



**The Sixth International Conference on
Bioinformatics of Genome Regulation
and Structure (BGRS'2008)**
Novosibirsk, Russia
June 22-28, 2008

June 26, Thursday

House of Scientists, Small Conference Hall Foyer

14:00-16:00

POSTER SESSION AND COMPUTER DEMONSTRATIONS

Poster Size: The maximum size allowed for each poster
is 0.7m wide × 1.2m high.

Please note that this is a portrait (vertical) poster.

Authors must bring their posters printed and ready, as no facilities to produce posters at the Conference are available. Organizers will provide boards and push pins to display your posters. Posters should be readable from a distance of about two to three feet—for easy reading by several people at one time.

Presentations may be posted starting from **10:00 on June 23** in the Small Conference Hall Foyer.

The posters will be displayed for the overall duration of the Conference.

A scheduled Poster Session, only one for all Conference sections, will be held on **June 26 from 14:00 to 17:00** in the Small Conference Hall Foyer.

During the allotted time, presenters are expected to remain at their individual displays to be available for questions and informal discussion of the poster content.

Material should be removed no later than **13.00 on June 27**.

In the case the author(s) does not take away the presentation, it will be removed and destroyed by the BGRS'2006 Organizing Committee.

Computer demonstrations will be held on **June 26 from 14:00 to 16:00** in the Small Conference Hall Foyer.

If you have any questions, please do not hesitate to contact the Organizing Committee in Room no. 200 at the House of Scientists.

POSTER PRESENTATIONS (BY SECTIONS)

GENOMICS AND TRANSCRIPTOMICS

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COMPARISON ANALYSING OF MUTANT GENE *cbn1* WITH MUTANT GENE *cao* AND MOLECULAR MAPPING OF *CAO* GENE IN *CHLAMYDOMONAS REINHARDTII*

A-2

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USING SVM AND A MEASURE OF MOTIF 'SURPRISE' TO DISTINGUISH REGULATORY DNA

A-3

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MODEL OF PERFECT TANDEM REPEAT WITH RANDOM PATTERN FOR LATENT PERIODICITY RECOGNITION IN BIOLOGICAL SEQUENCES

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A METHOD FOR THE ESTIMATION OF THE PARAMETERS OF THE LINEAR MODEL OF GENE NETWORK DYNAMICS

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RASDB – REGULATION OF ALTERNATIVE SPLICING DATABASE

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GENTOO PENGUIN'S POLYMORPHISM ON MOLECULAR-GENETIC LEVEL

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A.V. Fedorov*, O.I. Podgornaya

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**O.S. Glotov^{1,3*}, A.S. Glotov^{1,2}, G.S. Demin¹, Potulova S.V.^{1,2}, M.V. Moskalenko², N.Y. Shved¹,
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R. Ya. Golda

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K.A. Golovnina*, E.Y. Kondratenko, A.G. Blinov, N.P. Goncharov

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DISCOVERY OF PROPERTY-CONSERVED FUNCTIONAL ELEMENTS IN HUMAN

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T.M. Khlebodarova^{*1}, V.A. Likhoshvai^{1,2}, D.Y. Oshchepkov¹, A.V. Kachko¹, N.V. Tikunova¹

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O.V. Nikolaienko*, M.V. Dergay, O.V. Dergay, D.Y. Morderer, L.O. Tsyba, I.Y. Skrypkina, A.V. Rynditch

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D. Parkhomchuk*, M. Banaru, T. Borodina, V. Amstislavskiy, A. Soldatov, H. Lehrach

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N.L. Podkolodny^{1,2,3,*}, **E.V. Ignatieva^{1,2}**, **S.S. Nechkin^{1,2}**, **E.A. Ananko¹**, **O.A. Podkolodnaya¹**

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T.O. Pylnik*, **S.E. Smolenskaya**, **A.L. Markel**, **O.E. Redina**

