Abstract No.111

Identification of New Candidate Lung Cancer Genes by Network of Overexpressed Genes Obtained from EST Analysis

Faezeh Hosseinzadeh[*1], *Narges Shamabadi*[2], *Mansour Ebrahimi*[3]

1. Laboratory of Biophysics and Molecular Biology, Institute of Biophysics and Biochemistry, University of Tehran, Tehran, IR
2. Member of Young Researcher club, Qom Branch, Islamic Azad University, Qom, IR
3. Bioinformatics Research Group, Green Research Center, University of Qom, Qom, IR
(E-mail: hosseinzadeh1365@gmail.com)

Genes involved in related biological pathways and diseases are usually expressed cooperatively for their functions, and thus information on their coexpression is a key to understand the biological systems at the molecular level. Publicly available databases of coexpressed gene sets are a valuable resource for a wide variety of experimental studies, including gene targeting for functional identification, and for investigations of regulatory mechanisms or protein–protein interaction networks. Recent improvements in DNA EST techniques have made a large variety of gene expression data available in public databases. This data can be used to evaluate the strength of gene coexpression by calculating the correlation of expression patterns among different genes between many experiments. The original COXPRESdb (coexpressed gene database) (http://coxpresdb.jp) represented the coexpression relationship for human and mouse.In this study, we investigated new genes that may involve in lung cancer but hitherto haven't reported, by drawing coexpressed genes network. EST libraries analyzed by Digital Differential Display (DDD) to identify overexpressed genes turmeric comparing to normal lung tissues. IDS of sixteen overexpressed genes imported to COXPRESdb and gene networks drew. Forty eight genes linked and showed coexpression to our overexpressed genes and all coexpressed genes carefully examined. The results showed nine genes (EIF1B, PPP2R2B, BTK, ATXN1, GABARAPL2, MAP1LC3A, RANBP9, SNCA and LOC344887) have not so far reported as genes involved in lung cancer and could be considered as new candidate genes for being investigated their participation in lung cancer.

Keywords: Lung Cancer, EST Analysis, Gene Network, Coexpressed Genes.

Abstract No.112

Micellar SDS –TsIm – Hemin Complex as a Peroxidase-Like Nano Artificial Enzyme

Hanie Ahmadzade Kermani[*1], *Abbas Shockravi*[2], *Zeinab Moosavi-Movahedi*[3], *A. Khalafi-Nezhad*[4], *Ali Akbar Moosavi-Movahedi*[5]

1. Laboratory Of Biophysical Chemistry, Institute of Biochemistry and Biophysics, University of Tehran, IR
2. Faculty of chemistry, Tarbiat Moallem University, Tehran, IR
3. Department of Chemistry, College of Sciences, Shiraz University, Shiraz, IR
4. Chemistry and Chemical Research Center of Iran (CCERCI), Tehran, IR
5. Institute of Biochemistry & Biophysics (IBB), University of Tehran, IR
(E-mail: hanieahmadzade@yahoo.com)

Biomimetic chemistery tries to design novel system by using chemical strategies considering the chemistry of living systems and attempts to imitate enzymatic processes and improve the performance of chemical reactions and enzymes. Artificial enzymes are constructed from synthetic materials by functional simulation . In many hemoproteins such as peroxidasese heme group has the functional role. The catalytic activity of hemoproteins depends on the microenvironment surrounding the heme and also the heme ligands . Heme itself has catalytic property but it has tendency to dimerization in aqueous solutions, so its catalytic activity is decreased in aqueous solutions . It is known that porphyrins may be solubilized by detergents like sodium dodecyl sulfate (SDS). There are strong hydrophobic interactions between detergents and porphyrin which overcome the porphyrin – porphyrin forces and porphyrin is solubilized at detergent concentrations corresponding to critical micelle concentration (CMC) . Micelles mimic the polypeptide envelope in proteins as the heme environment. Hemoproteins containing heterocylic nitrogen like histidine as proximal ligands can catalyze the oxidation of variety of substrates through reacting with hydrogen peroxide as oxidatative enzymes . In biomimetic chemistery the coordination chemistery of histidine is stimulated by imidazole containing ligands . A surfactant – Imidazole – heme ternary complex is known as nano artificial enzyme which shows peroxidase activity in aqueous solutions . In this study the SDS – TsIm – heme ternary complex has been designed as a peroxidase like nano artificial enzyme. 1-tosyl-1H-Imidazole (TsIm) was employed as an imidazole moiety to mimics histidine ligand in the native horseradish peroxidase(HRP). Enzymatic activation parameters, using spectrophotometeric measurements showed that the catalytic efficiency of SDS – TsIm – heme enhancement up to 26.38% relative

to HRP efficiency and also that is more efficient in comparing with the catalytic efficiency of SDS – Imidazole – heme system.

