MATEMAATIKA-LOODUSTEADUSKONNA GEENITEHNOLOOGIA INSTITUUDI TEADUS- JA ARENDUSTEGEVUSE AASTAARUANNE 2011

1. Instituudi struktuur

Instituudi direktor Andres Veske

- Geenitehnoloogia õppetool , Chair of Gene Technology, Heiti Paves
- Molekulaarbioloogia õppetool , Chair of Molecular Biology, Tõnis Timmusk
- Molekulaardiagnostika õppetool , Chair of Molecular Diagnostics, Lilian Järvekülg
- Genoomika ja proteoomika õppetool , Chair of Genomics and Proteomics, Peep Palumaa

2. Instituudi teadus- ja arendustegevuse (edaspidi T&A) iseloomustus

(NB! punktid 2.1- 2.6 täidab struktuuriüksus)

2.1 struktuuriüksuse koosseisu kuuluvate uurimisgruppide

2.1.1 teadustöö kirjeldus *(inglise keeles*);

2.1.2 aruandeaastal saadud tähtsamad teadustulemused *(inglise keeles).*

Chair of Genomics and Proteomics

2.1.1 New ESI MS based methods for determination of protein midpoint redox potentials and metal-binding constants have been elaborated and midpoint redox potential for IGF_1 and Zn-binding constants for representative set of zinc finger proteins has been determined. Role of environmental factors on fibrillization of Alzheimers amyloid peptide (Aβ) has been studied and conditions for formation of oligomeric Aβ species have been established

2.1.2 Midpoint redox potential for IGF-1 equal to -332 mV has been determined, which shows that IGF-1 consists three structural disulphides, however, peptiide can be reduced in cytosolic reductive environment. Fully reduced IGF-1 exposed ability to bind 4 Cu(I) ions most probably into tetracopper-hexathiolate cluster. However, Cu(I) binding to the IGF-1 was threefold weaker compared to copper chaperone Cox17.

Metal-binding studies of zinc finger proteins (ZFP) demonstrated that ZFP with four Cys residues expose highest zinc-binding affinities and can compete even with metallothioneis. ZFPs with 2 Cys and 2 His residues expose weaker Zn-binding affinity and can not compete for metal with metallothioneis.

It has been established that environmental factors like temperature, pH, ionic strength, presence of organic solvents affect fibrillization of Alzheimers amyloid peptide (Aβ) by changing both – lag pahase of fibrillization and rate of fibril growth. Formation of oligomeric Aβ species have been observed in the presence of organic solvent and elevated temperatures.

Chair of Gene Technology

2.1.1 Studies on protein-RNA linkage and post-translational modifications of sobemovirus VPgs. Characterization of *Arabidopsis* class XI and VIII myosin double and triple mutants.Studies on wheat resistance to powdery mildew.

2.1.2 Sobemoviruses possess a viral genome-linked protein (VPg) attached to the 5' end of viral RNA. VPg is processed from the viral polyprotein. In the current study, Cocksfoot mottle virus (CfMV) and Rice yellow mottle virus (RYMV) VPgs were purified from virions and analysed by mass spectrometry. The cleavage sites in the polyprotein and thereof the termini of VPg were experimentally proven. The lengths of the mature VPgs were determined to be 78 and 79 aa residues, respectively. The amino acid residues covalently linked to RNA in the two VPgs were, surprisingly, not conserved; it is a tyrosine at position 5 of CfMV VPg and serine at position 1 of RYMV VPg. Phosphorylations were identified in CfMV and RYMV VPgs with two positionally similar locations T20/S14 and S71/S72, respectively. RYMV VPg contains an additional phosphorylation site at S41.

Simultaneous depletion of *Arabidopsis* class XI myosins XI-K, XI-1, and XI-2 in double and triple mutant plants affected the growth of different epidermal cells. The size and shape of trichomes, leaf pavement cells or the elongation of the stigmatic papillae of double and triple mutant plants were affected to different extent. Reduced cell size led to significant size reduction of shoot organs in the case of triple mutant, affecting bolt formation, flowering time and fertility. Phenotype analysis revealed that the reduced fertility of triple mutant plants was caused by delayed or insufficient development of pistils.