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DETECTION OF NEW POTENTIALLY ACTIVE DRE SITES IN REGULATORY REGION OF HUMAN GENES ENCODING COMPONENTS OF Ah RECEPTOR CYTOSOLIC COMPLEX

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EXPRESSION ANALYSIS OF NF- κ B-REGULATED GENES IN BREAST CANCER. META-ANALYSIS OF FIVE MICROARRAY DATA SETS

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DEVELOPMENT OF TEST-SYSTEMS FOR GENETICALLY MODIFIED CROP DIAGNOSTICS USING REAL-TIME PCR

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SITEGA METHOD APPLICATION FOR GENOME WIDE PREDICTION OF P53 BINDING SITES

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“PROMETHEUS” TOOLKIT FOR AGILE DEVELOPMENT OF BIOLOGICAL DATA STORING AND ACCESS SOFTWARE

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FINE STRUCTURE OF MAMMALIAN TRANSLATION INITIATION SIGNAL

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DROSOPHILA MELANOGASTER STRAIN *y cn bw sp*

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ANALYSIS OF A LIGHT ENTRAINMENT ON THE MATHEMATICAL MODEL OF MAMMALIAN
CIRCADIAN OSCILLATOR

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DATABASE NEUROGENESIS ON BRISTLE PATTERN FORMATION IN *D. melanogaster*

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MODELING AND VISUALISATION OF PATHWAYS USING PETRI NETS

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MGSmodeller – A COMPUTER SYSTEM FOR RECONSTRUCTION, CALCULATION AND ANALYSIS
MATHEMATICAL MODELS OF MOLECULAR GENETIC SYSTEM

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V.V. Lavreha^{1*}, **A.V.Penenko**², **S.V. Nikolaev**¹, **N.A. Kolchanov**¹

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MODELLING AND COMPARATIVE ANALYSIS OF AUXIN TRANSPORT MECHANISMS IN SHOOT AND ROOT

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MODELLING OF AUXIN CONTROL OF ROOT PATTERNING

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MODELING THE EXPRESSION OF THE DROSOPHILA *EVEN-SKIPPED (EVE)* GENE DRIVEN BY ITS PROXIMAL 1.7 KB UPSTREAM REGION.

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PGNS-ROOT – A DATABASE ON EXPRESSION OF GENES IN PLANT ROOT DEVELOPMENT.

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AGNS (ARABIDOPSIS GENENET SUPPLEMENTARY DATABASE), RELEASE 4.0

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AGNK: COMPUTER SYSTEM FOR AGNS DATA ANALYSIS

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WHOLE-GENOME COMPARISON OF TWO MYCOBACTERIUM TUBERCULOSIS STRAINS BY THE
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SDPFOX: A TOOL TO PREDICT PROTEIN SPECIFICITY AND SPECIFICITY DETERMINANTS FROM MULTIPLE SEQUENCE ALIGNMENT

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PROF_PAT, THE UPDATED DATABASE OF PROTEIN FAMILY PATTERNS – AN EFFECTIVE TOOL FOR GENOME ANNOTATION.

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INVESTIGATION OF THE AMINO ACID SEQUENCES OF HUMAN INFLUENZA VIRUS H5N1 WITH PROTEIN FAMILY PATTERNS BANK PROF_PAT.

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ACCELERATED ADAPTIVE EVOLUTION ON A NEWLY FORMED X CHROMOSOME

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ANALYSIS OF THE EVOLUTIONARY SPECIFICITIES OF THE YFIA И YHBH E. COLI GENES AND THEIR REGULATORY REGIONS.

