ESF Conference 2010
Poster Programme

	Bioinformatics
[P1.01]	**APOBEC1 editing of HIV1 RNA often leads to the destruction of linear B-cell epitopes: Case study of *env* gene region coding for gp120 protein** V.V. Khrustalev*[1], E.V. Barkovsky[1], [1]*Belarussian State Medical University, Belarus*
[P1.02]	**Identifying and analysing conserved modules in metabolic networks between different mycoplasma species** A. Gómez*[1], J. Cedano[1], E. Querol[1], [1]*Institut de Biotecnologia i Biomedicina, Spain,* [2]*Universitat Autònoma de Barcelona, Spain*
[P1.05]	**Structural fragment clustering reveals novel structural and functional motifs in alphahelical transmembrane proteins** A. Marsico*[1], A. Henschel[1], C. Winter[1], A. Tuukkanen[1], B. Vassilev[1], K. Scheubert[1], [1]*Biotechnology Center TU dresden, Germany*
[P1.07]	**Unraveling the structure and evaluating the quality of protein networks with power graph analysis** L.A. Royer*[1], M. Reimann[1], A.F. Stewart[1], M. Schroeder[1], [1]*Biotec, Germany*
[P1.10]	**Clusters of transcription start sites in human genomes exhibit a biased orientation of Sp1 binding site towards the template strand** Y. Medvedeva*[1], A. Favorov[1,2], N. Oparina[3], V. Makeev[1,3], [1]*GosNIIgenetika, Russia,* [2]*The Sidney Kimmel Comprehensive Cancer Center at Johns Hopkins, USA,* [3]*Engelhardt Institute of Molecular Biology, USA*
[P1.11]	**Prediction of disease-associated single nucleotide polymorphisms mapping on to human proteins** V. Acharya*, H.A. Nagarajaram, *Centre For DNA Fingerprinting and Diagnostics, India*
[P1.12]	**Evolution of glyceraldehyde-3-phosphate dehydrogenase family in deuterostomia** M.L. Kuravsky*, V.I. Muronetz, E.V. Schmalhausen, *Moscow State University, Russia*
[P1.14]	**Discovery and prioritization of human cellular factors required for HCV infection** H. Blankenburg*[1], S. Diehl[1], F. Ramírez[1], I. Wörz[2], M. Poenisch[2], R. Bartenschlager[2], [1]*Max Planck Institute for Informatics, Germany,* [2]*University of Heidelberg, Germany*
[P1.17]	**Prediction of enzyme classes in a hierarchical approach by using spmap** A. Yaman[2], V. Atalay[2], R. Atalay*[1], [1]*Bilkent University, Turkey,* [2]*Middle East Technical University, Turkey*
	Other
[P1.18]	**Comparative genomics reveals preferential distribution and domain organization of FYVE and PX domain proteins across eukaryotic lineages** S. Banerjee[1], S. Basu[2], S. Sarkar*[1], [1]*Indian Institute of Science Education and Research, India,* [2]*West Bengal University of Technology, India*
[P1.20]	**Genetic and epigenetic variation and toxicity and/or outcome during therapy in childhood acute lymphoblastic leukemia** E. Lopez-Lopez*[1], I. Martin-Guerrero[1], J. Ballesteros[1], J. Uriz[2], N. Garcia de Andoin[2], M.A. Pinan[3], [1]*University of the Basque Country, Spain,* [2]*Hospital Donostia, Spain,* [3]*Hospital de Cruces, Spain,* [4]*Hospital La Paz, Spain*
[P1.21]	**The comparison of the DNA ploidy distribution pattern in canine inflammatory lesions, benign tumors, sarcomas, and malignant thymomas** K.M. Boerkamp*[1], G.R. Rutteman[1], G. Grinwis[1], N.J. Kuipers-Dijkshoorn[1], C. Schulze[1], C.J. Cornelisse[1], [1]*Utrecht University, Netherlands,* [2]*University Medical Centre, Netherlands*
[P1.22]	**Characterization of altered process and protein modification in patients affected by inflammatory myopathies** S. Cagnin*[1], S. De Palma[2,3], P. Martini[1], C. Borsato[1], G. Sales[1], M. Vasso[2], et al [1]*University of Pavova, Italy,* [2]*CNR, Milan, Italy,* [3]*University of Milan, Italy,* [4]*University of Bologna, Italy*
