Results

MOLECULAR MODELING & COMPUTATIONAL CHEMISTRY

Vol. 15, No. 1 1 May 2006

Coverage period: 1 January 2006 through 30 April 2006
About 100 papers from 20 journals are cited.

Editorial and News

I am the new Editor for MMCC Results, the Molecular Modeling and Computational Chemistry News Letter. I have been working as an Assistant Editor of MMCC Results with Prof. David Busath from January 2004 to December 2005. Prof.David Busath has transferred the News Letter responsibility, starting from January this year.

In this issue we have covered more than 20 journals from January 2006 to April 2006. From next issue onwards, we will maintain the journal reviews section and increase the number of reviews related to structural biology and proteomics.

I sincerely hope that all the scientists from academic and industrial background will give your full support to this News Letter.

R.Nageswar, Editor

1. APPLICATIONS

1.1. *Small Molecules*

General and Model Systems

A theoretical model of *Aquifex pyrophilus* flagellin: Implications for its thermostability.

M.V. Raghu Ram and B.C. Tripp* [Western Michigan U]

J.Mol.Mod. **12,** 481-493 (2006)

The predictive 3D-structure of flagellin (FlaA) is developed using the structure of mesophilic Salmonella typhimurium flagellin as a template. The FlaA N- and C-termini have higher proportions of hydrophobic and charged residues at the expense of polar residues and higher non-polar surface areas.

Water and Solvation

A theoretical study of the interactions of water with gallic acid and a PEO/TGG complex.

R. Gaudreault* [McGill U], T.G.M. van de Ven, M.A. Whitehead

Mol. Sim., **32**, 17-27 (2006).

PM3, MM and MD calculations are performed to study the interaction of the hexamer of poly(ethylene oxide) $(PEO)_6$ and cofactor containing trigalloyl glucose (TGG). The results showed that $(PEO)_6$/TGG complexes do not form in aqueous solution, agreed well with the experimental results in pure water.

First and second hydration shell of Ni^{2+} studied by molecular dynamics simulations.

A.V. Egorov, A.V. Komolkin, A.P. Lyubartsev and A. Laaksonen* [Stockholm U]

Theor.Chem.Accounts., **115***,* 170-176 (2006)

MD simulations of a Ni^{2+} ion in water is carried out to investigate the structure and dynamics of water molecules around the nickel, extending the analysis to the second hydration shell. The structural parameters as well as the motions of water molecules in various sub-structures of the solution is evaluated giving a detailed picture of the motional modes of water molecules.

A molecular dynamics simulation of the structure and properties of a self assembled monolayer formed from an amphiphilic polymer on a water surface.

D. Leith* [Trinity Coll.]and D.A. Morton-Blake

Mol.Sim. **32**, 987-997 (2006)

MD simulations are applied to investigate the compression on the amphiphilic polymer. It is observed that there is a range of surface pressures in which the material possesses lattice order. As the compression is increased beyond a critical value breakdown occurs leading to the rupture of the surface layer.

MMCC Results
R.Nageswar, Editor
8013 Los Sabalos Street
San Diego, CA 92126
Tel. (858) 663-0162
e-mail: *drnageswar@yahoo.com*

R.Nageswar,Ph.D.
RR Labs Inc.,8013 Los Sabalso St.
San Diego, CA 92126
Editors Emeritus: Bruce Gelin, Ph.D.
David Busath,M.D.
Dr. Gelin was founder of MMCC Results and edited volumes 1-6.
Dr. David Busath edited volumes 7-14

MMCC Results (ISSN 1061-6381) is published ten times per year at the beginning of each month except January and August by the independent business, MMCC Results. Mention of software, hardware, or other products is for informational purposes only and does not constitute an endorsement or recommendation by MMCC Results nor by the authors of the paper cited. All product names are the trademarks or registered symbols of their respective holders.
Marginal symbols indicate that the authors acknowledged the use of a software package from a commercial sourse. **A** refers to Accelrys Inc. and **T** to Tripos Inc. Other companies are denoted by their name in a box. Papers of special interest are marked by an exclamation point [**!**].

Water and Solvation (cont'd)

A comparative theoretical study of dipeptide solvation in water.

H.W. Hugosson* [Swiss Federal Inst. of Tech.], A. Laio, P. Maurer, U. Rothlisberger

J.Comp.Chem. **27**, 672-684 (2006)

MD simulations are used to study the zwitterionic form of the dipeptide glycine-alanine in water focussed on solvation and electrostatic properties. The results showed that the solvation pattern is similar for all methods used for most atoms in the dipeptide, like the carboxy and aminoterminii, and the backbone amid NH group.

Medicinal Chemistry and Drug Design

Effective discrimination of antimalarial potency of artemisinin compounds based on quantum chemical calculations of their reaction mechanism.

S. Tonmunphean, V. Parasuk and S. Kokpol* [Chulalongkorn U]

Bioorg. Med. Chem. **14**, 2082-2088 (2006)

IMOMO (B3LYP/6-31(d,p):HF/3-21G) method is used to calculate the mechanism of 12 antimalarial artemisinin compounds. The energy profiles showed that the hemolytic C-C cleavage reaction is more preferable than an intramolecular 1,5-hydrogen shift process, correlated with the docking calculations.

Fragment-based drug discovery of carbonic anhydrase II inhibitors by dynamic combinatorial chemistry utilizing alkene cross metathesis.

Sally-Ann Poulsen* [Griffith U] and L.F. Bornaghi

Bioorg. Med. Chem. **14**, 3275-3284 (2006)

The classical bCA II recognition fragment is an aromatic sulfonamide moiety is incorporated into a scaffold building block. The allowed determination of the relative bCA II binding affinities of the cross metathesis products that contained the $ArSO_2NH_2$ fragment. A bCA II competitive binding assay validated the results with a representative number of pure compounds.

The effect of a tightly bound water molecule on scaffold diversity in the computer-aided de novo ligand design of CDK2 inhibitors.

A.T. García-Sosa* [U Cambridge] and R.L. Mancera

J.Mol.Mod. **12,** 422-431 (2006)

The effect of a specific water molecule on the chemical diversity and binding mode of ligands in the binding site of CDK2 was investigated. It is observed that the tightly bound water molecule modifies the size and shape of the binding site, indirect effect of reducing the chemical diversity of the underlying molecular scaffolds.

A!
Ligand design and synthesis of new imidazo[5,1-*b*]-quinazoline derivatives as α_1-adrenoceptor agonists and antagonists.

M.A.H. Ismail* [Ain Shams U], M.N.Y. Aboul-Enein, K.A.M. Abouzid and R.A.T. Serya

Bioorg. Med. Chem. **14**, 898-910 (2006)

CATALYST software is used to generate the hypotheses for a series of new imidazo[5,1-*b*]quinazoline derivatives. These are designed based upon the molecular modeling simulation of the fitting values and conformational energy values of the best-fitted conformers to both the α_1-adrenoceptor (α_1-AR) agonist and α_1-adrenoceptor (α_1-AR) antagonist. In vivo studies of these compounds for their effects on the blood pressure of normotensive cats was consistent with the results of molecular modeling studies.

De novo structure-based design of bisurea hosts for tetrahedral oxoanion guests.

V.S. Bryantsev and B.P. Hay* [Pacific Northwest Nat. Lab]

J. Am. Chem. Soc., **128**, 2035-2042 (2006)

De novo molecule building software, HostDesigner, is interfaced with MM software, GMMX, is used for generating and screening millions of potential structures. This computer-aided design methodology is illustrated with a search for bisurea podands that are structurally organized for complexation with tetrahedral oxoanions.

Medicinal Chemistry and Drug Design (cont'd)

Discovery of potent and selective PARP-1 and PARP-2 inhibitors: SBDD analysis via a combination of X-ray structural study and homology modeling.

J. Ishida, H. Yamamoto, Y. Kido, K. Kamijo, K. Murano, H. Miyake, M. Ohkubo, T. Kinoshita, M. Warizaya, A. Iwashita, K. Mihara, N. Matsuoka and K. Hattori* [Fujisawa Pharm.Co. Ltd.]

Bioorg. Med. Chem. **14**, 1378-1390 (2006)

In structure-based drug design, X-ray structure is used to study the complexes of inhibitors and human PARP-1 catalytic domain. Homology modeling is used for murine PARP-2 suggested distinct interactions of inhibitors with PARP-1 and PARP-2. The results provided a new structural framework for the design of selective inhibitors for PARP-1 and PARP-2.

Can we rationally design promiscuous drugs?

A.L. Hopkins* [Pfizer], J.S. Mason and J.P. Overington

Curr.Opi.Str.Biol.**16**, 127-136 (2006)

Recent advantages in post-genomic biology indicated that polypharmacology is necessary trait for the efficacy of many drugs through rational drug design. Chemoinformatics and structural biology advances are combined together in rational drug design to find out the next generation of promiscuous drugs with polypharmacology.

Quantitative Structure-Activity Relations

Effect of cholesterol on DMPC phospholipid membranes and QSAR model construction in membrane-interaction QSAR study through molecular dynamics simulation.

Jianzhong Liu* [U Delware] and Liu Yang

Bioorg. Med. Chem. **14**, 2225-2234 (2006)

MD simulations and normal mode analysis are used to compare the physico-chemical properties of DMPC and DMPC/cholesterol mixed membrane monolayer. The area of per molecule of membrane is decreased with the addition of the cholesterol, increases the lipid amplitude motion, solute diffusion coefficient is changed. MI-QSAR models are constructed based on solute–membrane interaction energy descriptors and other intramolecular descriptors. The short range solute–membrane interaction energy changes due to the uptake of the solute on permeability in DMPC/cholesterol membrane.

!
Antimalarial activity: A QSAR modeling using CODESSA PRO software.

A.R. Katritzky* [Univ. of Florida], O.V. Kulshyn, D.C. Fara I. Stoyanova-Slavova, D.A. Dobchev, M. Kuanar, and M. Karelson

Bioorg. Med. Chem. **14**, 2333-2357 (2006)

QSAR is proposed for two diverse sets of compounds for each of two strains D6 and NF54 of Plasmodium falciparum. CODESSA PRO software is used to calculate the molecular descriptors like geometrical, topological, quantum mechanical, and electronic properties of these compounds.

Binding free energy calculations of adenosine deaminase inhibitors.

A. Coi, M. Tonelli, M.L. Ganadu and A.M. Bianucci* [Univ. di Pisa]

Bioorg. Med. Chem. **14**, 2636-2641 (2006)

MD simulations are used to calculate the binding free energies between four inhibitors and adenosine deaminase (ADA). The calculated values are correlated with the experimental values and non-polar contributions have an important role for ADA-inhibitor interactions.