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ABOUT EVOLUTIONARY CONSTRUCTOR

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COMPARATIVE PHYLOGENETIC ANALYSIS OF OPISTHORCHIID SPECIES BASED ON NUCLEAR AND MITOCHONDRIAL SEQUENCES

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AN INFORMATION ENTROPY MODEL FOR THE PHYLOGENESIS OF THE 1918 INFLUENZA VIRUS

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POLYMORPHISM OF LIPOPROTEIN LIPASE GENE IN WEST SIBERIA CAUCASIAN POPULATION AND ITS ASSOCIATION WITH PLASMA LIPID LEVELS

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ANALYSIS OF FACTORS AFFECTING THE ACCURACY PREDICTIONS FOR PROTEIN-PROTEIN INTERACTIONS BASED ON THE MIRROR TREE APPROACH

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TEpredict: SOFTWARE FOR PREDICTING T-CELL EPITOPES

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BIOINFORMATIONAL MODELS FOR TESTING OF MEDICINAL PLANTS

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MACHINE LEARNING TECHNIQUES FOR NUCLEAR HORMONE RESPONSE ELEMENT PREDICTION

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WEB-TOOL FOR PROTEIN DESIGN BY THE ANIS-METHOD.

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QUALITY OF LOCAL AND GLOBAL PAIR-WISE ALIGNMENTS OF AMINO ACID SEQUENCES

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PREDICTION OF FUNCTIONALLY RELATED PROTEINS: PHYLOGENETIC PROFILES AND CLUSTER ANALYSIS

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FUNCTIONAL ANNOTATION OF AMINO ACID SEQUENCES USING THE LOCAL SIMILARITY

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QUANTUM-CHEMICAL ANALYSIS OF ZN²⁺ BINDING IN WILD-TYPE AND G245C MUTANT OF P53 PROTEIN

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BIOINFORMATIONAL MODELS FOR TESTING OF MEDICINAL PLANTS

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IN SILICO DESIGN OF PRIMER FOR 28 KDA ANTIGEN PRECURSOR PROTEIN OF *MYCOBACTERIUM LEPRAE*

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MODELLING OF REGULATORY NETWORKS TO IDENTIFY PROMISING DRUG TARGETS FOR BREAST CANCER THERAPY

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ESTIMATION OF MINIMAL DRUG TREATMENT DURATION FOR CLEARANCE OF AN HUH-7 CELL FROM HEPATITIS C VIRUS REPLICON BASED ON MATHEMATICAL MODELLING

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THE NEW TOOL FOR OLIGONUCLEOTIDE DESIGN FOR VIRUS GENOTYPING USING MULTIPLE ALIGNMENT

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MOSAIC NATURE OF THE WATER-LIPID INTERFACE AFFECTS A BEHAVIOR OF MEMBRANE-ACTIVE PEPTIDES.

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CELL VOLUME AND SODIUM CONTENT IN RAT KIDNEY COLLECTING DUCT PRINCIPAL CELLS
DURING HYPOTONIC SHOCK

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PREDICTION OF SPATIAL STRUCTURE OF TRANSMEMBRANE HELICAL DIMERS USING
MOLECULAR MODELING TECHNIQUES

COMPUTER ANALYSIS AND IMAGE RECOGNITION IN SYSTEMS BIOLOGY

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SYSTEMS BIOLOGY STUDIES OF THE EFFECTS OF LEPTIN REPLACEMENT ON HUMAN GLUCOSE
HOMEOSTASIS

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DEVELOPMENT OF THE COMPUTER PROGRAM FOR DEFINING LEAF HAIRINESS IN WHEAT BASED
ON ITS MICROSCOPE IMAGE PROCESSING

G-3

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ANNOTATION OF LUNG-SCREENING IMAGES AND 2D-E PROTEOMIC ANALYSIS FOR EARLY
DIAGNOSIS OF LUNG CANCER THROUGH FEDERATED BIOBANKS

G-4

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CENTRALITY ANALYSIS OF GENE REGULATORY NETWORKS

G-5

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AGNS (ARABIDOPSIS GENENET SUPPLEMENTARY DATABASE), RELEASE 4.0

G-6

R.N. Sharipov^{1,2,3}, I.S. Yevshin^{1,2}, T.I. Leonova^{1,3}, B.V. Semisalov^{1,3}, E.A. Biberdorf⁴, Y.L. Trakhinin⁴, M.V. Puzanov^{1,3}, A.M. Blokhin⁴, A.L. Markel², L. N. Ivanova², F.A. Kolpakov^{1,3,*}