It was shown that introgression from tetraploid *Triticum militinae* into bread wheat has increased resistance to powdery mildew in a race-nonspecific manner, and the main locus responsible for resistance has been located in a 3 Mb region on chromosome 4AL in the introgression line.

Chair of Molecular Biology

2.1.1 The complex structure of the adult brain is the product of genetic instructions, cellular interactions, and also interactions between the organism and the external environment. We are studying themolecular mechanisms of the regulation of gene expression and signaling in mammalian nervous system. Specifically we study: (I) Molecular mechanisms controlling the tissue-specific and neural activity-regulatedexpression of genes for the neurotrophic factors BDNF and GDNF; (II) BDNF receptor TrkB signaling; (III) Transcriptional dysregulation in Huntington’s disease; (IV) The leucine-rich repeat transmembrane protein (LRRTM)/alpha catenin gene loci and their role in different nervous system diseases.

We have demonstrated that transcriptional interference (TI) induced by intronic L1s (or other repeated DNAs) and nested genes could be characterized by intron retention, forced exonization and cryptic polyadenylation. These molecular effects were revealed from the analysis of endogenous prematurely terminated transcripts derived from different cell lines and tissues and confirmed by the expression of three minigenes in cell culture. While intron retention and exonization were comparably observed in introns upstream to L1s, forced exonization was preferentially detected in nested genes. TI induced by L1 or nested genes was dependent on the presence or absence of cryptic splice sites, affected the inclusion or exclusion of the upstream exon and the use of cryptic polyadenylation signals. Our results suggest that TI induced by intronic L1s and nested genes could influence the transcription of the large number of genes in normal as well as in tumor tissues.

2.1.2 Novel mechanisms of neuronal-activity-dependent transcriptional regulation of BDNF in cortical neurons was characterized (Pruunsild et al, 2011).Bidirectional transcription from the schizophrenia associated human *LRRTM2*/*CTNNA1* and *LRRTM1*/*CTNNA2* gene loci was shown to lead to expression of N-terminally truncated CTNNA1 and CTNNA2 isoforms (Kask et al., 2011). Functional diversity of the protein isoforms derived from human basic helix-loop-helix transcription factor TCF4 gene, that is mutated in Pittt-Hopkins syndrome and associated with schizophrenia, was shown to be generated by alternative 5' exon usage and splicing (Sepp et al., 2011).FoxO3a levels were shown to be increased in Huntington's disease cells due to overactivated positive autofeedback loop (Kannike et al., manuscript).

We also extended our TI studies to intronic Alu repeats and non-coding RNA genes by showing their orientational bias effects suggesting widespread occurrence of gene regulation and/or interference. In addition, we further developed the double stranded RNA isolation and cloning protocol

Chair of Molecular Diagnostics

2.1.1 During year 2011, RGS16-/- mice were characterized with the aim to clarify the role of this regulator of G-protein signaling in the immune system. Leukocyte composition and activation were analyzed. In addition, two pathological situations were applied in order to assess the impact of RGS16 during immunological challenge. PCV2 virus was used as a model of infection, whereas histocompatible melanoma was chosen for the estimation of cancer progression. ELISA and HI methods were used to screen both Estonian human and porcine blood samples from different origins for the presence of anti-H1N1 (Influenza A) antibodies.

The 28 rDNA D3 motif together with the flanking regions was sequenced for the Geodia species *G. atlantica*, *G. barretti*, *G. cydonium* ja *G. neptuni*. The applicability of this sequence for the discrimination between these sponge species was demonstrated. The main research was focused on the 2-5A synthetase (2',5' oligoadenylate synthetase, OAS). Sets of specific and/or degeneranted primers were used to amplify OAS fragments from different species of Geodia. Because of the high variability of primary structures the set of full coding sequences for OAS1 were obtained for *G. baretti* only. The genomic structure of the OAS1 from sponge was also elucidated and the presence of trancriptable pseudogenes in the genome was established. In parallel the analysis of OAS genes in other metazoan throughout the phylogeny was started by cloning OAS cDNAs from *Mytilus californicus* (a mussel), *Ambystoma mexicanum* (a salamander) and *Leucoraja erinacea* (litte skate) for their heterologous expression.