Quantitative Structure-Activity Relationships (cont'd)

!
3D-QSAR and docking studies of aldehyde inhibitors of human cathepsin K.

X. Pan, Ninghua Tan* [Chinese Acad. of Sci.], G. Zeng, H. Han and H. Huang.

Bioorg. Med. Chem. **14**, 2771-2778 (2006)

Gold 2.2 is used to identifying the conformations of 59 aldehyde compounds into the active sites of CatK. 3D-QSAR studies are performed on the docking confirmations resulted the aldehyde group is an important pharmacophore because of electrostatic effect. The inhibitory activities are well agreed with the calculated binding free energies, are further useful to deign and finding new potential CatK inhibitors.

QSAR models for Daphnia toxicity of pesticides based on combinations of topological parameters of molecular structures.

A.A. Toropov* [Inst. Ricerche Farmacol.] and E. Benfenati.

Bioorg. Med. Chem. **14**, 2771-2778 (2006)

The vertex degrees (0EC), the extended connectivity of first order (1EC), and the numbers of paths of length two (P2) are considered for QSAR studies. These descriptors are used to predict toxicity toward Daphnia magna for a set of pesticides. Based on the correlation weight of local topological parameters together with the global topological parameters, statistical characteristics of the best model with n = 220, $r^2 = 0.7822$, s = 0.849, F = 783 (training set); n = 42, $r^2 = 0.7388$, s = 0.941, F = 113 (test set).

Quantitative structure-activity relationship of spirosuccinimide type aldose reductase inhibitors diminishing sorbitol accumulation in vivo.

Kwangseok Ko, Hoshik Won* [Hanyang Univ.] and Y. Won

Bioorg. Med. Chem. **14**, 3090-3097 (2006)

QSAR studies are used to calculate spirosuccinimide type aldose reductase inhibitors and the in vivo inhibitory activity of sorbitol accumulation. The hydrophobic character of Aldose reductase inhibitor is the major contributing factor to enhance in vivo activity. The high correlation between ED50 and the Caco-2 cell permeability of in vitro active compounds indicated that the membrane permeability is essential for in vivo efficacy.

3D QSAR on a library of heterocyclic diamidine derivatives with antiparasitic activity.

P. Athri, T. Wenzler, Patricia Ruiz, Reto Brun, D.W. Boykin, R. Tidwell and W. D. Wilson* [Georgia State Univ.]

Bioorg. Med. Chem. **14**, 3144-3152 (2006)

CoMFA and CoMSIA 3D QSAR analyses are performed with furamidine and a set of 25 other structurally related compounds. An extended CoMSIA model with additional descriptors for hydrophobic, donor, and acceptor properties had good predictive ability with a $q^2 = 0.699$, $r^2 = 0.974$, SEE, standard error of estimate = 0.1, and $F = 120.04$. The results are further useful to design compounds that, potentially, have better activity against African trypanosomes.

Prediction of hERG potassium channel affinity by the CODESSA approach.

A. Coi, I. Massarelli, L. Murgia, M. Saraceno, V. Calderone and A.M. Bianucci* [Univ. di Pisa]

Bioorg. Med. Chem. **14**, 3153-3159 (2006)

QSAR studies are performed on a series of hERG K^+ channel blockers using CODESSA program. The results obtained for a *blind set*, disjoined from the whole dataset initially considered, confirmed the predictive potency of the models. The results suggested that they are valuable tool for practical applications in predicting the blockade of hERG K^+ channels.

Quantitative Structure-Activity Relationships (cont'd)

QSAR for *anti*-malarial activity of 2-aziridinyl and 2,3-bis(aziridinyl)-1,4-naphthoquinonyl sulfonate and acylate derivatives.

M. Zahouily* [Chem. & Env. Maroc] , M. Lazar, J. Rakik, A. Elmakssoudi, S. Elaychi and A. Rayadh.

J.Mol.Mod. **12,** 398-405 (2006)

QSAR studies are performed on 63 analogues of 2-azaridinyl and 2,3-bis(aziridinyl)-1,4-napthoquinonyl sulfonate and acyl derivatives. The antimalarial activity of 2-aziridinyl and 2,3-bis(aziridinyl)-1,4-naphthoquinonyl sulfonate and acylate derivatives is strongly dependent on hydrophobic character, hydrogen-bond acceptors and also steric factors of the substituents.

A 4D-QSAR study on anti-HIV HEPT analogues.

A. Bak and J. Polanski* [Univ. of Silesia].

Bioorg. Med. Chem. **14**, 273-279 (2006)

4D-QSAR method with the PLS analysis is used to investigate the antiviral activity of HEPT. This method showed the mode of interaction revealed by X-ray studies and allowed to calculate highly predictive QSAR models.

Quantitative structure-activity relationships for small non-peptide antagonists of CXCR2: Indirect 3D approach using the frontal polygon method.

A.I. Khlebnikov* [Altai State Tech.Univ.], I.A. Schepetkin and M.T. Quinn.

Bioorg. Med. Chem. **14**, 352-365 (2006)

QSAR model is developed for 59 nonpeptide antagonists of CXCR2 using a partial 3D- comparison of the antagonists. Structural fragments are responsible for the antagonist activity is identified by this model. QSAR models are useful in the design of CXCR2 antagonists from molecular fragments.

Two- and three-dimensional quantitative structure-activity relationships for a series of purine nucleoside phosphorylase inhibitors.

M.S. Castilho, M.P. Postigo, C.B.V. de Paula, G. Oliva, C.A. Montanari , and A.D. Andricopulo* [Univ. São Paulo].

Bioorg. Med. Chem. **14**, 516-527 (2006)

CoMFA, CoMSIA, and HQSAR studies are performed on a series of 52 training set inhibitors of calf spleen purine nucleoside phosphorylase. Significant cross-validated correlation coefficients of CoMFA with $q^2 = 0.68$; CoMSIA, with $q^2 = 0.66$; and HQSAR with $q^2 = 0.70$ are obtained and the results are further useful for the design of novel inhibitors of PNP having improved potency.

Molecular modeling and 3D-QSAR studies of indolomorphinan derivatives as kappa opioid antagonists.

Wei Li, Yun Tang, You-Li Zheng and Zhui-Bai Qiu* [Fudan Univ.].

Bioorg. Med. Chem. **14**, 601-610 (2006)

CoMFA and CoMSIA methods are used in 3D-QSAR studies and obtained the models with $q^2 = 0.693$, $N = 4$, $r^2 = 0.900$ and $q^2 = 0.617$, $N = 4$, $r^2 = 0.904$ respectively. The 3D structure of human κ opioid receptor is constructed based on the crystal structure of bovine rhodopsin. CoMSIA contour plots are mapped into the structural model of κ opioid receptor-GNTI complex to identify key residues, which might account for κ antagonist potency and selectivity.

Constructing plasma protein binding model based on a combination of cluster analysis and 4D-fingerprint molecular similarity analyses.

J. Liu* [Univ. of Delware], L. Yang, Yi Li, D. Pan and A.J. Hopfinger.

Bioorg. Med. Chem. **14**, 611-621 (2006)

Four different predictive schemes (SM, SA, SR, and SC) were applied to the test set based on the similarity measures of each compound to the compounds in the training set. The 4D-fingerprints provided 36 different individual IPE/IPE type molecular similarity measures. The results showed that the NP/HA, HS/HA, and HA/HA IPE/IPE type measures predict the test set well. The 4D-fingerprints have relatively high predictivity for this particular dataset.

Quantitative Structure-Activity Relationships (cont'd)

T!
3D-QSAR study of ring-substituted quinoline class of anti-tuberculosis agents.

Amit Nayyar, M. Alpeshkumar, Rahul Jain* [NIPER, Punjab] and E. Coutinho.

Bioorg. Med. Chem. **14**, 847-856 (2006)

CoMFA, CoMSIA methods are evaluated in 3D-QSAR studies. CoMFA model generated with database alignment is the best model for the prediction of activity for a set of test molecules and also identified some novel features that are incorporated into the quinoline framework to improve the activity.

A QSAR study on influenza neuraminidase inhibitors.

R.P. Verma and Corwin Hansch* [Pomona Coll.].

Bioorg. Med. Chem. **14**, 982-996 (2006)

17 QSAR's are developed for different sets of compounds to understand chemical-biological interactions governing their activities toward influenza neuraminidase.

QSPR models for polychlorinated biphenyls: *n*-Octanol /water partition coefficient.

J. Padmanabhan, R. Parthasarathi, P.K. Chattaraj and V. Subramanian* [Central Leather Res.Inst.].

Bioorg. Med. Chem. **14**, 1021-1028 (2006)

The lipophilic behavior of the data set containing 133 polychlorinated biphenyl (PCB) congeners is analyzed using the conceptual DFT based global reactivity parameter in QSPR model. The results made good agreement between the coefficient of determination and the internal predictive ability values indicating the significance of the considered descriptors in the property analysis of PCBs. The proposed method has the applicability from chemical reactivity to toxicity analysis and various studies of physicochemical properties in the series of dioxins and other polyaromatic hydrocarbons.

QSAR by LFER model of HIV protease inhibitor mannitol derivatives using FA-MLR, PCRA, and PLS techniques.

J. Thomas Leonard and Kunal Roy* [Jadavpur U].

Bioorg. Med. Chem. **14**, 1039-1046 (2006)

QSAR studies are performed to investigate the structural and physicochemical properties of mannitol derivatives for HIV protease inhibitory activity. QSAR models are developed using electronic (σ), hydrophobicity (π), and steric parameters of phenyl ring substituents of the compounds along with appropriate dummy variables. Whole molecular descriptors and statistical techniques are applied to identify the structural and physicochemical requirements for HIV protease inhibitory activity.

High-throughput screening of ecdysone agonists using a reporter gene assay followed by 3-D QSAR analysis of the molting hormonal activity.

C.E. Wheelock, Y. Nakagawa* [Kyoto U], T. Harada, N. Oikawa, M. Akamatsu, G. Smagghe, D. Stefanou, K. Iatrou and L. Swevers.

Bioorg. Med. Chem. **14**, 1143-1159 (2006)

172 diacylhydrazine analogs were tested for their ability to activate an ecdysone (molting hormone) dependent reporter gene in a silkworm (Bombyx mori) cell-based high-throughput screening assay. CoMFA model is used to visualize the steric and electrostatic potential fields, which is supported the physicochemical parameters required for activity. These studies are useful to discover novel agonists of molting hormone activity.

Quantitative Structure-Activity Relationships (cont'd)

QSAR analysis of phenolic antioxidants using MOLMAP descriptors of local properties.