[P1.24]	**Polymorphic retroelements - a useful tool for human genetic studies** I.Z. Mamedov*[1], S.V. Ustyugova[1], D.A. Shagin[1], Y.B. Lebedev[1], [1]*Shemiakin-Ovchinnikov Institute of Bioorganic Chemistry RAS, Russia*
[P1.25]	**Molecular characterization of carboxypeptidase B (CPB) of *An.stephensi* with respect to TBV strategy in states under WHO/EMRO** A. Raz*[1], N. Dinparast Djadid[1], S. Zakeri[1], [1]*Pasteur Institute of Iran, Iran*
[P1.28]	**The plumage colour Dark Brown in chicken is caused by an 8 kb deletion upstream of SOX10** S. Kerje*[1], [1]*Uppsala University, Sweden,* [2]*UMR Genetique et Diversite Animales, France,* [3]*Uppsala University, Sweden*

[P1.29]	**Improving manual genome annotation: Challenges and opportunities of new technologies** L.G. Wilming*, G. Saunders, M. Brosch, A. Frankisch, J.L. Harrow, *Wellcome Trust Sanger Institute, UK*
[P1.30]	**Ciliates as models to study diversities in microtubule functions by functional genomics** S. Pucciarelli, P. Ballarini, S. Barchetta, D. Sparvoli*, M. Montani, C. Miceli, *University of Camerino, Italy*
	RNA World
[P1.31]	**Identification of genes involved in cisplatin resistance by screening of an shRNA library generated by several enzymatic steps** D. Hertfelder*, T. Hees, K.A. Boehme, *University of Tübingen, Germany*
[P1.32]	**Co-transcriptional spliceosome assembly on mammalian model genes** N.I. Bardehle*, K.M. Neugebauer, *Max Planck Institute of Molecular Cell Biology and Genetics, Germany*
[P1.33]	**MicroRNA and cancer progression in breast tumours** C. De Pittà*[1], D. Cimino[2], E. Pinatel[2], S. Casara[1], M. Zampini[1], C. Romualdi[1], *[1]University of Padova, Italy, [2]University of Torino, Italy*
[P1.34]	**Conservation and evolution of tRNA transcription in mammals** C. Kutter*[1,2], G.D. Brown[1,2], S.B. Watt[1,2], D.T. Odom[1,2], *[1]Cambridge Research Institute, UK, [2]University of Cambridge, UK*
[P1.35]	**Identification of targets of microRNA-21 by 2-DIGE analysis** K. Schramedei*[1], N. Mörbt[2], M. von Bergen[2], F. Horn[1], K. Brocke-Heidrich[1], *[1]University of Leipzig, Germany, [2]UFZ-Helmholtz-Centre for Environmental Research, Germany*
[P1.36]	**Genome-wide expression profile associated with renal aging** S.J. Noppert*[1], M. Rudnicki[1], J. Enrich[1], P. Perco[2], I. Muehlberger[2], G. Mayer[1], *[1]Medical University Innsbruck, Austria, [2]emergentec biodevelopment GmbH, Austria, [3]Medical University of Vienna, Austria*
[P1.37]	**MiR-101 is dysregulated in malignant melanoma and targets MITF** C. Luo*, P. Merz, D. Schadendorf, S.B. Eichmüller, *German Cancer Research Center, Germany*
[P1.38]	**A set of tolerance values for identifying shared motifs in RNA tertiary structures** Z.U.A. Khuhro*, A.P. Harrison, *University Of Essex, UK*
[P1.39]	**Mirnas in huvecs: Differential microRNA expression in replicative vs stress-induced premature cell senescence.** S. Mariotti*[1,2], F. Olivieri[3], R. Recchioni[1], F. Marcheselli[1], A.D. Procopio[1,3], *[1]Center of Clinical Pathology and Innovative Therapies, Italy, [2]University of Camerino, Italy, [3]Polytechnic University of Marche, Italy*
	Sequencing and other high throughput technologies
[P1.40]	**Integrated analysis of ERBB receptor activation and downstream signaling with EXTassays** A. Botvinnik*, S.P Wichert, T.M. Fischer, M.J. Rossner, *Max Planck Institute for Experimental Medicine, Germany*
[P1.41]	**Screening genomic libraries by recombineering** M. Nedelkova*, F. Stewart, *Biotechnology Center, Germany*
[P1.42]	**High-throughput function-based gene identification using enzymatically generated short hairpin RNA library and massive parallel sequencing** M. Shtutman*[1], A. Maliyekkel[1], E. Levina[1], P. Ohouo[1], Y. Shao[2], S. Carmack[2], *[1]Ordway Research Institute, USA, [2]New York State Department of Health, USA*