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⁴Sobolev Institute of Mathematics SB RAS, Novosibirsk, Russia

INTEGRATED APPROACH FOR MODELLING PHYSIOLOGICAL, BIOMECHANICAL, AND
MOLECULAR-GENETIC ASPECTS OF HUMAN CARDIOVASCULAR SYSTEM IN HEALTH AND
ESSENTIAL HYPERTENSION

G-7

Yu.V. Shatalin¹, A.A. Naumov¹, T.K. Sukhomlin¹, G.L. Ermakov¹, M.M. Potselueva¹, R.N. Sharipov^{2,3,4}, I.S. Yevshin^{2,3}, F.A. Kolpakov^{2,4,*}

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DISBALANCE BETWEEN INNATE IMMUNITY RESPONSE AND ANTIOXIDANT DEFENCE IN BLOOD AND ASCITES: INTEGRATION OF EXPERIMENTAL AND MATHEMATICAL MODELING

G-8

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CONDITIONS OF CORRECTNESS OF MODELLING OF NON-LINEAR AND REVERSIBLE MATRIX PROCESSES BY THE DELAY EQUATION

G-9

I.S. Yevshin^{1,2}, R.N. Sharipov^{1,2,3}, Yu.V. Shatalin⁴, A.A. Naumov⁴, G.L. Ermakov⁴, M.M. Potselueva⁴, T.K. Sukhomlin⁴

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THE MODEL OF TRANSFERRIN UPTAKE BY CELL: A NOVEL MODE OF TFR2-MEDIATED IRON SEQUESTRATION IN OXIDATIVE STRESS

HIGH-PERFORMANCE COMPUTING IN BIOINFORMATICS

H-1

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OPENMP+MPI PARALLEL IMPLEMENTATION OF THE "MOLKERN" MOLECULAR MODELLING SOFTWARE PACKAGE

H-2

A.A. Dibert, A.Yu. Palyanov*

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COMPUTER SIMULATION OF *C. ELEGANS* MUSCULAR SYSTEM AND NEURAL NETWORK

H-3

A.S. Karyagina^{1*}, A.S. Ershova^{1,2}, R.N. Nurtdinov², M.O. Vasiliev³, A.B. Merkov⁴, I.S. Lossev⁵

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MALE/FEMALE DISCRIMINATION: USAGE OF PROBE-LEVEL AFFYMETRIX EXPRESSION DATA

H-4

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A GRID ORIENTED EVOLUTION STRATEGY TO APPROACH THE PARAMETER ESTIMATION PROBLEM IN SYSTEMS BIOLOGY MODELS

NANOBIOENGINEERING

I-1

A.I. Davidovskii, V.G. Veresov*

Institute of Biophysics and Cell Engineering NASB, Minsk, Belarus

MONTE CARLO SIMULATIONS OF THE 3D STRUCTURE OF THE PROTEIN BAK ASSOCIATED WITH MITOCHONDRIAL OUTER MEMBRANE

I-3

E.V. Dmitrienko^{1,2}, I.A. Pyshnaya¹, M.N. Repkova¹, A.S. Levina¹, Y.S. Gashnikova³, M.R. Kabilov¹, D.V. Pyshnyi^{1,2*}, V.F. Zarytova¹

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²Novosibirsk State University, Russia