S. Gupta* [U Nova de Lisboa], S. Matthew, P.M. Abreu and J. Aires-de-Sousa.

Bioorg. Med. Chem. **14**, 1199-1206 (2006)

MOLMAP descriptors applicability is used to describe QSAR with a study of the radical scavenging activity of 47 naturally occurring phenolic antioxidants. Counterpropagation neural networks are trained with MOLMAP descriptors selected using genetic algorithms to predict antioxidant activity. The model is subsequently validated by the leave-one-out procedure obtaining a q^2 of 0.71. In this, how MOLMAPs are used for data mining of structural and biological activity data, leading to the extraction of relationships between local properties and activity.

A!
The 3D-QSAR analysis of 4(3*H*)-quinazolinone derivatives with dithiocarbamate side chains on thymidylate synthase.

S. Liu, F. Liu, X. Yu, G. Ding, P. Xu, Jian Cao and Yuyang Jiang* [Tsinghua U].

Bioorg. Med. Chem. **14**, 1425-1430 (2006)

FlexiDock and SCORE2.0 are used to investigate the binding model of 14 antifolates of 4(3*H*)-quinazolinone derivatives with dithiocarbamate side chains. The calculated binding energies of these antifolates complexed with TS and their inhibitory activities are correlated with each other. The robust QSAR model, its 3-D contour map, and binding score for these antifolates derived from SCORE2.0 provided the structural optimization of current antifolates.

Understanding the structure-activity and structure-selectivity correlation of cyclic guanine derivatives as phosphodiesterase-5 inhibitors by molecular docking, CoMFA and CoMSIA analyses.

Guang-Fu Yang, Hai-Ting Lu, Ying Xiong and Chang-Guo Zhan* [U Kentucky].

Bioorg. Med. Chem. **14**, 1462-1473 (2006)

3D-QSAR and molecular docking are used to study the interaction between PDE5 and PDE6 for a series of (49) cyclic guanine derivatives. CoMFA and CoMSIA were performed to develop QSAR and QSSR models from the conformations of the docking structures to predict the inhibitory activity against PDE5 and the selectivity against PDE6. The results are further useful for rational design and development of more active and more selective PDE5 inhibitors for the therapeutic treatment of erectile dysfunction.

3D QSAR study of hypolipidemic asarones by comparative molecular surface analysis.

T. Magdziarz, B. Łozowicka, R. Gieleciak, A. Bąk, J. Polański* [U Silesia] and Z. Chilmonczyk.

Bioorg. Med. Chem. 14, 1630-1643 (2006)

CoMSIA is used to develop a 3D-QSAR model for α-asarone derivatives. The results showed that a correlation between the activity of these compounds and the electrosraric potential at the molecular surface. The grid formalism (s-CoMSA) gave the activity of the compound.

A combined approach of docking and 3D QSAR study of β-ketoacyl-acyl carrier protein synthase III (FabH) inhibitors.

A. Ashek and S. Joo Cho* [Korea Inst. of Sci. & Tech.]

Bioorg. Med. Chem. **14**, 1474 -1482 (2006)

CoMFA and CoMSIA and docking simulations are performed on a series of potent benzoylaminobenzoic acids. Docking studies are employed to position the inhibitors into the FabH active site to determine the probable binding conformation. The predicated binding free energy is well agreed with the inhibitory activity. The predictive ability of the models is validated using a set of compounds that were not included in the training set and progressive scrambling test. Mapping the 3D-QSAR models to the active site of FabH related that some important amino acid residues are responsible for protein-inhibitor interaction.

Quantitative Structure-Activity Relationships (cont'd)

3D-QSAR studies on tripeptide aldehyde inhibitors of proteasome using CoMFA and CoMSIA methods.

Yong-Qiang Zhu, Jian-Feng Pei, Zhen-Ming Liu, Lu-Hua Lai, Jing-Rong Cui and Run-Tao Li* [Peking U Health Sci.Cent.].

Bioorg. Med. Chem. **14**, 1483-1496 (2006)

CoMFA and CoMSIA are applied to analyze the binding affinity of a set of tripeptide aldehyde inhibitors of 20S proteasome. These models are validated by a test set of eight molecules that were not included in the training set. The CoMFA and CoMSIA field contour maps are agreed well with the structural characteristics of the binding pocket of β5 subunit of 20S proteasome. The results suggested that the 3D-QSAR models built are further used for the development of novel inhibitors of 20S proteasome.

The development of 3D-QSAR study and recursive partitioning of heterocyclic quinone derivatives with antifungal activity.

Su-Young Choi, J. Hong Shin, C. Kyu Ryu, Ky-Youb Nam, K. Tai No and Hea-Young Park Choo* [Ewha Womans U].

Bioorg. Med. Chem. **14**, 1608-1617 (2006)

CoMFA is used for a series of compounds. The results are reliable to the prediction of inhibitory activity of a series of compounds. The results are reliable to the prediction of inhibitory activity of a series of compounds. Recursive partitioning is used for the classification of molecules with activity using CART methods.

Anthrax lethal factor protease inhibitors: Synthesis, SAR, and structure-based 3D QSAR studies.

S.L. Johnson, D. Jung, Martino Forino, Ya Chen, A. Satterthwait, D.V. Rozanov, A.Y. Strongin, and M. Pellecchia* [Burnham Inst. for Med.Res.].

J. Med. Chem. **49**, 27-30 (2006)

A series of compounds are identified that efficiently inhibit anthrax lethal factor (LF) metallo-protease. CoMFA studies are performed and obtained 3D QSAR model, compared with the X-ray structure of the complex between LF and a representative compound. These studies form the basis for the rational design of additional compounds with improved activity and selectivity.

3D-QSAR studies on cannabinoid CB1 receptor agonists: G-protein activation as biological data.

O.M. H. Salo* [U Kuopio], J.R. Savinainen, T. Parkkari, T. Nevalainen, M. Lahtela-Kakkonen, J. Gynther, J.T. Laitinen, T. Järvinen, and Antti Poso.

J. Med. Chem. **49**, 554-566 (2006)

Automated docking is used to obtain a common alignment of endocannabinoid and classical cannabinoid derivatives. The endocannabinoid headgroup occupies a unique region distinct from the classical cannabinoid structures. Both CoMFA and CoMSIA produce statistically significant models based on the manual alignment and a docking alignment at one receptor conformer.

Soft quaternary anticholinergics: Comprehensive quantitative structure-activity relationship (QSAR) with a linearized biexponential (LinBiExp) model.

P. Buchwald* [IVAX Research Inc.,] and N. Bodor.

J. Med. Chem. **49**, 883-891 (2006)

QSAR studies are used for quaternary soft anticholinergics including two distinctly different classes designed on the basis of the soft analogue and the inactive metabolite approaches. Linearized biexponential (LinBiExp) model showed a maximum/minimum around a given parameter value but tend to show linearity away from this turning point. LinBiExp represents a natural extension of linear models, and a direct correspondence between its parameters.

Host-Guest Systems

Incorporation of impurity anions into DSP: Insights into structure and stability from computer modeling.

J.L. Lowe* [Curtin U Tech.], A.L. Rohl , J.D. Gale, P.G. Smith, G.M. Parkinson.

Mol. Sim., **32**, 35-44 (2006).

MM calculations are used to examine the interaction energy between a series of anions and the sodalite framework, as a measure of the affinity of the anions for the sodalite cage. These calculations predicted that the ions have an increased affinity for the cage along the series aluminate, chloride, carbonate, sulfate and hydroxide.

Some physical properties of the Weeks-Chandler-Andersen fluid.

D.M. Heyes* [U Surrey] and H. Okumura.

Mol. Sim., 32, 45-50 (2006).

MD simulations are carried out of some properties of a Weeks-Chandler-Andersen system in its fluid phase. The scaling behaviour of these quantities using reduced variables, such as an effective hard sphere diameter was investigated. It was observed that the infinite frequency Poisson's ratio increases with packing fraction and temperature towards the incompressible fluid limit value of 1/3.

Carbon Nanoparticles

Directed assembly of carbon nanotubes at liquid-liquid interfaces: Nanoscale conveyors for interfacial biocatalysis.

A. Prashanth, S.S. Karajanagi, J.S. Dordick* [Rensselaer Polytech. Inst.] and Ravi S. Kane.

J. Am. Chem. Soc., **128**, 1046 -1047 (2006)

Single-walled carbon nanotubes (SWNT)-enzyme conjugates enhanced the rate of catalysis up to 3 orders of magnitude relative to the rates obtained with native enzymes in similar biphasic systems. The ability to direct the assembly of nanotubes at the interface also provides an attractive route to organizing these nanomaterials into 2D architectures.

1.2. *Biopolymers*

Bioinformatics

2D Autocorrelation modeling of the negative inotropic activity of calcium entry blockers using Bayesian-regularized genetic neural networks.

J. Caballero, M. Garriga and M. Fernández* [U Matanzas].

Bioorg. Med. Chem. **14**, 3330-3340 (2006)

Autocorrelation vectors in the nonlinear model contained information regarding 2D spatial distributions on the CEB structure of van der Waals volumes, electronegativities, and polarizabilities. A sensitivity analysis of the network inputs pointed out to the electronegativity and polarizability 2D topological distributions at substructural fragments of sizes 3 and 4 as the most relevant features governing the nonlinear modeling of the negative inotropic potency.

Modeling of farnesyltransferase inhibition by some thiol and non-thiol peptidomimetic inhibitors using genetic neural networks and RDF approaches.

M.P. González, J. Caballero, A. Tundidor-Camba, A.M. Helguera and M. Fernández* [U Matanzas].

Bioorg. Med. Chem. **14**, 200-213 (2006)

Radial distribution function descriptors are used in Genetic neural network (GNN) approach to model the inhibition of farnesyltransferase (FT) enzyme by thiol and non-thiol peptidomimetic inhibitors. This model suggested the occurrence of a strong dependence of FT inhibition on the molecular shape and size rather than on electronegativity or polarizability characteristics of the reported inhibitors.

Bioinformatics (cont'd)

Modeling of activity of cyclic urea HIV-1 protease inhibitors using regularized-artificial neural networks.

M. Fernández and J. Caballero* [U Matanzas].

Bioorg. Med. Chem. **14**, 280-294 (2006)

HIV-1 protease inhibition and inhibition of HIV replication for 55 cyclic urea derivatives are modeled with Artificial neural networks approach using constitutional and 2D descriptors. The inhibition of HIV replication was dependent on the occurrence of five-member rings. It was observed that the inhibitors were well distributed regarding its activity levels in a Kohonen self-organizing map built using the input variables of the best non-linear models.

Protein Sequence Analysis and Alignment

Clustering of domains of functionally related enzymes in the interaction database PRECISE by the generation of primary sequence patterns.