[P1.43]	**Alu insertion site profiling in the human genome** M. Cardelli*[1], F. Marchegiani[1], C. Franceschi[2], F. Lattanzio[3], M. Provinciali[1], *[1]Italian National Research Center on Aging, Italy, [2]University of Bologna, Italy, [3]Roma, Italy*
[P1.44]	**Synthesis of four colour labelled reversible terminators useful in array based sequencing-by-Synthesis** J. D'Onofrio*[1], D.C. Knapp[1], A. Keller[1], A. Lubys[2], S. Serva[2], J.W. Engels[1], et al, *[1]J. W. Goethe Universität, Germany, [2]Fermentas UAB, Lithuania, [3]Asper, Estonia, [4]University of Tartu, Estonia*
[P1.45]	**Tissue-specific transcript annotation and expression profiling with complimentary next-generation sequencing technologies** M.S. Hestand[1], A. Klingenhoff[2], M. Harbers[3], G.J.B. Van Ommen*[1], J.T. Den Dunnen[1], P.A.C. 't Hoen[1], *[1]Leiden University Medical Center, Netherlands, [2]Genomatix Software GmbH, Germany, [3]DNAFORM Inc, Japan*
[P1.46]	**Highly sensitive detection of genomic instability by ultradeep sequencing** A. De Grassi*[1], C. Segala[1], F. Iannelli[1], S. Volorio[2], P. Radice[2,3], F.D. Ciccarelli[1], *[1]European Institute of Oncology, Italy, [2]IFOM, Italy, [3]Fondazione IRCCS Istituto Nazionale dei Tumori, Italy*

[P1.47]	**The role of sequence analysis of wild-type varicella-zoster virus (VZV) in epidemiological and evolutionary characterization of VZV: Focus on epidemiologic situation in Czech Republic** V. Bostikova*[1], [1]*University of Defence, Czech Republic,* [2]*Charles University, Czech Republic*
[P1.50]	**Improving the quality of DNA libraries in the next-generation sequencing workflow** R. Salowsky*[1], M. Gassmann[1], S. Glueck[1], [1]*Agilent Technologies, Germany*
[P1.51]	**Both copy number and sequence variation determine expression of human DEFB4** K. Huse[1], M. Groth[1], C. Wiegand[2], K. Szafranski[1], P. Rosenstiel[3], M. Platzer*[2], [1]*Leibniz Institute for Age Research Jena, Germany,* [2]*Friedrich Schiller University Jena, Germany,* [3]*Institute of Clinical Molecular Biology Kiel, Germany*
[P1.52]	**Motif discovery for transcription factor binding sites using a priori information on potential similarity regions at different resolution scales** I.V. Kulakovskiy*[1], V.A. Boeva[1,2], A.V. Favorov[1,3], V.J. Makeev[1], [1]*State Scientific Institute of Genetics and Selection of Industrial Microorganisms, Russia,* [2]*Curie Institute, France,* [3]*The Sidney Kimmel Comprehensive Cancer Center at Johns Hopkins, USA*
[P1.53]	**"Proteome scale" in vitro antibody selections - Lessons from pilot projects and use of the antibody genes for functional genomics** J. Mersmann*, *Technical University Braunschweig, Germany*
	Systems biology
[P1.54]	**Length of exons and introns in protozoa genes** A.A. Kabdullina*[1], A.T. Ivachshenko[1], [1]*Al-Farabi Kazakh National University, Kazakhstan*
[P1.55]	**Twin research in functional genomics: More than just two-pronged** A. Busjahn*, *HealthTwiSt GmbH, Germany*
[P1.57]	**The ERGoncogene modulates WNT signaling and cell adhesion in human prostate cancer cells** S. Gupta*[1,2], K. Ilkin[1,2], H. Sara[1], M. John[4], T. Mirtti[2], P. Vanio[1,2], [1]*VTT Medical Biotechnology, Finland,* [2]*University of Turku, Finland,* [3]*Institute for Molecular Medicine, Finland*
[P1.58]	**An integrative network based approach to analyze type 2 diabetes** B. Coskunkan*[1], D. Rende[1,2], N. Baysal[1], B. Kirdar[2], [1]*Yeditepe University, Turkey,* [2]*Bogazici University, Turkey*
[P1.59]	**A molecular systems biomedicine approach to diabetes: Characterization, prioritization and network analysis of new candidate genes from the apoptotic machinery** D. Barbagallo*[1], S. Piro[1], M. Ragusa[1], C. Di Pietro[1], F. Purrello[1], M. Purrello[1], [1]*Università di Catania, Italy*
