program implementation are briefly mentioned. The demonstration of the working program (and also of its simplified, "lite" version) can be additionally organized by request.

Открытое акционерное общество «ИнтерХим»

Основано - 11.12.1992 г.

Председатель Правления, генеральный директор, к.х.н. Редер Анатолий Семенович.

Председатель Совета, академик НАН Украины, д.х.н. Андронати Сергей Андреевич.

Основными видами деятельности предприятия являются производство фармацевтических субстанций и готовых лекарственных средств.

ОАО «ИнтерХим» давно известно на фармацевтическом рынке как один из ведущих производителей фармацевтических субстанций. Предприятие производит такие фармацевтические субстанции, как феназепам, клоназепам, гидазепам, циназепам, амиксин, транквилар, клофелин, прозерин. Фармацевтические субстанции предприятие реализует ведущим фармацевтическим заводам Украины, России и Латвии.

ОАО «ИнтерХим» имеет свои научно-исследовательскую, фармакологическую, аналитическую и микробиологическую лаборатории. В сотрудничестве с Физико-химическим институтом им. А.В.Богатского Национальной академии наук Украины (ФХИ) ОАО «ИнтерХим» занимается разработкой новых оригинальных лекарственных средств.

В 2003 г. введен в эксплуатацию Участок по производству готовых лекарственных средств. Участок спроектирован и построен (с нулевого цикла) в соответствии с требованиями надлежащей производственной практики (GMP) и сертифицирован МОЗ Украины как полностью отвечающий требованиям GMP. Мощность участка составляет 2 000 000 таблеток в год, ассортимент выпускаемой продукции насчитывает 15 наименований. ОАО «ИнтерХим» - одно из двух украинских фармацевтических предприятий, имеющих лицензию на выпуск психотропных препаратов.

Технический, технологический и нормативно-организационный уровень производства ОАО «ИнтерХим» полностью соответствует всем самым строгим международным требованиям. За время работы участка предприятие не получило ни одной рекламации.

В составе ОАО "ИнтерХим" работает аттестованный Исследовательский центр, выполняющий анализы сточных, грунтовых и питьевых вод, косметических и моющих средств, удобрений и др. ОАО «ИнтерХим» имеет свою розничную аптечную сеть в Одессе.

Также ОАО «ИнтерХим» производит продукты тонкого органического синтеза. Основными потребителями химической продукции в странах Западной Европы являются фирмы «Акрос Органикс», Бельгия; «СиЭмСи», Германия; «Флука Кеми», Швейцария и др.

ОАО "ИнтерХим" является официальным партнером компаний «Меггле» (Германия) – производство вспомогательных веществ для фармацевтической промышленности и «Акрос Органикс» (Бельгия) – химические реактивы.

В ОАО "ИнтерХим" работает более 300 человек, в том числе: специалистов с высшим образованием - 172, кандидатов и докторов наук - 22.

Генеральный директор Анатолий Редер: «В 2008 году мы опередили все предприятия отрасли по темпам роста в розничном сегменте фармацевтического рынка – 75,17%, в то время. По итогам 1-го квартала 2009 г наша компания впервые вошла в двадцатку лидеров, заняв 18 место в рейтинге спростом 116% и долей рынка 1,27% (по данным маркетинговой компании SMD)».

ОАО "ИнтерХим": 65080, г. Одесса, Люстдорфская дорога, 86. Тел. (048) 777-29-50, (0482) 34-08-04, факс (0482) 34-08-03. E-mail: info@interchem.com.ua; Web: http://www.interchem.com.ua

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