M.R. Landon, D.R. Lancia, Jr., K.H. Clodfelter and S. Vajda* [Boston U].

J. Mol. Graph. Mod. 24, 426-433 (2005)

To generate the primary sequence patterns for each poorly aligned cluster in PRECISE to assess the extent to which multi-domain proteins that are incorrectly aligned contributes to poor pair-wise alignments of each cluster member to its representative. The poor alignments in PRECISE are caused most frequently by the misalignment of multi-domain proteins. The generation of primary sequence patterns for the assignment of sequence family membership yields better alignments for the functionally related enzyme clusters in PRECISE than our original alignment algorithm.

Protein Secondary Structure

Support-vector-machine classification of linear functional motifs in proteins.

D. Plewczynski* [BioInfo Bank Inst.], A. Tkacz, L.S. Wyrwicz, A. Godzik, A. Kloczkowski and L. Rychlewski.

J.Mol.Mod. **12,** 459-461 (2006)

Swiss-Prot database is used to build the statistical models for short linear functional motifs in proteins. The query protein sequence is dissected into short overlapping fragments, all segments are represented as vectors. Each vector is then classified by a machine learning algorithm as potentially modifiable or not. A study of the human protein kinase C family as a biological application of this method is presented.

Comparative or Homology Modeling

A modelling study of a non-concerted hydrolytic cycloaddition reaction by the catalytic antibody H11.

R.L. Clark, B.F. Johnston, C.J. Suckling and S.P. Mackay* [U Strathclyde].

Bioorg. Med. Chem. **14**, 2674-2683 (2006)

Homology modeling is used to construct H11, to calculate the antibody-ligand complexes in the docking studies. It was found that the hydrolytic nature of H11 was due to Glu 95H acting as a catalytic base, and evaluation of the shape complementarity of the proposed antibody–ligand complexes confirmed at a semi-quantitative level.

Cannabinoid CB2/CB1 selectivity, receptor modeling and automated docking analysis.

T. Tuccinardi, P.L. Ferrarini, C. Manera, G. Ortore, G. Saccomanni, and A. Martinelli* [U di Pisa].

J. Med. Chem. **49**, 984-994 (2006)

Homology modeling is used to build the 3D-models of the CB1 and CB2 cannabinoid receptors based on the structure of bovine rhodopsin. AUTODOCK used to study several ligands into the CB2 model. The results are correlated between the estimated free energy binding and the experimental binding data confirmed the binding hypothesis and the reliability of the model.

Comparative or Homology modeling (cont'd.)

S!
New insights about HERG blockade obtained from protein modeling, potential energy mapping, and docking studies.

R. Farid* [Schrödinger, Inc.], T. Day, R.A. Friesner and R.A. Pearlstein.

Bioorg. Med. Chem. **14**, 3160-3173 (2006)

Homology modeling is used to build the homo-tetrameric pore domain of HERG using the crystal structure of the bacterial potassium channel, KvAP, using Glide and Prime programs. Hydrophilic iso-potential contours define a 'propeller-shaped' volume at the selectivity filter entrance. Hydrophobic contours define a hollow 'crown-shaped' volume located above the 'propeller', whose hydrophobic 'rim' extends along the pore axis between Tyr652 and Phe656. Terfenadine, cisapride, sertindole, ibutilide, and clofilium adopt similar docked poses, in which their N-substituents bridge radially across the hollow interior of the 'crown', and project aromatic/hydrophobic portions into the hydrophobic 'rim'.

T-cell epitopes of the La/SSB autoantigen: Prediction based on the homology modeling of HLA-DQ2/DQ7 with the insulin-B peptide/HLA-DQ8 complex.

A.Kosmopoulou, M.Vlassi, A. Stavrakoudis* [U Ioannina], C.Sakarellos, M. Sakarellos-Daitsiotis.

J.Comp.Chem. **27**, 1033-1044 (2006)

Homology modeling is used to build DQ2 and DQ7 based on the crystal structure of HLA-DQ8, an HLA molecule. The reliability of the modeled DQ2 and DQ7 was confirmed by the TINKER. Common and/or similar candidate T-cell epitopes, obtained by comparing three different approaches the Taylor's sequence pattern, the TEPITOPE quantitative matrices, and the MULTIPRED artificial neural network, and the best superposed candidate epitopes were placed into the modeled HLA-DQ2 and DQ7 binding grooves to perform energy minimization calculations.

Protein Folding

Studies of folding and misfolding using simplified models.

N.V. Dokholyan* [The U North Carolina]

Curr.Opin.Stru.Biol.**16**, 79-85 (2006)

Advanced computer simulations are provided the information to understand the biological phenomena. The simplified models are accurate as traditional MD approaches in identifying native conformations of proteins. Protein structure prediction yielded phenomenal accuracy in recapitulating native protein conformations. New studies that utilize the synergy of simplified protein models with all-atom models and experiments yielded novel insights into complex biological processes, such as protein folding, aggregation and the formation of large protein complexes.

Protein Dynamics

Flap opening mechanism of HIV-1 protease.

Gergely Tóth* [Locus Pharm.] and Attila Borics

J. Mol. Graph. Mod. **24**, 465-474 (2005)

MD simulations are used to study the mechanism of flap opening and the structure and dynamics of HIV-1 PR with semi-open and open flap conformations. The flaps showed complex dynamic behavior as two distinct mechanisms of flap opening and various stable flap conformations were observed during the simulations. It is assumed from the obtained results that such interactions could be responsible for making flap opening a highly sensitive gating mechanism which control access to the active site.

Protein Dynamics (cont'd)

Insights into the induced fit mechanism in antithrombin-heparin interaction using molecular dynamics simulations.

Hugo Verli and J.A. Guimarães* [U Federal do Rio Grande do Sul].

J. Mol. Graph. Mod. **24**, 203-212 (2005)

MD simulations are used to describe the interaction between the synthetic pentasaccharide and AT. The results showed a solvent-exposed P1 residue instead of a hided conformation. The results are used to characterize and quantify the interaction of synthetic compounds with AT, predicting its specific capacity to induce conformational changes in AT structure. MD simulations of heparin -AT interactions are proposed as a powerful tool to assist and support drug design of new antithrombotic agents.

Molecular dynamics simulations of ligand dissociation from thyroid hormone receptors: Evidence of the likeliest escape pathway and its implications for the design of novel ligands.

L. Martínez, P. Webb, I. Polikarpov, and M.S. Skaf* [U Sao Paulo].

J. Med. Chem. **49**, 23-26 (2006)

The dissociation is favored via rearrangements in a mobile part of the LBD comprising H3, the loop between H1 and H2, and nearby β-sheets, contrary to current models in which the H12 is mostly involved. Dissociation is favorable through the interaction of the hydrophilic part of the ligand with external water molecules, suggested strategies to enhance ligand binding affinity.

Free Energy

Free energies of molecular crystal surfaces by computer simulation: Application to tetrathiophene.

V. Marcon and Guido Raos* [Polytech. di Milano].

J. Am. Chem. Soc., **128**, 1408 -1409 (2006)

A generalized simulation method is described to evaluate the surface free energies of molecular crystals like polymorphism and crystal growth. The results showed the importance of temperature-dependent entropic contribution to the surface free energies, which is not included in widely used static simulations of surface structure and energetics.

Studies on binding free energies and the binding mode by docking and MM-PBSA in gp41-ligand complex.

J. J. Tan* [Beijing U of Tech.], R. Kong, W. Z. Chen, C. X. Wang.

Mol.Sim. **31**, 1050-1056 (2006)

Autodock is used to dock a small inhibitor (TP1) into the hydrophobic grooves of gp41. The molecular mechanics-Poisson Boltzmann surface area method is applied to calculate the binding free energies. It was observed that only one binding mode is supported by the experimental evidence. The model is used to design more effective HIV-1 inhibitors targeted to the HIV-1 gp41 core structure.

Ligand Binding

Exploring protein-ligand recognition with binding MOAD.

R.D. Smith, Liegi Hu, J.A. Falkner, M.L. Benson, J.P. Nerothin and H.A. Carlson* [U Michigan].

J. Mol. Graph. Mod. **24**, 414-425 (2005)

The results of mining binding MOAD to map the degree of solvent exposure for binding sites are presented. The most cavities and ligands are well buried in the complexes are determined. This fits with the common paradigm that a large degree of contact between the ligand and protein is significant in molecular recognition. GoCAV and the GoCAV viewer are the tools are created for this study. To share the data and make online dataset more useful to other research groups, an integration is made to the viewer into the Binding MOAD website.

Ligand Binding (cont'd)

The environment of amide groups in protein-ligand complexes: H-bonds and beyond.

S. Cotesta* [Novartis] and M. Stahl.

J.Mol.Mod. **12,** 436-444 (2006)

Most of the amide C=O and NH groups at the protein–ligand interface are highly buried within the binding site and involved in H-bonds with corresponding counter-groups. C=O groups show a higher propensity is solvated or embedded in a hydrophobic environment than NH groups do. A small percentage of carbonyl groups is involved in weak hydrogen bonds with CH. Dipolar interactions, involving carbonyl oxygen and electrophilic carbon atoms, such as amide, amidinium, guanidium groups, are also identified.

Semiempirical comparative binding energy analysis (SE-COMBINE) of a series of trypsin inhibitors.

M.B. Peters and K.M. Merz, Jr.* [The Pennsylvania State U].

J. Chem. Theory Comput., **2**, 383-399, 2006

SE-COMBINE method is coupled with the comparative binding energy analysis and the semiempirical quantum mechanical method pairwise energy decomposition. This approach is useful to calculate the residue pairwise electrostatic interaction energies. QSAR models are built with the energies as descriptors using partial least squares. The intermolecular interactions between 88 benzamidine inhibitors and trypsin and to test the ability of this novel method to predict binding free energies are investigated.

Cu, Zn superoxide dismutase: Distorted active site binds substrate without significant energetic cost.

R.J.F. Branco, P.A. Fernandes and M.J. Ramos* [U do Porto].

Theor.Chem.Accounts., **115***,* 27-31 (2006)

Distorted geometry is the basis for the catalytic efficiency of the enzyme by allowing substrate binding without extensive geometric reorganization of the copper complex. The results showed that a lower limit for the reorganization energy is calculated here in 22 kcal/mol, slow down the reaction kinetics by more than 13 orders of magnitude, transforming a perfect enzyme into an inefficient one.

Matrix metalloproteinase target family landscape: A chemometrical approach to ligand selectivity based on protein binding site analysis.

Bernard Pirard* [Aventis Pharma.] and Hans Matter.

J. Med. Chem. **49**, 51-69 (2006)

Molecular interaction fields are used to characterize the binding sites of 56 matrix metalloproteinase structures and one tumor necrosis factor α-converting enzyme. Consensus principal component analysis is provided the ranking of the six subpockets based on the selective interactions with different MMP's.