³State center of virology and biotechnology "Vector", Koltsovo, Russia

UNIVERSAL METHOD FOR REVEALING OF DRUG-RESISTANT FORMS OF HIV-1

I-4

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SELECTIVITY OF ALLELE SPECIFIC HYBRIDIZATION OF DNA PROBES

I-5

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3-D MODEL FOR AGROBACTERIAL T-DNA-BINDING VIRE2 PROTEIN

I-6

S.V. Rahmanov*, V.Y. Makeev

GosNIIGenetika Research Institute, Moscow, Russia

EMPIRICAL POTENTIALS FOR INTERACTION OF PROTEINS WITH WATER MOLECULES AND IONS

MICROSYMPOSIUM "GENETIC COLLECTIONS AND BIODIVERSITY OF CULTIVATED PLANTS: PRODUCING, PRESERVATION AND CRYOCONSERVATION"

June 27, Friday

Institute of Cytology and Genetics, Conference Hall

12:05-14:00

A.Artemyeva¹, Y.Chesnokov¹, E.Klocke²

¹ N.I.Vavilov Institute of Plant Industry (VIR), S-Petersburg, Russia

²Institute of Horticultural Crops, Erwin-Baur-Str.27, D-06484 Quedlinburg, Germany

GENETIC DIVERSITY OF BRASSICA RAPA CROPS AND THEIR RELATIONSHIPS USING SSR MARKERS

E.D. Badaeva

Engelhardt Institute of Molecular Biology RAS, Moscow, Russia

DEVELOPMENT OF A NEW APPROACH TO STUDY INTRASPECIFIC DIVERGENCE IN WHEAT ON THE BASIS OF CHROMOSOME ANALYSIS

J.V. Chudinova, G.A. Michkina, G.A. Popova, L.N. Rogdestvina, N.A. Arhipov

Tomsk State University, Tomsk, Russia

GENETIC VARIETY OF FLAX TOMSK SELECTION SORTS

M. Dshunusova

Kyrgyz Agricultural Co-Operative "MIS", Kyrgyzstan

GENETICS METHODS OF WHEAT IN KYRGYZSTAN

A.A. Konovalov, E.A. Moisseeva, E.Ya. Kondratenko, A.I. Shchapova

Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia

ENZYME POLYMORPHISM IN GENETIC COLLECTIONS OF *TRITICUM AESTIVUM*, *SECALE CEREALE*, THE RYE -WHEAT SUBSTITUTION LINES AND THE *TRITORDIUM* ACCESSIONS WITH DIFFER RATIO OF PARENTAL GENOMES

T.V. Lebedeva, E.V. Zuev

N.I. Vavilov All-Russian Research Institute of Plant Industry, St. Petersburg, Russia
GENETIC DIVERSITY OF TRITICUM AESTIVUM L. ON POWDERY MILDEW RESISTANCE (*BLUMERIA GRAMINIS* DC. F. SP. *TRITICI* GOLOVIN)

E.G. Pestsova

Heinrich-Heine-University, Germany
SEED QUALITY MODIFYING TREATMENTS, LIKE PRIMING AND DETERIORATION, CAUSE CHARACTERISTIC CHANGES OF GENE EXPRESSION PROFILES IN SUGAR BEET SEEDS (*BETA VULGARIS* L.)

E.P. Razmakhnin

Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
GENEPOL OF AGROPYRUM GLAUCUM AS RESOURCES OF INCREASING WHEAT BIODIVERSITY

B.V. Rigin, V.A. Koshkin, Nguen Din Lam, I.I. Matvienko

N.I. Vavilov All-Russian Research Institute of Plant Industry, St. Petersburg, Russia
THE GENES *EPS*, CONTROLLING ULTRA-EARLINESS OF WHEAT TRITICUM AESTIVUM L. THEIR EXPRESSION AND EVOLUTION

Y.N. Shavrukov

Australian Centre for Plant Functional Genomics, Australia
BIODIVERSITY OF SALINITY TOLERANCE IN WHEAT AND BARLEY FROM DIFFERENT GENE BANK COLLECTIONS

O.G. Silkova

Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
WHEAT-RYE SUBSTITUTION LINES AS THE MODEL FOR INVESTIGATION MEIOTIC RESTITUTION - A POTENT EVOLUTIONARY FORCE