Conversion of a normal cell into a malignant tumor cell is a multi-step process requiring several genetic mutations. The first of those mutations that are limiting for further progression cause the loss of normal growth control mechanisms of the cell, either by eliminating the function of tumor suppressor genes or by activating oncogenes that act positively on cell growth. However, what makes cancer a deadly disease is the next set of mutations that lead to malignant tumor progression and the formation of metastases; these latter processes have proven far more difficult to analyze. Successful establishment of metastases requires sequential and coordinated regulation of a whole set of genes that in contrast to growth control genes do not convey a selective advantage for stationary tumor growth and may even be counterproductive. Therefore it has been postulated that important metastasis genes are only

transiently activated/inactivated during metastasis. Recently there have been suggestions in the literature that “metastasis genes” as such do not exist. Instead it has been proposed that tumor metastasis is determined by the specific set of mutations in oncogenes/tumor suppressor genes early in tumor development. There is some evidence to support both models. The current project is set up to test these possibilities and to contribute to our understanding of tumor progression and metastasis in a significant manner. Specifically we want to further characterize CD44 as a transient metastasis molecule and study the role of PTCH1 in angiogenesis and metastasis models. The underlying hypothesis is that both metastasis genes and metastasis-suppressing gatekeeper genes exist with CD44 representing an example of the former and PTCH1 of the latter class

2.1.2 We could show that, RGS16-/- splenocytes produce larger amounts of KC in response to LPS than their WT counterparts, implying an involvement for RGS16 in the regulation of KC synthesis/secretion. Our results indicate that viral load is significantly higher in the tissues of RGS16-/- compared to wild type mice. Experiments with melanoma showed that tumor progression is promoted in RGS16-/- mice, (Pahtma, 2011). We could establish that both humans and pigs had been infected by the H1N1 virus (during pandemi 2009-2010) often in absence of clinical signs, which may indicate that an attenuated virus was circulated in the Estonian population during this period.

We have shown that sponge 2-5A synthetases (OASs) form a distinct subgroup of the 2-5A synthetase family. OAS proteins from different genera of Demospongia show rather low similarities in their primary structures. To ascertain divergence of the OAS genes within a particular sponge genus, we identified the OAS genes from the marine sponge *Geodia barretti* and compared them with those from another member of the genus Geodia, *Geodia cydonium*. The identity and similarity of these OAS sequences were considerably higher that with those from other sponges. We also established the presence of a transcriptionally active polymorphic OAS pseudogene in the genome of *G. baretti*.

In addition to the purine metabolic enzymes we also performed a study of a survivin-like protein of the marine sponge *Suberites domuncula*. The data show that poriferan survivin exhibits a conserved regulatory role in the interconnected pathways of cell cycle and apoptosis.

While studying the the functions in CD44 on endothelial cells and its role in inhibiting tumor angiogenesis and metastasis, we have identified the receptor for CD44 on endothelial cells as cell surface vimentin. We mapped the region in vimentin responsible for binding to CD44 hyaluronan binding domain. We studied the role of CD44-vimentin interaction in the context of the cell and organism. For this purpose we created CD44 and vimentin double knockout mice. The results of this study have been reorted in an article published in PloS One. In order to find possible new molecules affecting metastasis we have foused our attention on finding new molecules affecting SHH-PTCH signalling. By screening different compounds we manage to discover that chelidonine, an alkaloid from *Chelidonium majus*, is capable of affecting SHH signalling in mammalian cells.

2.2 Uurimisgrupi kuni 5 olulisemat publikatsiooni läinud aastal.

Chair of Genomics and Proteomics

Tõugu, Vello; Tiiman, Ann; Palumaa, Peep (2011). Interactions of Zn(II) and Cu(II) ions with Alzheimer's amyloid-beta peptide. Metal ion binding, contribution to fibrillization and toxicity. Metallomics, 3, 250 - 261.