S!
Protein structures in virtual screening: A case study with CDK2.

M.P. Thomas* [Cyclacel Ltd.], C. McInnes, and P.M. Fischer.

J. Med. Chem. **49**, 92-104 (2006)

GOLD and Glide are used to dock a set of CDK2 inhibitors of known bound pose into 20 different CDK2 structures. The numbers of docked poses that reproduced the known pose are reported. Depending on the program and protein structure, 0.3%-96.2% of the ligands docked with the correct pose. It is identified that the volume of the binding site into which the ligands are docked and the exact orientation of the residues forming the binding site.

Ligand Binding (cont'd)

Combination of a modified scoring function with two-dimensional descriptors for calculation of binding affinities of bulky, flexible ligands to proteins.

C. Hetényi* [Eotvos Lorand U], G. Paragi, U. Maran, Z. Timár, M. Karelson, and B. Penke.

J. Am. Chem. Soc., **128**, 1233 -1239 (2006)

AutoDock is used to modify the scoring function of the popular docking program and the involvement of ligand-based two-dimensional descriptors. QSAR's are derived with good predictive power and the results of lead design are contributed to precise predictions, correct selections, and consequently a higher success rate of rational drug discovery.

Protein-Protein Interactions

An agent-based system to discover protein-protein interactions, identify protein complexes and proteins with multiple peptide mass fingerprints.

Tzong-Yi Lee, Jorng-Tzong Horng* [Nati. Cent. U], Hsueh-Fen Juan, Hsien-Da Huang, Li-Cheng Wu, Meng-Fong Tsai, Hsuan-Cheng Huang.

J.Comp.Chem. **27**, 1020-1032 (2006)

An agent-based system is developed, namely AgentMultiProtIdent, which integrated two protein identification tools and a variety of databases storing relations among proteins. This is used to discover protein-protein interactions and protein functional associations, and to identifying protein complexes and proteins with multiple peptide mass fingerprints as input. The system takes Multiple Peptide Mass Fingerprints as a whole in the protein complex or protein identification.

Nucleic Acids

A study on chirality in biomolecules: the effect of the exchange of L amino acids to D ones in Sso7d ribonuclease.

J.J. Ladik* [Friedrich - Alexander - U – Erlangen] and Z. Szekeres.

J.Mol.Mod. **12,** 462-467 (2006)

The conformational behavior of ribonuclease Sso7d is studied as a function of chirality of its constituting amino acids. CHARMM force field and MD simulations are used and both optimized structures are compared.

On 3DD-curves of DNA sequences.

Y. Zhang* [Shandong U], B. Liao, K. Ding.

Mol. Sim., **32**, 29-34 (2006).

The 3DD-curves, a new 3D graphical representation of DNA sequences, resolves degeneracy completely and is mathematically proved to eliminate circuit formation. This is applicable to a comparison for the mitochondrial sequences belonging to 11 different species based on the new 3D graphic representation.

1.3. Polymers

Prediction of polyamide properties using quantum-chemical methods and BP artificial neural networks.

Jinwei Gao, Xueye Wang* [Xiangtan U], Xiaobing Li, Xinliang Yu and Hanlu Wang.

J.Mol.Mod. **12,** 513-520 (2006)

Quantitative structure property relationships are determined for glass translation temperatures (T_g), density (ρ) and indices of refraction (n) of the polyamides. All descriptors are calculated from molecular structures at the B3LYP/6-31G(d) level. These models are generated by two methods: multiple linear regression (MLR) and error back-propagation artificial neural networks (BPANN) and are useful to predict T_g, ρ and n values.

Polymers (cont'd)

Calculation of polyamides melting point by quantum-chemical method and BP artificial neural networks.

Jinwei Gao, Xueye Wang* [Xiangtan U], Xinliang Yu, Xiaobing Li and Hanlu Wang.

J.Mol.Mod. **12,** 521-527 (2006)

B3LYP/6-31G(d) level is used to generate the model by multiple linear regression to determine the QSPR. The number of benzene rings in the backbone chain, the proportion of methylene and acylamino in the backbone chain, the total molecular energy and the atomic charge for the oxygen atom in the acylamino group descriptors are considered. Melting-point temperatures for polyamides are described by molecular chain rigidity and interchain attractive interactions.

Molecular dynamics simulations of polyampholyte solutions: osmotic coefficient.

J. Feng*[East China U of Sci. &Tech.], H. Liu, Y. Hu.

Mol. Sim., **32**, 51-57 (2006).

MD simulations are used to obtain osmotic coefficients of solutions containing neutral or non-neutral polyampholyte chains with different segment sizes and charged sequences. Molecular thermodynamic model is developed based on chemical association theory where the polyampholyte molecules are modeled as positively and negatively charged hard-sphere chains with a chain length *l*. The predicted osmotic coefficients by the model well agreed with those obtained from MD simulation for neutral polyampholytes.

Periodic and high-temperature disordered conformations of polytetrafluoroethylene chains: An ab initio modeling.

M. D'Amore, G. Talarico, and V. Barone* [U of Stud. of Napoli].

J. Am. Chem. Soc., **128**, 1099 -1108 (2006)

DFT is applied with the proper choice of periodic boundary conditions, functional, basis set, and model system size and validated for saturated polymers such as polyethylene and isotactic/syndiotactic polypropylenes. Poly(tetrafluoroethylene) chains in both regular periodic and disordered conformations is studied. A statistical approach is used to obtain the thermal concentration of defects and to reproduce the thermal behavior of the investigated polymer.

1.4. Surfaces, Catalysts, and Material Subjects

What role do surfaces play in GB models? A new-generation of surface-generalized born model based on a novel gaussian surface for biomolecules.

Zhiyun Yu, M.P. Jacobson, R.A. Friesner* [Columbia U].

J.Comp.Chem. **27**, 72-89 (2006)

An efficient algorithm is designed to construct and triangulate the Gaussian surface for large biomolecules with arbitrary shapes, and to compute the various terms required for energy gradients. The Gaussian surface showed to better mimic the boundary between the solute and solvent by properly addressing solvent accessibility, as is demonstrated by comparisons with standard Poisson-Boltzmann calculations for proteins of different sizes. The results showed that the surface definition is a dominant contribution to differences between GB and PB calculations, especially if the system is large.

A molecular-dynamics simulation study of diffusion of a single model carbonic chain on a graphite (001) surface.

H. Yang, Z.-Yuan Lu, Ze-Sheng Li* [Jilin U] and Chia-Chung Sun.

J.Mol.Mod. **12,** 432-435 (2006)

MD simulations are used to study the diffusion of a short single carbonic chain on the graphite surface. An abnormal behavior is observed i.e., firstly diffusion coefficient increases, then decreases with increasing chain length.

Surfaces, Catalysts, and Material Subjects (cont'd)

Theoretical study of aluminum arsenide clusters: Equilibrium geometries and electronic structures of Al_nAs_n (n = 1–4).

Yuhui Qu* [Shandong Inst. of Light Indu.], Wanyong Ma, Xiufang Bian, Hongwei Tang and Weixing Tian.

J. Mol. Graph. Mod. **24**, 167-174 (2005)

DFT is used to investigate the geometry, electronic configurations, harmonic vibrational frequencies and stability of the structural isomers of Al_nAs_n clusters (n = 1–4). The Al-As bond dominates the structures for many isomers and compared with valence-isoelectronic Si_{2n}, Al_nP_n and Ga_nAs_n clusters of same size, the properties of the aluminum arsenide clusters are analogous to those of their corresponding Al_nP_n, Si_{2n}. The results explained the modification and refinement of Si phase in Al-Si alloy in the molecular level.

Molecular dynamics simulation of shell-symmetric Pd nanoclusters.

Y. Pan* [Beijing U of Chem.Tech.], S. Huang, Z. Liu, W. Wang.

Mol.Sim. **31**, 1057-1061 (2006)

MD simulation with Sutton-Chen many-body potential (SC) is used to study the interaction between the Pd atoms of shell-symmetric cubooctahedron and icosahedron nanoclusters. The cubooctahedron nanocluster melts around 1040 K, much lower than the melting point of bulk Pd system. The icosahedron nanocluster melts around 1070 K. The outer two shells of the shell-symmetric nanocluster melt prior to their homogeneous melting of the whole nanoclusters.

Effect of surface roughness on slip flows in hydrophobic and hydrophilic microchannels by molecular dynamics simulation.

S.C. Yang* [Chien Kuo Tech.U] and L.B. Fang.

Mol.Sim. 32, 971-977 (2006)

MD simulations are used to investigate the influences of surface roughness on the boundary conditions. The slip boundary condition is strongly depends on the shear rate near the surface. For hydrophobic surfaces, apparent fluid slips are observed on smooth and rough surfaces. It is observed that there is a no-slip boundary condition only when shear rate is low, and partial slip occurs when it exceeds a critical level.

2. METHODOLOGY

Quantitative Structure-Activity Relations

QSPR analysis for infinite dilution activity coefficients of organic compounds.

K. Tämm* [Tartu U] and P. Burk.

J.Mol.Mod. **12,** 417-421 (2006)

CODESSA PRO program is used for QSAR studies and molecular descriptors are correlated with the activity coefficients. The fractional partial negative surface area and the count of hydrogen donor sites describe the dilution process in ILs.

Insight into the structural requirements of urokinase-type plasminogen activator inhibitors based on 3D QSAR CoMFA/CoMSIA models.

B.A. Bhongade and A.K. Gadad* [The West Indies U]

J. Med. Chem. **49**, 475-489 (2006)

CoMFA/CoMSIA techniques are performed to investigate the structural requirements for substrates and derive a predictive model that is used for the design of novel uPA inhibitors. 3D QSAR models were derived for 2-pyridinylguanidines, 4-aminoarylguanidines and 4-aminoarylbenzamidines, thiophene-2-carboxamindines, 2-naphthamidines, and 1-isoquinolinylguanidines. 3D contour maps generated from these models were analyzed individually, provides the regions in space where interactive fields may influence the activity.

Conformational Search and Analysis

Study of peptide conformation in terms of the ABEEM/MM method.

Zhong-Zhi Yang* [Liaoning Normal U], Qiang Zhang.

J.Comp.Chem. **27**, 1-10 (2006)

The atom-bond electronegativity equalization method fused into molecular mechanics (ABEEM/MM) model is applied to study of the polypeptide conformations. The Lennard-Jones and torsional parameters were optimized to consistent with the ABEEM/MM fluctuating charge electrostatic potential.

Potentials and Parameters

Reparameterized Austin Model-1 for quantitative structure-property relationships in liquid media.