[P1.61]	**Protein domain cooccurences reveal functional changes of regulatory mechanisms during evolution** A.A. Parikesit*, S. Prohaska, P. Stadler, *University of Leipzig, Germany*
[P1.62]	**Improved modulon identification from bacterial gene expression array data using operon-based correlation reference set** S. Hedge[1], E.A. Permina*[2], Y.A. Medvedeva[2], S.C. Mande[1], V.J. Makeev[1,3], [1]*The Centre for DNA Fingerprinting and Diagnostics (CDFD), India,* [2]*State Research Center of Genetics and Selection of Industrial Microorganisms, Russia,* [3]*Russian Academy of Sciences, Russia*
[P1.63]	**Mutated genes, pathways and processes in tumours** A. Baudot*, A. Valencia, *Spanish National Cancer Research Centre (CNIO), Spain*
[P1.64]	**Systems biology of nuclear hormone receptors in caenorhabditis** M. Kostrouchova*, Z. Kostrouch, *Charles University in Prague, Czech Republic*
[P1.65]	**Reconstruction of a genome-wide protein-protein functional linkage map: A computational approach to study cellular physiology** V.Y. Muley*, A. Ranjan, *Centre for DNA Fingerprinting and Diagnostics, India*
[P1.66]	**Identification of composite elements in eukaryotic transcription regulatory regions using protein-protein interaction data** A.A. Belostotsky*[1], I.V. Kulakovskiy[1], V.J. Makeev[1], [1]*State Research Center of Genetics and Selection of Industrial Microorganisms, Russia*
	Transcriptomics
[P1.68]	**Studying the functions of yeast Sac3p using functional genomics** P. Palit*[1], A. Koehler[1,2], O. Antúnez[1], V. Pelechano[1], J.E. Perez-Órtin[1], E. Hurt[1,2], [1]*Universitat de Valencia, Spain,* [2]*Universität Heidelberg, Germany*

[P1.69]	**Quantitative analysis of gene expression in porcine articular cartilage from healthy and osteochondrosis joints** W. Laenoi[1], M.U. Cinar*[1], D. Tesfaye[1], H. Juengst[1], A.M. Scholz[3], E. Tholen[1], *[1]University of Bonn, Germany, [2]Fakultät der Ludwig-Maximilians-Universität, Germany, [3]University of Bonn, Germany*
[P1.70]	**Pathogen load and expression of immune-related genes in mesenteric lymph-nodes of pigs experimentally infected with *Salmonella Typhimurium*** R.P. Martins*[1], M. Collado-Romero[1], C. Arce[1], J.J. Garrido[1], *[1]University of Córdoba, Spain*
[P1.72]	**Unsynapsed chromatin, meiotic transcriptional silencing and intrameiotic arrest of spermatogenesis in mouse interspecific hybrids** T. Bhattacharyya*[1], P. Simecek[1], S. Gregorova[1], M.A. Handel[2], J. Forejt[1], *[1]Institute of Molecular Genetics AS CR, Czech Republic, [2]The Jackson Laboratory, USA*
[P1.73]	**Mapping of a trans-acting regulatory locus of bone gamma carboxyglutamate protein-related sequence 1 (Bglap-rs1) mRNA levels in mouse chromosome substitution strains** M. Dzur-Gejdosova*, P. Simecek, I. Chvatalova, J. Forejt, *Institute of molecular genetics, Czech Republic*
[P1.74]	**Type 1 diabetes and graves' disease transcriptomic analysis show common contibuting disease pathways** M. Ruiz, R. Planas, R. Colobran*, A. Marín, M. Vives, R. Pujol-Borrell, *Universitat Autònoma de Barcelona (UAB), Spain*
[P1.77]	**Comparison of testicular transcriptome between two mouse species shows dysregulation of protein-non-coding RNAs and confirms continuous evolution of the X chromosome** D. Homolka*, R. Ivanek, J. Forejt, P. Jansa, *Academy of Sciences of the Czech Republic, Czech Republic*
[P1.78]	**The effect of different statins on gene expression profile of human hepatoma cells** A. Leszczynska*[1], G. Hoser[3], M. Kotlinski[1,2], M. Prymakowska-Bosak[1,2], A. Szkopinska[1], B. Burzynska[1], *[1]Polish Academy of Sciences, Poland, [2]University of Warsaw, Poland, [3]The Medical Centre of Postgraduate Education, Poland*