S.E. Smolenskaya, E.V. Kvasova, O.E. Redina

Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
USING OF MOLECULAR MARKERS FOR POLYMORPHISM STUDYING IN PERENNIAL CV. OMSKAJA 192 POPULATION

M.A. Vishnyakova

Vavilov Institute of Plant Industry, St-Petersburg, Russia
GENETIC DIVERSITY INVESTIGATION AND PASPORTIZATION OF REPRESENTATIVES TRIBE VICIEAE (ADANS.) BRONN FROM VIR COLLECTION BY MEANS OF RAPD-ANALYSIS

N. Watanabe

College of Agriculture, Ibaraki University, Ami, Inashiki Ibaraki, Japan
GENETIC COLLECTION AND DEVELOPMENT OF NEAR-ISOGENIC LINES IN WHEAT

COMPUTER DEMONSTRATIONS (BY SECTIONS)

Computer demonstrations will be held on **June 26** from 14:00 to 16:00 in the Small Conference Hall Foyer.

GENOMICS AND TRANSCRIPTOMICS

N. Ju. Oparina

Engelhardt Institute of Molecular Biology RAS, Moscow, Russia
EST-BASED ANALYSIS OF HUMAN CANCERS TRANSCRIPTOME

PROTEOMICS

A.S. Chirtsov¹, E.S. Fomin^{2*}

¹ Novosibirsk State University, Novosibirsk, Russia

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AN ALGORITHM FOR PROTEIN CONFORMATIONAL FLEXIBILITY PREDICTION

I.V. Dobrokhotov

Institute of Medicobiological. Problems RAS (IMBP), Moscow, Russia

T.V. Kirys^{*1,2}, A.V. Tuzikov¹, D.K. Voytekhovsky¹, Y.E. Grushetsky¹

¹United Institute of Informatics Problems BAS, Minsk, Belarus

²Belarusian State University, Minsk, Belarus

PREDICTION OF PROTEIN INTERACTIONS USING HOMOLOGOUS INTERFACES

S. Ramachandran^{*}, R. Gorai[§], S. Ahmed[§], F.A. Ansari[§]

G.N. Ramachandran Knowledge Centre for Genome Informatics, Institute of Genomics and Integrative Biology, Delhi, India

MALVAC: DATABASE OF MALARIAL VACCINE CANDIDATES

EVOLUTIONARY AND POPULATION COMPUTATIONAL BIOLOGY

D.M. Larkin^{1,2}, M.V. Tarasova³, N.S. Zhdanova^{1*}

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² Laboratory of Mammalian Genome Biology, University of Illinois, Urbana, IL

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ANCESTRAL ARCHITECTURE OF THE HUMAN CHROMOSOME 17 SYNTENY GROUP IS NON-RANDOMLY MAINTAINED IN MOUSE CHROMOSOME 11.

INTELLIGENT DATA ANALYSIS AND PATTERN RECOGNITION IN BIOINFORMATICS

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² Physical-Technical Institute of NTUU "KPI", Kiev, Ukraine

A PROTOCOL TO DEMONSTRATE SEQUENCE MATCHING

COMPUTER ANALYSIS AND IMAGE RECOGNITION IN SYSTEMS BIOLOGY

Yu.S. Bukin^{*}, A.V. Natyaganova

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«KARYOSTATANALYSIS» - A SOFTWARE FOR CHROMOSOMAL SETS MORPHOMETRIC ANALYSIS

I. Glotova*¹, V. Lyubetsky²

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CLASSICAL ATTENUATION REGULATION MODEL

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BMOND – A NEW APPROACH TO FORMALIZED DESCRIPTION AND SIMULATION OF BIOLOGICAL SYSTEMS

HIGH-PERFORMANCE COMPUTING IN BIOINFORMATICS

M. Fursov *¹, O. Novikova²

¹Novosibirsk Center of Information Technologies ‘UniPro’

MULTITASKING SOFTWARE SYSTEM FOR DNA ANALYSIS