D.A. Dobchev and M. Karelson* [Tallinn U of Tech].

J.Mol.Mod. **12,** 503-512 (2006)

QSPR equation is obtained for the b.p's of organic compounds for the one-electron resonance integral parameters (β_s and β_p) and core-core repulsion atomic parameters α were obtained for the elements H, C, N, O, Cl and Br. The QSPR equation employs two molecular descriptors, a bulk cohesiveness descriptor, and the area-weighted surface charge of hydrogen-bonding donor atom(s) in the molecule. The new parameters were tested on the critical temperatures of 165 organic compounds.

Molecular parameter optimization using simulated annealing and evolutionary algorithm techniques in a quantum parametric method (CATIVIC).

M. Sánchez*[IUT Federico Rivero-Palacio], L.S. Rodríguez, G. Larrazabal, L. Galean, N. Bello, F. Ruette.

Mol. Sim., **32**, 65-70 (2006).

The parametric quantum chemistry method (CATIVIC) is applied with simulated annealing (SA) and evolutionary algorithm (EA) techniques for optimization of parameters for a set of organic and gold clusters. The results showed that EA is more efficient than SA and are having some differences in the set of parameters.

***Ab initio* calculations of intramolecular parameters for a class of arylamide polymers.**

V. Satyavani* [U Pennsylvania], I. Ivanov , K. Spiegel, V. Pophristic, M.L. Klein.

J.Comp.Chem. **27**, 693-700 (2006)

MD simulations are used to study the zwitterionic form of the dipeptide glycine-alanine in water focussed on solvation and electrostatic properties. The results showed that the solvation pattern is similar for all methods used for most atoms in the dipeptide, like the carboxy and aminoterminii, and the backbone amid NH group.

Solvation Energy

Linear interaction energy models for β-secretase (BACE) inhibitors: Role of van der Waals, electrostatic, and continuum-solvation terms.

B.A. Tounge, R. Ramkumar, E.W. Baxter, A.B. Reitz and C. H. Reynolds* [Johnson & Johnson Pharm.].

J. Mol. Graph. Mod. **24**, 475-484 (2005)

The computed interaction energies of a series of β-secretase (BACE) inhibitors in terms of van der Waals, coulombic, and continuum-solvation contributions to ligand binding are studied. The effect of different protonation states of the protein and ligands are systematically studied. It was find out that the binding affinities are relatively insensitive to the protonation state of the protein when neutral ligands are considered. The best models are obtained when the protein is judiciously charged and the potentially charged ligands are treated as neutral.

Molecular Dynamics

The simulation of imidazolium-based ionic liquids.

P. A. Hunt* [Imperial Coll.]

Mol. Sim., **32**, 1-10 (2006).

Design and development of force fields for the simulation of imidazolium-based ionic liquids is presented. The efficacy of these models is assessed with respect to the prediction of structural and dynamical properties and compared with *ab initio* molecular dynamics studies.

Molecular dynamics simulation of Henry's constant of argon, nitrogen, methane and oxygen in ethylene oxide.

M. Krishnamurthy* [Illinois U at Chicago], S. Murad, J. D. Olson.

Mol. Sim., **32**, 11-16 (2006).

MD simulations are used to calculate the Henry's constants and solubilities of a range of small non-polar molecules in ethylene oxide. The results showed that the method is reliable for polar-nonpolar sytems, and validated for several gases. It is observed that for gas solubilities, small diatomics are effectively approximated by central Lennard-Jones potential models.

Monte-Carlo Simulation

Monte Carlo simulations of biomolecules: The MC module in CHARMM.

Jie Hu , Ao Ma, A.R. Dinner* [U Chicago],

J.Comp.Chem. **27**, 203-216 (2006)

Implementation of CHARMM with general and flexible Monte Carlo module is described. Sampling is enhanced by noncanonical acceptance criteria, automatic optimization of step sizes, and energy minimization. A systematic procedure for improving MC move sets is introduced and applied to simulations of two peptides. The resulting move sets allow MC to sample the configuration spaces of these systems much more rapidly than Langevin dynamics.

Free Energy Methods

QM/MM free-energy perturbation compared to thermodynamic integration and umbrella sampling: Application to an enzymatic reaction.

J. Kästner, H. Martin Senn, Stephan Thiel, Nikolaj Otte, and Walter Thiel* [Max-Planck-Inst.]

J. Chem. Theory Comput., **2**, 452-461, 2006

QM/MM integrated free energy perturbation method is used to calculate the free-energy profile of the hydroxylation reaction in the enzyme *p*-hydroxybenzoate hydroxylase. The results of QM/MM-FEP for PHBH are in good agreement with those of thermodynamic integration and umbrella sampling.

Computation of hydration free energies of organic solutes with an implicit water model.

M.V. Basilevsky, I.V. Leontyev, S.V. Luschekina* [Algodign], O.A. Kondakova, V.B. Sulimov

J.Comp.Chem. **27**, 552-570 (2006)

A new method combines a conventional polarizable continuum model computation for the electrostatic component ΔG_{el} of ΔG_{solv} and a specially detailed algorithm for treating the complementary non-electrostatic contributions ΔG_{nel}. The special features are two different cavities are used for treating ΔG_{el} and ΔG_{nel}, the cavitation component of ΔG_{nel} is taken to be proportional to the volume of the large cavity, in the treatment of van der Waals interactions, all solute atoms are counted explicitly.

QM/MM

Density functional computations of enantioselective alkynylation of aldehyde catalyzed by chiral zinc(II)-complexes.

Q. Meng, Ming Li* [Southwest-China Normal U] and J. Zhang

J.Mol.Mod. **12,** 494 -502 (2006)

DFT is used to study the alkynylation of aldehyde catalyzed by chiral zinc(II)-complexes. B3LYP/6-31G(d,p) level is used to optimized all the structures and to obtain more exact energies, geometries. The chirality-determining step for the alkynylation was the formation of the catalyst–ethanol complexes and the transition states for this step involved a six-membered ring.

Path integral simulations of proton transfer reactions in aqueous solution using combined QM/MM potentials.

D. Thomas Major, M. Garcia-Viloca, and Jiali Gao* [U Minnesota].

J. Chem. Theory Comput., **2**, 236-245, 2006

A combined QM/MM method is used to study the convergence of the bisection method for two proton-transfer reactions in aqueous solution at room temperature. The first reaction involves the symmetrical proton transfer between an ammonium ion and an ammonia molecule, and the second reaction is the ionization of nitroethane by an acetate ion. It was observed that a sufficient number of polymer beads along with a large number of configurations to achieve convergence.

Ab initio quantum mechanical charge field (QMCF) molecular dynamics: A QM/MM – MD procedure for accurate simulations of ions and complexes.

B.M. Rode*[U Innsbruck], T.S. Hofer, B.R. Randolf, C.F. Schwenk, D. Xenides and V. Vchirawongkwin.

Theor.Chem.Accounts., **115***,* 77-85 (2006)

The new formalism is tested with some hydrated ions, for which accurate conventional ab initio QM/MM simulations are performed, the comparison shows equivalence and in some aspects superiority of the new method. This simulation procedure does not require any tedious construction of two-and three-body interaction potentials inherent to conventional QM/MM approaches, it opens the straightforward access to ab initio molecular dynamics simulations of any kind of solutes, such as metal complexes and other composite species in solution.

Catalytic mechanism and product specificity of the histone lysine methyltransferase SET7/9: An ab initio QM/MM-FE study with multiple initial structures.

Po Hu and Yingkai Zhang* [New York U]

J. Am. Chem. Soc., **128**, 1272 -1278 (2006)

Ab initio QM/MM free energy calculations and MD simulations are used to investigate the reaction mechanism and product specificity of histone lysine methyltransferase SET7/9. The methyl-transfer reaction catalyzed by SET7/9 is a typical in-line S_N2 nucleophilic substitution reaction with a transition state of 70% dissociative character. The results showed the product specificity of SET7/9 as a monomethyltransferase is achieved by disrupting the formation of near-attack conformations for the dimethylation reaction.

Comparative or Homology Modeling

Three-dimensional models of histamine H_3 receptor antagonist complexes and their pharmacophore.

F.U. Axe* [Axe Consult. Services], S.D. Bembenek and Sándor Szalma

J. Mol. Graph. Mod. **24**, 456-464 (2005)

Homology modeling is used to build the H_3 receptor based on the X-ray structure of bovine rhodopsin. MD simulations are applied and a pharmacophore model is calculated by mapping the features common to three active compounds three-dimensionally in space. The H_3 antagonist pharmacophore consists of two protonation sites connected by a central aromatic ring or hydrophobic region.

Comparative or Homology Modeling (cont'd)

A!
Structural insights into human 5-Lipoxygenase inhibition: Combined ligand-based and target-based approach.

C. Charlier, Jean-Pierre Hénichart, F. Durant, and J. Wouters* [U Lille]

J. Med. Chem. **49**, 186-195 (2006)

HipHop module of the Catalyst is used to generate a pharmacophore model for 16 non redox 5-LOX inhibitors. 3D structure of human 5-LOX is modeled based on the structure of rabbit 15-LOX crystal structure. Molecular docking is used to study the binding modes of representative ligands. The docking results with the pharmacophore model allowed the weighting of the pharmacophoric features and the integration of structural information.

Homology modeling of the Serotonin 5-HT_{1A} receptor using Automated docking of bioactive compounds with defined geometry.

M. Nowak* [Polish Acad. of Sci.], M. Pawlowski, M. Kolaczkowski and A.J. Bojarski

J. Med. Chem. **49**, 205-214 (2006)

A rhodopsin-based model of 5-HT_{1A} serotonin receptor is described and validated by automated docking of conformationally restricted arylpiperazines. The model reproduced the binding affinity of the test group of ligands. It gave the enrichment in virtual screening-like experiment, in which 34 high-affinity compounds were found among 50 top-scored ligands.

Ligand Docking

Essential structural profile of a dual functional inhibitor against cyclooxygenase-2 (COX-2) and 5-lipoxygenase (5-LOX): Molecular docking and 3D-QSAR analyses on DHDMBF analogues.

Mingyue Zheng, Zhenshan Zhang, Weiliang Zhu, Hong Liu, Xiaomin Luo, Kaixian Chen and Hualiang Jiang* [Chinese Acad. of Sci.]

Bioorg. Med. Chem. **14**, 3428-3437 (2006)

Homology modeling is used to built a 3D-model of 5-LOX based on the X-ray structure of rabbit reticulocyte 15-lipoxygenase. Molecular docking was then applied to locate the binding orientations and conformations of DHDMBF analogues with COX-2 and 5-LOX respectively. CoMFA models constructed on the basis of the binding conformations with q^2 values of 0.782 and 0.634 for COX-2 and 5-LOX, respectively. The 3D-QSAR models and the inhibitor-enzyme interaction are useful in developing new NSAIDs as anti-inflamation drugs.