Chair of Gene Technology

Olspert A, Arike L, Peil L, Truve E. Sobemovirus RNA linked to VPg over a threonine residue. FEBS Lett. 2011 Oct 3;585(19):2979-85.

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Chair of Molecular Biology

Pruunsild, P.; Sepp, M.; Orav, E.; Koppel, I.; Timmusk, T. (2011). Identification of cis-elements and transcription factors regulating neuronal activity-dependent transcription of human BDNF gene. Journal of Neuroscience, 31, 3295 - 3308.

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Kask, M.; Pruunsild, P.; Timmusk, T. (2011). Bidirectional transcription from human LRRTM2/CTNNA1 and LRRTM1/CTNNA2 gene loci leads to expression of N-terminally truncated CTNNA1 and CTNNA2 isoforms. Biochemical and Biophysical Research Communications, 411, 56 - 61

Kaer Kristel, Branovets Jelena, Hallikma Anni, Nigumann Pilvi and Speek Mart (2011). Intronic L1 retrotransposons and nested genes cause transcriptional interference by inducing intron retention, exonization and cryptic polyadenylation. PLoS ONE, 6(10):e26099.

Chair of Molecular Diagnostics

Saar, R.; Põdersoo, D.; Järvelaid, M.; Tuubel, L.; Suurväli, J.; Nutt, A.; Saaremäe, M.; Saar, T.; Rüütel Bodinot, S. (2012). The Estonian H1N1 Influenza 2009 outbreak was highly underestimated. Proceedings of the Estonian Academy of Sciences (April,2012)

Vallmann, K., Aas, N., Reintamm, T., Lopp, A., Kuusksalu, A., Kelve, M. (2011) Expressed 2-5A synthetase genes and pseudogenes in the marine sponge *Geodia barretti*. Gene 18, 201-213

Luthringer, B., Isbert, S., Müller, W.E.G., Zilberberg, C., Thakur, N.L., Wörheide, G., Stauber, R.H., Kelve' M., Wiens, M. (2011) Poriferan survivin exhibits a conserved regulatory role in the interconnected pathways of cell cycle and apoptosis. Cell Death Differ. 18, 201-213

Päll, Taavi; Pink, Anne; Kasak, Lagle; Turkina, Marina; Anderson, Wally; Valkna, Andres; Kogerman, Priit (2011). Soluble CD44 Interacts with Intermediate Filament Protein Vimentin on Endothelial Cell Surface. PLoS ONE, 6(12), e29305

Kulp, M.; Bragina, O.; Kogerman, P.; Kaljurand, M. (2011). Capillary electrophoresis with led-induced native fluorescence detection for determination of isoquinoline alkaloids and their cytotoxicity in extracts of Chelidonium majus L. . Journal of Chromatography A, 1281(31), 5298 - 5304.

2.3 Loetelu struktuuriüksuse töötajate rahvusvahelistest tunnustustustest.

Prof. Peep Palumaa valiti EMBO organisatsiooni liikmeks.

Heiti Paves sai Bioimaging konkursil contest "When Life is Art 2011" 1. koha.

2.4 Loetelu struktuuriüksuse töötajatest, kes on välisakadeemiate või muude oluliste T&A-ga seotud välisorganisatsioonide liikmed.

Prof. Peep Palumaa on EMBO organisatsiooni liige.

2.5 Aruandeaasta tähtsamad T&A finantseerimise allikad.

Vaata punkti 2.7, kus kõik rahastamisallikad ka kirjas.

2.6 Soovi korral lisada aruandeaastal saadud T&A-ga seotud tunnustusi (va punktis 2.3 toodud tunnustused), ülevaate teaduskorralduslikust tegevusest, teadlasmobiilsusest ning anda hinnang oma teadustulemustele.