[P1.79]	**Endometrial gene expression analysis in infertile women in natural vs artificial cycles** S. Altmäe*[1,2], J.A. Martinez-Conejero[3], F.J. Esteban[4], A. Salumets[2], J.A. Horcajadas[3], A. Stavreus-Evers[5], *[1]Karolinska Institutet, Sweden, [2]University of Tartu, Estonia, [3]iGenomix, Spain, [4]University of Jaén, Spain, [5]Uppsala University, Sweden*
[P1.80]	**Two subtypes of serous ovarian cancer with different gene expression pattern** K. Lisowska*[1], M. Olbryt[1], M. Jarzab[1], K. Simek[2], E. Nowara[1], J. Kupryjanczyk[1], *[1]Maria Sklodowska-Curie Memorial Center, Poland, [2]Silesian University of Technology, Poland*
[P1.82]	**Transcriptional differences in genes regulating atrial fibrosis and mitochondrial energetics in patients at risk of development of atrial fibrillation** C. Preston, A. Gupta, S. Sultan, V. Maria, A. Jahangir*, *Mayo Clinic, USA*
	RNA world
[P1.83]	**Non-coding RNAs controlled in cell cycle and cancer related pathways** K. Reiche*[1], L. Böhlig[2], K. Schutt[1,2], A.K. Kretzschmar[3], K. Engeland[2], J Hackermüller[1,2], *[1]Fraunhofer Institute for Immunology and Cell Therapy, Germany, [2]University of Leipzig, Germany, [3]Universität München, Germany*
	Disease specific studies
[P2.01]	**Molecular markers development for early diagnostics of human colon cancer** A.A. Kabdullina*, O. A. Berillo, V. A. Khailenko, A.S. Achsheulov, M.K. Tauasarova, S.A. Atambayeva, *Al-Farabi Kazakh National University, Kazakhstan*
[P2.02]	**Atopy controlling loci in Czech and Russian populations** E.S. Gusareva*[1], J. Badalová[1], H. Havelková[1], E.J. Bragina[2], L.M. Ogorodova[3], M. Lipoldová[1], *[1]Academy of Sciences of the Czech Republic, Czech Republic, [2]Russian Academy of Medical Sciences, Russia, [3]Siberian State Medical University, Czech Republic*
[P2.03]	**Early age of onset, more primary malignancies, and worse prognosis are indicative of inherited predisposition to oesophageal squamous carcinoma for the familail as opposed to the sporadic cancer form** S. Wang*, D. Wen, L. Zhang, Y. Cao, L. Wei, W. Yu, *4th Hospital of Hebei Medical University, China*
[P2.04]	**Comparison of epidemiological features between oesophageal squamous carcinoma and adenocarcinoma at the oesophagogastric junction in a surgical cohort for genetic revelation from a chinese high-risk area** D. Wen*, S. Wang, L. Zhang, W. Yu, L. Wei, W. Zou, *4th Hospital of Hebei Medical University, China*

[P2.05]	**Spinal muscular atrophy: Oxidative stress modulating the pathogenesis?** A.S. Köstel*, G. Bora-Tatar, H. Erdem-Yurter, *Hacettepe University Medical Faculty, Turkey*
[P2.06]	**Expression profiling of defined projection neurons and oligodendrocytes in dys- and demyelinated genetic mouse models** S.P. Wichert*, K.A. Nave, M.J. Rossner, *Max Planck Institute, Germany*
[P2.07]	**Genetics and genomics of leishmaniasis** V.S. Volkova*[1], M. Slapnicková[1], T. Kobets[1], H. Havelková[1], P. Demant[2], M. Lipoldová[1], *[1]Academy of Sciences of the Czech Republic, Czech Republic, [2]Roswell Park Cancer Institute, USA*
[P2.09]	**ERGIC2, a new member of the OTOF interactome connected with the DFNB9 form of hearing impairment** M. Zak*, A. Bress, M. Pfister, M. Knipper, N. Blin, *University of Tuebingen, Germany*
[P2.10]	**Leigh syndrome leads to severe defects in the incorporation of Atp6p within the ATP synthase and mitochondrial morphology in Saccharomyces cerevisiae** R Kucharczyk*[1,2], B.S. Salin[1], J.P. di Rago[1], *[1]Institut de Biochimie et Génétique Cellulaires CNRS, France, [2]Institute of Biochemistry and Biophysics PAS, Poland*