A!
Investigation of the binding mode of (−)-meptazinol and bis-meptazinol derivatives on acetylcholinesterase using a molecular docking method.

Qiong Xie, Yun Tang, Wei Li, Xing-Hai Wang and Zhui-Bai Qiu* [Fudan U]

J.Mol.Mod. **12,** 373-389 (2006)

FlexX and GOLD programs were used to investigate the binding mode of (−)-meptazinol (MEP) with acetylcholinesterase (AChE) and to screen bis-meptazinol (bis-MEP) derivatives. GOLD fitness values of known ligands were correlated with their activities, (−)-MEP is binding with the enzyme catalytic site in an open-gate conformation through strong hydrophobic interactions and a hydrogen bond.

Study on improving the selectivity of compounds that inhibit two PI3Ks (gamma and delta).

Rong-Ren Kuang, Feng Qian, Zhong Li and Dong-Zhi Wei* [New World Inst. of Biotech.]

J.Mol.Mod. **12,** 445-452 (2006)

GRID/PCA and docking methods are used to investigate the detail interactions of the two PI3Ks with various chemical groups. 3 D-model of the PI3Kδ catalytic subunit is constructed with the program Modeller7.0, and GRID is employed and PCA to reveal the most relevant structural and physicochemical differences between the two PI3Ks related to their selectivity.

Molecular Graphics

Tools for building a comprehensive modeling system for virtual screening under real biological conditions: The computational titration algorithm

G.E. Kellogg* [Virginia Commonwealth U], D. L. Chen, M. Fornabaio, D. J. Abraham, F. Spyrakis, P. Cozzini and A. Mozzarelli.

J. Mol. Graph. Mod. **24**, 434-439 (2005)

Computational tools utilizing a unique empirical modeling system based on the hydrophobic effect and the measurement of $\log P_{o/w}$ are described. The comprehensive modeling system for virtual screening that incorporates these features is described and a detailed description of the computational titration algorithm is given.

Computational tools for the analysis and visualization of multiple protein-ligand complexes.

S.E. O'Brien* [Pfizer Global], D.G. Brown, J.E. Mills, C. Phillips and G. Morris

J. Mol. Graph. Mod. **24**, 186-194 (2005)

Computational tools are analyzed, display multiple protein-ligand interactions and their properties are presented with an illustrative example. It was also showed that how 2D- and 3-D similarities are combined to provide enhanced understanding of 33 factor Xa inhibitor complexes. This methodology has enabled to identify pharmaceutically relevant relationships between ligands and their binding modes.

Graphs to chemical structures 3. General theorems with the use of different sets of sphericity indices for combinatorial enumeration of nonrigid stereoisomers.

Shinsaku Fujita* [Kyoto Inst. of Tech.]

Theor.Chem.Accounts., **115***,* 37-53 (2006)

Two theorems for enumerating nonrigid stereoisomers are proved by adopting two schemes of their derivation, *i.e.*, the scheme ``positions of a skeleton ⇐ proligands ⇐ ligands and the scheme ``(positions of a skeleton ⇐ proligands ⇐ ligands (positions of a ligand)) ⇐ sub-proligands". The theorems are applied to the stereoisomerism of trihydroxyglutaric acids.

3. ADDRESSES OF PRINCIPAL AUTHORS

The production sites for the corresponding or principal authors are given in brackets in the citations. When not designated by the publisher, the first author is assumed to be the principal. Current addresses are listed here.

Aaron R. Dinner
dinner@uchicago.edu
Dept. of Chem.
The Univ. of Chicago
Chicago, Illinois 6063, USA.

Aatto Laaksonen
aatto@physc.su.se
Div. of Phys. Chem.
Arrhenius Lab.
Stockholm Univ.
Stockholm, 106 91, Sweden

Adriano Martinelli
Dept. di Sci. Farma.
Univ. di Pisa
via Bonanno 6
56126 Pisa, Italy

Alan R. Katritzky
Cent. for Het. Comp.
Dept. of Chem.
Univ. of Florida
Gainesville, FL 32611, USA

A.D. Andricopulo
Lab. de Química Med. e Comp.
Cent. de Biotech. & Mol. Estrut.
Inst. de Física de São Carlos
Univ. de São Paulo
Av. Trabalhador São-carlense 400
13560-970, São Carlos-SP
Brazil

A.M. Bianucci
Dept. Sci. & Pharm.
Univ. di Pisa
Via Bonanno 6
56126 Pisa, Italy

Benjamin P. Hay
ben.hay@pnl.gov
Chem. Sci. Div.
Pacific Northwest Nati. Lab.
Richland, Washington 99352
USA.

Bernd M. Rode
Bernd.M.Rode@uibk.ac.at
Theor. Chem. Division
Inst. of Gen.Inorg. & Theor. Chem.
Univ. of Innsbruck
Innrain 52a, A-6020 Innsbruck
Austria

Bernard Pirard
Sci. & Med. Affairs, Chem. Sci.,
Drug Design
Aventis Pharm.
Deutschland GmbH
D-65926 Frankfurt am Main
Germany

Brian C. Tripp
brian.tripp@wmich.edu
Dept. of Biol. Sci.
Mailstop 5410
1903 West Michigan Avenue
Western Michigan Univ.
Kalamazoo, MI 49008-5410
USA

Charles H. Reynolds
Drug Discov.
Johnson & Johnson Pharma.
L.L.C., P.O. Box 776
Welsh and McKean Roads
Spring House, PA 19477-0776,
USA

Corwin Hansch
Dept of Chem.
Pomona Coll.
Claremont, CA 91711, USA

Csaba Hetényi
csabahete@yahoo.com
Dept. of Biochem.
Eötvös Loránd Univ.
1/C Pázmány P. sétány
H-1117 Budapest
Hungary

H.A. Carlson
Biophys. Res. Division
Univ. of Michigan
Ann Arbor, MI 48109-1055
USA

Chang-Guo Zhan
Dept. of Pharm. Sci.
Coll. of Pharm.
Univ. of Kentucky
725 Rose Street
Lexington, Kentucky 40536
USA

Dong-Zhi Wei
dzhwei@ecust.edu.cn
State Key Lab. of Bioreactor Engg.
New World Inst. of Biotech.
130 Mei-Long Road
Shanghai, 200237
P.R. China

W. David Wilson
Dept. of Chem.
Georgia State Univ.
Atlanta, GA 30303, USA

N.V. Dokholyan
Dept. of Biochem. & Biophys.
The Univ. of North Carolina at
Chapel Hill
Sch. of Med., Chapel Hill
NC 27599, USA

Frank U. Axe
Axe Consult. Services
14595 Surrey Junction Lane
Sutter Creek, CA 95685, USA

J. Feng
Dept. of Chem. and State Key Lab.
of Chem. Engg.
East China Univ. of Sci. & Tech.
Shanghai, 200237, P.R. China

M. Fernández
Mol.Model. Group
Cent. for Biotech.Studies
Univ. of Matanzas
Matanzas, C.P. 44740, Cuba

R.A. Friesner
rich@chem.columbia.edu
Dept. of Chem. & Cent. for
Biomol. Sim.
Columbia Univ., New York
New York 10027,U.S.A.

A.K. Gadad
Pharm. Program
Facu. of Med. Sci.
The Univ. of The West Indies
St. Augustine
Champs Fleurs, Mount Hope
Trinidad, W.I.

A.T. García-Sosa
atgs@cantab.net
Dept. of Pharmacology
Univ. of Cambridge
Tennis Court Road
Cambridge, CB2 1PD, UK

R. Gaudreault
Dept. of Chem.
McGill Univ.
801 Sherbrooke Street West
Montreal, Que.
Canada, H3A 2K6

Gergely Tóth
Locus Pharm.
Four Valley Square
512 Township Line Rd.
Blue Bell, PA 19422
USA

Glen E. Kellogg
Dept. of Med. Chem. & Inst. for
Stru. Biol. and Drug Discov.
Sch. of Pharm.
Virginia Commonwealth Univ.
Box 980540, Richmond
VA 23298-0540
USA

Guido Raos
guido.raos@polimi.it
Dept. of Chem.
Mat. Engg. Chem. "Giulio Natta"
Politecnico di Milano
Via L. Mancinelli 7
20131 Milano, Italy

Hanlu Wang
wxueye@xtu.edu.cn
Coll. of Chem.
Xiangtan Univ.
Xiangtan, 411105, P.R. China

D. M. Heyes
Div. of Chem.
Sch. of Biomed. & Mol. Sci.
Univ. of Surrey
Guildford, GU2 7XH, UK

Hoshik Won
Dept. of Chem.
Hanyang Univ.
Seoul 133-791, Republic of Korea

Hualiang Jiang
Drug Discov. and Design Cent.
State Key Lab. of Drug Res.
Shanghai Inst. of Mat. Medica
Shanghai Inst. for Biol. Sci.
Chinese Acad. of Sci., Shanghai
201203, PR China

H.W. Hugosson
hakan@theochem.kth.se
Lab. of Comp. Chem. & Biochem.
Inst. of Mol. and Biol. Chem.
Swiss Federal Inst. of Tech. EPF
Lausanne, Switzerland

P. A. Hunt
Dept. of Chem.
Imperial Coll. London
London, SW7 2AZ, UK

Hea-Young Park Choo
Sch. of Pharm.
Ewha Womans Univ.
Seoul 120-750
Republic of Korea

A.L. Hopkins
Pfizer Global (R &D)
Sandwich
Kent CT13 9NJ, UK

M.A.H. Ismail
Dept. of Pharm. Chem.
Facu. of Pharm.
Ain Shams Univ.
Cairo, Egypt

János J. Ladik
janos.ladik@chemie.uni-erlangen.de
Chair for Theor. Chem. and Lab. of the Nat. Found. for Cancer Res.
Friedrich - Alexander - Univ. – Erlangen
Nürnberg, Egerlandstraße 3
D-91058 Erlangen, Germany

Jaroslaw Polanski
Dept. of Org. Chem.
Inst. of Chem.
Univ. of Silesia
PL-40-006 Katowice
Poland

Jianzhong Liu
Dept. of Chem. & Biochem.
Univ. of Delaware
Newark, Delaware 19716, USA

Jiali Gao
Dept. of Chem. and Supercomp. Inst.
Digital Tech. Center
Univ. of Minnesota
Minneapolis, Minnesota 55455
USA.