Keywords: Nano Artificial Enzyme, SDS Micelle, Heme, Imidazole-Tosyl Group, Enzymatic Efficiency, Biomimetic.

Abstract No.113

Semi-empirical Analysis of Interaction Between Bisphosphonates and Farnesyl Pyrophosphate Synthase

Mohammad Hossein Karimi-Jafari [1], *Rohouhollah Firouzi** [2]

1. Institute of Biochemistry and Biophysics, University of Tehran, Tehran, IR
2. Chemistry and Chemical Engineering Research Center of Iran (CCERCI), Tehran, IR
(E-mail: Firouzi.chemist@yahoo.com)

Nitrogen-containing bisphosphonates (N-BPs) are important pharmaceuticals in treatment of various bone related diseases. Major molecular target of N-BPs is the enzyme farnesyl pyrophosphate synthase (FPP_S). Here, we conducted quantum mechanical calculations for several N-BPs and their surrounding residues in the active site of FPPS.

X-ray structures of all complexes were obtained from PDB and were saturated for missing hydrogen atoms and a computationally tractable model was built by cutting all residues within 4.5 Å of the ligand. Dangling bonds in the N and C terminals of selected residues were capped by CH_3-CO- and –NH-CH_3 fragments, respectively. PM6 semiempirical Hamiltonian was used for optimization of added hydrogen atoms and calculation of interaction energies. Different computational tasks in this work were performed by VMD-1.9, MATHEMATICA-8, REDUCE-3.14 and MOPAC-2009 programs.

Optimized structures show that the phosphonate groups interact mainly with an aspartate-rich region in the active site of FPPS via bridges of divalent metal ions. In addition, the hydroxyl group of N-BPs show direct interaction with proximally located, positively charged lysine residues. This study also reveals a strong dependence of number of hydrogen bonding interactions of the phosphonate groups with FPPS and the side chain of N-BPs. The heterocyclic N-BPs (such as Minodronate) make more hydrogen bonding.

Keywords: Bisphosphonates, FPPS, Computational, Osteoporosis.

Abstract No.114

Mammalian Intestinal Alpha Glucosidase Inihibitory Activity of Novel Pyrimidine Fused Heterocycles

*Mohamad Mehraban** [1], *Reza Yousefi* [1], *Farhad Panahi* [2], *Ali Khalafi-Nezhad* [2]

1. Protein Chemistry Laboratory (PCL), Dept. of Biology, College of Sciences, Shiraz University, Shiraz, IR
2. Dept. of Chemistry, College of Sciences, Shiraz University, Shiraz, IR
(E-mail: saido666@gmail.com)

The prevalence of diabetes which is partly associated to the amount of carbohydrates in the diet has risen at alarming rate. Mammalian starch digestion primarily occurs in lumen of the small intestine by α-amylase to yield both linear and branched chain oligosaccharides, neither of which can be absorbed into the blood-stream without further hydrolysis by α-glucosidases (EC 3.2.1.20) to release glucose. In this regard, intestinal α-glucosidases plays a critical role in carbohydrate digestion and absorption, and therefore, the inhibition of this enzyme provides an effective anti-diabetic option by targeting postprandial hyperglycaemia. In this study a novel class of pyrimidine fused heterocyclic compounds were synthesized and their inhibitory effect against mouse alpha-glucosidase examined spectroscopically. Both kinetic- and pharmacologic parameters including mode of inhibition, inhibition constant (Ki) and half maximal inhibitory concentration (IC50) were calculated for the synthetic compounds, presenting promising inhibitory effect against the mammalian enzyme. This study suggests a novel molecular scaffold as template for synthesis of anti-diabetic compounds with promising inhibitory activity against alpha-glucosidase.

Keywords: Alpha-glucosidase, Inhibition, Diabetes, Pyrimidine-Fused Heterocycles.

Abstract No.115

Antibacterial Activity and Conformational Study of Brevinin-2R

*Robab Hasanvand** [1], *Asadollah Asadi* [1], *Hashem Yaghoubi* [2], *Saber Zahri* [1]

1. Department of Biology, Faculty of Science, Mohaghegh Ardabili University, Ardabil, IR
2. Department of Biology, Faculty of Science, Islamic Azad University of Ardabil, Ardabil, IR