[P2.11]	**Comparative analysis of cancer related signalling pathways in humans and zebrafish** R.A. Gadkari*, N. Srinivasan, *Indian Institute of Science, India*
[P2.12]	**Involvement of KIR3D receptor functional variants in ankylosing spondylitis initiation** I.V. Zvyagin*, I.Z. Mamedov, A.V. Chkalina, D.M. Chudakov, S.A. Lukyanov, Y.B. Lebedev, *Shemiakin-Ovchinnikov Institute of Bioorganic Chemistry RAS, Russia*
[P2.15]	**A genetic screen for mutations in genes, interacting with fragile x mental retardation 1 in drosophila melanogaster (DFMR1)** D. Georgieva*, G. Genova, *University of Sofia, Bulgaria*
[P2.16]	**TBX1 gene structure among patients with thyroid hemiagenesis in polish population** E. Szczepanek, M. Ruchala, M. Jaroniec*, W. Szaflarski, M. Zabel, J. Sowinski, *Poznan University of Medical Sciences, Poland*
[P2.17]	**Analysis of patients with renal hypouricemia in Czech population** B. Stiburkova*[1], I. Sebesta[1,2], K. Ichida[4], M. Hosoyamada[3], *[1]Charles University in Prague, Czech Republic, [2]Institute of Clinical Biochemistry and Laboratory Medicine, Czech Republic, [3]Keio University, Japan, [4]Tokyo University, Japan*
[P2.18]	**BDNF Val66Met polymorphism is not associated with coronary atherosclerosis in Czech patients** M Petrek*[1,2], N Motakova[1], A Stahelova[1], F Mrazek[1], J Petrkova[1,2], *[1]Palacky University, Czech Republic, [2]Hospital Olomouc, Czech Republic*
[P2.19]	**A direct link between growth retardation and inflammation? Identification of a splice mutation in the bovine RNF11 gene** A. Sartelet, C. Fasquelle, N. Tamma, W. Coppieters, M. Georges, C. Charlier*, *University of Liège, Belgium*
[P2.21]	**Elucidating the chromatin architecture of loci associated with blood traits and coronary artery disease** D.S. Paul*[1], N. Soranzo[1,2], W.H. Ouwehand[1,3], P. Deloukas[1], *[1]Wellcome Trust Sanger Institute, UK, [2]King's College London, UK, [3]University of Cambridge and National Health Service Blood and Transplant, UK*
[P2.22]	**Prospective validation of a prognostic gene expression signature and identification of EGFR as a drug target in uveal melanoma** V. Mirisola*[1], P. Perri[1], S. Coupland[4], C. Mosci[3], M. Truini[2], U. Pfeffer[1], *[1]National Cancer Research Institute, Italy, [2]National Cancer Research Institute, Italy, [3]National Cancer Research Institute, Italy, [4]University of Liverpool, UK*
[P2.23]	**Deficiency in the glycolytic enzyme GAPDS in sperms with dysplasia of fibrous sheath** Y.L. Elkina*, E.E. Bragina, E.V. Schmalhausen, *Moscow State University, Russia*
[P2.24]	**Detailed analysis of chromosome rearrangements in patients with autism and mental retardation** Z. Sedlacek*[1], M. Vlckova[1], M. Hancarova[1], J. Drabova[1], Z. Zmitkova[1], P. Hedvicakova[1], *[1]Charles University, Czech Republic, [2]University Hospital Motol, Czech Republic*
[P2.25]	**The investigation of CD36 scavenger receptor and MSR1 scavenger receptor gene expression level in patients with atherosclerosis** M. Piechota*[1], A. Banaszewska[1], E. Guzniczak[2], G. Rosinski[1], T. Siminiak[2], R. Plewa[1], *[1]Adam Mickiewicz University, Poland, [2]Poznan University of Medical Sciences, Poland*

[P2.27]	**Characterization of mtor kinase activity induced by kainic acid evoked seizures** M. Blazejczyk*[1,2], M. Macias[1,2], M. Piechota[3], M. Korostynski[3], R. Przewlocki[3], J. Jaworski[1], *[1]International Institute of Molecular and Cell Biology, Poland, [2]Nencki Institute of Experimental Biology, Poland, [3]Institute of Pharmacology, Poland*