Jorng-Tzong Horng
horng@db.csie.ncu.edu.tw
Dept. of Comp. Sci. & Info. Engg.
Nat. Central Univ.
No. 320, Jung-do Road
Jungli 320, Taiwan
P.R. China

Johan Wouters
Inst. de Chim. Pharm.
Albert Lespagnol
EA 2692, Univ. de Lille 2
BP 83, F-59006 Lille, France

Jonathan S. Dordick
dordick@rpi.edu
Dept. of Chem. & Biol. Engg.
Rensselaer Polytech. Inst.
Troy, New York 12180, USA.

S. Joo Cho
Biochem. Res. Cent.
Korea Inst. of Sci. & Tech.
PO Box 131, Cheongryang
Seoul 130-650
Republic of Korea

Jorge A. Guimarães
Cent. de Biotech.
Univ. Federal do Rio Grande do Sul, Av.
Bento Gonçalves 9500
CP 15005, Porto Alegre 91500-970, RS, Brazil

Julio Caballero
Molecular Modeling Group
Cent. for Biotech. Studies
Univ. of Matanzas
Matanzas, Cuba

Kaido Tämm
kaido@alfanet.ee
Univ. of Tartu
2 Jakobi str., Tartu
51014, Estonia

Kenneth M. Merz, Jr.
Dept. of Chem.
104 Chem. Building
The Pennsylvania State Univ.
Univ. Park, Pennsylvania 16802
USA.

A.I. Khlebnikov
Dept. of Chem.
Altai State Tech. Univ.
Barnaul 656099
Russia

Kouji Hattori
Med. Chem.Res. Labs
Fujisawa Pharma. Co. Ltd
5-2-3 Tokodai, Tsukuba
Ibaraki 300-2698, Japan

M. Krishnamurthy
Dept. of Chem. Engg
Univ. of Illinois at Chicago
Chicago, IL, 60607, USA

Kunal Roy
Drug Theor. and Cheminfo. Lab
Div. of Med. & Pharm. Chem.
Dept of Pharm.Tech.
Jadavpur Univ.
Kolkata 700 032, India

D. Leith
Dept. of Chem.
Trinity College
Dublin 2, Ireland

J. L. Lowe
Nanochem. Res. Inst.
Curtin Univ. of Tech.
AJ Parker Co-operative Res. Cent. for Hydrometal.
Kent Street, Bentley
WA, 6102, Australia

S.V. Luschekina
sonya@mccme.ru
Dept. of Quantum Chem.
Algodign, LLC,
Bolshaya Sadovaya 8
123001 Moscow, Russia

A.Maria Bianucci
Dept. di Sci. Pharm.
Univ. di Pisa, 56126 Pisa
Italy

S.P. Mackay
Dept. of Pharm. Sci.
Univ. of Strathclyde
Glasgow G4 0NR, UK

Mateusz Nowak
Dept. of Med.Chem.
Inst. of Pharm.
Polish Acad. of Sci.
12 Smetna Street
31-343 Kraków, Poland

Maurizio Pellecchia
Cancer Res.Cent. and Infect. and Inflam. Disease Cent.
Burnham Inst. for Med. Res.
10901 North Torrey Pines Road
La Jolla, California 92037, USA.

Michael Fernández
Mol. Mod. Group
Cent. for Biotech. Studies
Fac. of Agronomy
Univ. of Matanzas
44740 Matanzas, Cuba

Mohamed Zahouily
mzahouily@yahoo.fr
UFR Chimie Appliquée
Lab. de Catalyse
Chim. et Environment
Dépt. de Chimie
B.P. 146, 20650 Mohammadia
Maroc

Ming Li
liming@swnu.edu.cn
Dept. of Chem.
Southwest-China Normal Univ.
Chongqing, 400715, P.R. China

Mati Karelson
mati.karelson@ttu.ee
Dept. of Chem.
Tallinn Univ. of Tech.
Ehitajate tee 5, Tallinn
19086, Estonia

Munir S. Skaf
Inst. de Física de São Carlos
Univ. de São Paulo
Av. Trabalhador São Carlense
400, São Carlos, SP 13560-970
Brazil

Ninghua Tan
State Key Lab of Phytochem. & Plant Resources in West China
Kunming Inst. of Botany
Chinese Acad. of Sci.
Kunming 650204, China

Outi M. H. Salo
Dept. of Pharm. Chem. & Physiol.
Univ. of Kuopio
P.O. Box 1627
FIN-70211 Kuopio, Finland

Y. Pan
Min. of Edu.
Beijing Univ. of Chem. Tech.
Key Lab for Nanomat.
Div. of Mol. & Mat. Sim.
Beijing, 100029, P.R. China

Peter Buchwald
IVAX Research, Inc.,
4400 Biscayne Boulevard
Miami, Florida 33137

D. Plewczynski
darman@icm.edu.pl
BioInfoBank Inst.
Limanowskiego 24A/16
60-744 Poznan, Poland

Ramy Farid
Schrödinger, Inc.
120 West Forty-Fifth St.
32nd Floor, New York
NY 10036, USA

M.J. Ramos
mjramos@fc.up.pt
Requimte, Dept. de Química
Facu. de Ciências
Univ. do Porto
Rua do Campo Alegre, 687
4169-007 Porto, Portugal

Rahul Jain
Dept. of Med.Chem.
Nat. Inst. of Pharm. Edu. & Res.
Sector 67, S.A.S. Nagar
Punjab 160 062, India

Run-Tao Li
Sch. of Pharm.Sci.
Peking Univ. Health Sci. Cent.
Beijing 100083, China

Sean E. O'Brien
Dept. of Med. Info. Stru. and Design
Pfizer Global R & D,
Sandwich, Kent, UK

Sirirat Kokpol
Dept. of Chem.
Facu. of Sci.
Chulalongkorn Univ.
Patumwan
Bangkok 10330, Thailand

Sally-Ann Poulsen
Chem. Biol. Group
Eskitis Inst. for Cell and Mol.Therapies, Griffith Univ.
Nathan Campus
Brisbane 4111, Australia

Sandor Vajda
Grad. Progr. in Bioinfo. & Sys. Biol.
Boston Univ., Boston 02215, MA, USA

V. Satyavani
vani@cmm.upenn.edu
Dept. of Chem.
Univ. of Pennsylvania
Philadelphia, Pennsylvania 19104
USA

M. Sánchez
IUT Federico Rivero-Palacio
Dept. de Química
Apartado 40347
Caracas, Venezuela

Simona Cotesta
simonacotesta@novartis.com
Mol. Design, Pharm. Division
F. Hoffmann-La Roche AG
Discov. Tech.
Bldg. 092/2.10D, CH-4070 Basel
Switzerland

Shinsaku Fujita
fujitas@chem.kit.ac.jp
Dept. of Chem. & Mat. Tech.
Kyoto Inst. of Tech.
Matsugasaki, Sakyoku
Kyoto 606-8585, Japan

A. Stavrakoudis
astavrak@cc.uoi.gr
Dept. of Economics
Univ. of Ioannina
Ioannina 44110, Greece.

V. Subramanian
Chem. Lab.
Central Leather Res. Inst.
Adyar, Chennai - 600 020, India

Sunil Gupta
REQUIMTE, CQFB
Dept. de Quím.
Facu. de Ciências e Tecn.
Univ. Nova de Lisboa
2829-516 Caparica, Portugal

J. J. TAN
Coll. of Life Sci. & Bioengg.
Beijing Univ. of Tech.
Beijing, 100022
P.R. China

A.A. Toropov
Lab. of Env. Chem. and Toxicol.
Inst. Ricerche Farma.
'Mario Negri,' Via Eritrea 62
20157 Milan, Italy

M.P. Thomas
Cyclacel Ltd.
James Lindsay Place
Dundee, DD1 5JJ, U.K.

Vincenzo Barone
baronev@unina.it
Dept. di Chem.
Univ. degli Stud. di Napoli "Federico II"
via Cintia, 80126 Napoli, Italy

Walter Thiel
Max-Planck-Inst. für Kohlenforschung
Kaiser-Wilhelm-Platz 1
D-45470 Mülheim an der Ruhr
Germany

Xueye Wang
wxueye@xtu.edu.cn
Coll. of Chem.
Xiangtan Univ.
Xiangtan, 411105
P.R. China

Yingkai Zhang
yingkai.zhang@nyu.edu
Dept. of Chem.
New York Univ.
New York, New York 10003

Yoshiaki Nakagawa
Div. of Appl. Life Sci.
Grad. Sch. of Agri.
Kyoto Univ.
Kyoto 606-8502, Japan

Yuhui Qu
Dept. of Chem.
Shandong Inst. of Light Industry
Shandong
Jinan 250100, PR China

S.C. Yang
ChienKuo Tech. Univ.
Dept. of Mech. Engg.
Changhua, 50094, Taiwan,
Republic of China.

Yuyang Jiang
The Key Lab. of Chem. Biol.
Guangdong Province
Grad. Sch. at Shenzhen
Tsinghua Univ.
Shenzhen 518055, China

Zhui-Bai Qiu
ytang234@yahoo.com.cn
School of Pharmacy
Fudan Univ., Shanghai, 200032
P.R. China

Ze-Sheng Li
zeshengli@mail.jlu.edu.cn
Inst. of Theor. Chem.
State Key Lab. of Theor. & Comp. Chem.
Jilin Univ., 130023 Changchun
PR China

Y. Zhang
Sch. of Inform. & Engg.
Shandong Univ. at Weihai
Weihai, 264209, P.R. China

Zhong-Zhi Yang
zzyang@lnnu.edu.cn
Dept. of Chem.
Liaoning Normal Univ.
Dalian 116029, P.R. China

Zhui-Bai Qiu
Dept. of Med.Chem.
Sch. of Pharm.
Fudan Univ.
138 Yixueyuan Road
Shanghai 200032, China

4. DISCLAIMER, COPYRIGHT, AND PUBLISHER INFORMATION

MMCC Results (ISSN 1061-6381), published by MMCC Results, RR Labs Inc., 8013 Los Sabalos Street, San Diego, CA 92126, is a private business independent of all software and hardware vendors, companies, government laboratories, universities, and other institutions whose products or publications may be cited herein. R.Nageswar, Senior Research Manager, RR Labs Inc., 8013 Los Sabalos Street, San Diego, CA 92126. Mention of a software product is for information purposes only and does not constitute an endorsement or recommendation by either MMCC Publishing or the authors of the paper cited. All product names are the trademarks or registered symbols of their respective organizations.

MMCC Results is published ten times per year, at the beginning of each month except January and August. For subscription information, please contact MMCC Publishing:

Editor:

R.Nageswar Ph.D. Tel. (858) 663-0162
MMCC Results E-mail: drnageswar@yahoo.com
RR Labs Inc.,
8013 Los Sabalos Street
San Diego, CA 92126