[P2.28]	**ZNF750 is a nuclear protein whose promoter sequence variants are found in psoriasis patients** I. Cohen[1], R.Y. Birnbaum[1], A.M. Bowcock[2], S. Sivan[1], O.S. Birk*[1], *[1]Ben Gurion University, Israel, [2]Washington University School of Medicine, USA*
[P2.29]	**MicroRNA expression profile and network in colorectal carcinoma after chemotherapy** M. Ragusa[1], A. Majorana[1], L. Statello[1], D. Barbagallo*[1], C. Di Pietro[1], M. Purrello[1], *[1]Sezione di Biologia Generale, Italy*
[P2.30]	**Unique spectrum of spast variants in estonian hsp patients: Presence of benign missense changes but lack of exonic rearrangements** R. Tamm*[1], M. Braschinsky[2], C. Beetz[2], E. Sachez-Ferrero[1], *[1]University of Tartu, Estonia, [2]University Hospital Jena, Germany, [3]Hospital Central Universitario de Asturias, Spain, [4]Estonian Biocentre, Estonia*
[P2.32]	**RNA-interference based screen identifies new factors important for NF-kappaB activation and termination** S. Bartfeld*[1], C. Rechner[1], B. Bauer[1], S. Hess[1], A. Maeurer[1], N. Machuy[1], *[1]Max Planck Institute for Infection Biology, Germany*
[P2.33]	**Towards a genetic screening test for dyslexia allowing functional regeneration: A strategy for identification and analysis of genetic risk factors** K. Holger*[1,2], A. Wilke[1,2], P. Ahnert[3], J. Boltze[1], *[1]TRM Leipzig, Germany, [2]IZI Fraunhofer Leipzig, Germany, [3]IMISE, Germany*
	Epigenetics
[P2.35]	**Conserved elements in imprinted genes** B. Hutter*, M. Bieg, V. Helms, M. Paulsen, *Saarland University, Germany*
[P2.36]	**Differential allelic expression of genes associated with asthma** J. Burkhardt*[1], H. Kirsten[2,3], G. Wolfram[3], E. Quente[2,3], P. Ahnert[4], *[1]University Leipzig, Germany, [2]Fraunhofer IZI Leipzig, Germany, [3]TRM Leipzig, Germany, [4]IMISE Leipzig, Germany*
[P2.37]	**Histone H3 lysine 4 methyltransferase hybrid sterility 1 (Hst1/Prdm9/Meisetz) activates small RNA genes** P. Flachs*, Z. Trachtulec, O. Mihola, P. Simecek, J. Forejt, *Institute of Molecular Genetics, ASCR, Czech Republic*
[P2.38]	**Copy number variations and chromatin structure** R.M. Witwicki*, G. Didelot, C. Howald, L. Harewood, A. Reymond, *University of Lausanne, Switzerland*
[P2.39]	**Loss of the histone methyltransferase Setd1a leads to embryonic lethality around gastrulation** A.S. Bledau*[1,2], A.F. Stewart[1], K. Anastassiadis[1,2], *[1]Centre for Regenerative Therapies Dresden, Germany, [2]Technische Universität Dresden, Germany*
	Proteomics
[P2.40]	**Lipopolysaccharide stimulation of swine neutrophils: A proteomic approach by time-course comparison** G. Sanz*, Á. Jimenez-Marin, Á. Moreno, J.J. Garrido, *University of Córdoba, Spain*
[P2.41]	**Increased reactive oxygen species formation in murine cardiac mitochondria after irradiation: A functional and proteomic analysis** Z. Barjaktarovic*[1], D. Schmaltz[1], O. Azimzadeh[1], A. Shyla[1], H. Zischka[1], J. Haagen[2], *[1]German Research Center for Enviromental Health, Germany, [2]Dresden University of Technology, Germany*
[P2.44]	**A label-free method identified differentially abundant proteins in related M.tuberculosis Beijing strains** G.A. De Souza[1], S. Fortuin*[2], et al *[1]University of Bergen, Norway, [2]Stellenbosch University, South Africa, [3]National Institute of Medical Sciences and Nutrition Salvador Zubiràn, Mexico, [4]University of Oslo, Norway, [5]University Hospital, Norway*
[P2.45]	**Antibody microarrays: Profiling cancer proteomes in a dual-colour mode** C. Schröder*, *Deutsches Krebsforschungszentrum, Germany*
[P2.46]	**Defining the role of the two distinct fragments of the histone methyltransferase Mll2 and their activities in regulating and maintaining mouse ES cells** H. Hofemeister*, J. Fu, K. Anastassiadis, F. Stewart, *TU-Dresden, Germany*

[P2.48]	**Molecular study of phytoplasma-lime interactions via proteomics approach** M. Alikhani*[1,2], S.M. Alavi[3], H. Askari[4], E. Majidi Heravan[2], M. Mardi[2], *[1]Royan Institute, Iran, [2]Agricultural Biotechnology Research Institute of Iran, Iran, [3]University of Agricultural Sciences and Natural Resources of Sari, Iran, [4]Shahid Beheshti University, Iran*
[P2.49]	**Biomarkers discovery for evidence-based Chinese medicines using the proteomic technology platform** W.C.S. Tai*[1], W.Y. Wong[1], J.F. Chiu[1], W.L.W. Hsiao[1], *[1]Hong Kong Baptist University, Hong Kong*
[P2.50]	**Multidimensional antibody array analysis** A. Holm*[1], W. Wu[1], H.S. Slaastad[1], L. Goullart[1], D. Carrillo[1], F. Lund-Johansen *[1]Oslo University Hospital, Norway, [2]Charles University Prague, Czech Republic*
[P2.51]	**Specific detection of proteins by immunoprecipitation combined with high sensitivity protein sizing on microchips** C. Wenz[1], E. Herwig[2], M. Marchetti-Deschmann[2], G. Allmaier[2], A. Ruefer[1], R. Salowsky*[1], *[1]Agilent Technologies, Germany, [2]Vienna University of Technology, Austria*
[P2.52]	**Proteome profiling in the elucidation of the modulation role of cathepsin B cysteine proteases in leishmnia donovani parasites** T.K. Gerbaba*, L. Gedamu, *University of Calgary, Canada*
[P2.53]	**Some like it hot: Molecular interaction studies using microscale thermophoresis** P. Baaske*[1], C.J. Wienken[2], S. Duhr[1] *[1]NanoTemper Technologies GmbH, Germany, [2]Center for NanoScience, Germany*
	Whole genome association studies
[P2.54]	**Genes expression in the frontal cortex of mice lacking the noradrenaline transporter - microarray study** J. Solich*, P. Palach, M. Gaska, M. Kusmider, M. Dziedzicka-Wasylewska, *Polish Academy of Sciences, Poland*
[P2.55]	**Shar Pei dogs – a model for hereditary periodic fevers and amyloidosis** M. Olsson[1], K. Truvé[2], G.R. Pielberg*[1], L. Andersson[1,2], Å. Hedhammar[2], K. Lindblad-Toh[1,3], *[1]Uppsala University, Sweden, [2]Swedish University of Agricultural Science, Sweden, [3]Broad Institute of Harvard and Massachusetts Institute of Technology (MIT), USA*
[P2.57]	**Functional heterogeneity of gene effects in *Leishmania major*-induced disease** I. Kurey*[1], H. Havelková[1], J. Badalová[1], T. Kobets[1], P. Demant[2], M. Lipoldová[1], *[1]Institute of Molecular Genetics AS CR, Czech Republic, [2]Roswell Park Cancer Institute, USA*
[P2.58]	**Novel loci controlling lymphocyte production of interferon γ after alloantigen stimulation in vitro** M. Lipoldová[1], Y. Sohrabi*[1], H. Havelková[1], J. Vojtíšková[1], A.P. Stassen[2], P. Demant[3], *[1]Academy of Sciences of the Czech Republic, Czech Republic, [2]Maastricht University, Netherlands, [3]Roswell Park Cancer Institute, USA*
[P2.59]	**Analysis of genetic changes in small intestinal carcinoid tumors** J.L. Cunningham*, T. Díaz de Ståhl, T. Sjöblom, J. Dumanski, E. Tiensuu Janson, *Uppsala University, Sweden*
[P2.60]	**Towards positional identification of susceptibility loci for white heifer disease in belgian blue cattle** A. Sartelet*, T. Druet, W. Coppieters, M. Georges, C. Charlier, *University of Liège, Belgium*
[P2.61]	**RNAi loss-of-function screen reveals RAS/RAF independent MEK/ERK signaling during chlamydia trachomatis infection** R.K. Gurumurthy*, A.P. Mäurer, N. Machuy, T.F. Meyer, *Max Planck Institute for Infection Biology, Germany*
[P2.62]	**Functional assessment of S100B as a susceptibility gene for bipolar disorder** E. Dagdan*[1,3], M. Hill[3], P. McKeon[1,2], D. Morris[3], S. Roche[1], *[1]Trinity College Dublin, Ireland, [2]St. Patrick's Hospital, Ireland, [3]Neuropsychiatric Genetics Research Group, St. James' Hospital, Ireland*