Prof. Peep Palumaa sai Eesti riikliku teauspreemia keemia ja molekulaarbioloogia alal. Instituudi teadlased viibisid paljudel rahvusvahelistel konverentsidel ja seminaridel. Samuti võeti vastu mitmeid külalisteadlasi, kes esinesid instituudi seminarides. Doktoritööde kaitsmine on olnud jätkuvalt hea. Instituudi teadlaste töötulemused on avaldatud erinevates hea mainega rahvusvaheliselt tunnustatud teadusajakirjades.

Kokkuvõtvalt võib hinnata instituudi 2011 aasta teadustegevust heaks ja jääb vaid loota, et kasvab väga heades teadusajakirjades publitseertavate artikllite arv.

2.7 Instituudi teadus- ja arendustegevuse teemade ja projektide nimetused *(Eesti Teadusinfosüsteemi, edaspidi ETIS, andmetel)*

- Haridus- ja Teadusministeerium

sihtfinantseeritavad teemad:

- T108,N ukleotiidide metabolismis osalevad ensüümid - võrdlev biokeemia, molekulaarbioloogia ja evolutsioonilised aspektid , Kelve Merike
- T145A, Tuumorprogressiooni molekulaarbioloogia: molekulaarsed mehhanismid ja biomeditsiinilised rakendused, Kogerman Priit
- T055, Struktuurne ja meditsiiniline metalloproteoomika, Palumaa Peep
- T143, Geeniregulatsioon ja signaaliülekanne närvisüsteemis, Timmusk Tõnis
- T106, Taim-patogeen molekulaarsed interaktsioonid , Truve Erkki
- T066, Tsirkoviiruse bioloogia ja vaktsinoloogia, Rüütel Boudinot Sirje

baasfinantseerimise toetusfondist rahastatud projektid (sh TTÜ tippkeskused):

- B11, Professor Tõnis Timmuski poolt juhitava uurimisgrupi toetamine
- B12, Professor Peep Palumaa poolt juhitava uurimisgrupi toetamine

riiklikud programmid:

- Teiste ministeeriumide poolt rahastatavad riiklikud programmid:
- 556L, Põllumajanduskultuuride geneetilise ressursi kogumine ja säilitamine, Järve Kadri
- RP9010, Sordiaretusprogramm aastatel 2009 - 2019, Järve Kadri

- Uurija-professori rahastamine:

- SA Eesti Teadusfond

grandid:

- ETF7421, Nukleotiidide metabolismis osalevate ensüümide genoomse struktuuri ja aktiivsuse iseloomustamine madalaimates hulkraksetes loomades - käsnades , Kelve Merike
- ETF8385, Amüloidsete peptiidide konformatsiooni ja agregatsiooni uurimine.,Kumm Tiina
- ETF7711,Madalaeelarveliste in ovo tuumorite kuvamismudelite väljatöötamine (MRT, ultraheli), Nairismägi Jaak
- ETF8381, Transkriptsiooniline interferents – kompleksne regulatsioon geenide ja mobiilsete elementide vahel , Speek Mart
- ETF7363, Sobemoviirused: paljunemine ning interaktsioonid peremehega,Truve Erkki
- ETF8844,Regulation of the neurotrophic factor BDNF gene expression in health and nervous system diseases, Tõnis Timmusk
- ETF8811, Uudsed mass-spektroskoopial põhinevad metoodikad vase ja tsingi valkude metallide sidumisomaduste ja redoksregulatsiooni uurimiseks, Peep Palumaa
- ETF8604, Arabidopsis thaliana müosiinid, Heiti Paves
- ETF8914, RGS16 osalus immuunregulatsioonis, Sirje Rüütel Boudinot

ühisgrandid välisriigiga:

järeldoktorite grandid (SA ETF ja Mobilitas):

- MJD37, High-throughput screening of inhibitors of A? peptide aggregation, Kumm Tiina
- JD155, Cloning, overexpression and labelling of intracellular C-terminal domain of human Smoothened (a receptor protein synthesised from proto-oncogene) in Escherichia coli system for functional and structural studies, Tomson Katrin
- MJD121, Studies on function of human RNase L inhibitor (RLI), Toompuu Marina

tippteadlase grandid (Mobilitas):

- MTT4, CO-OPERATION OF INTEGRINS AND RECEPTOR TYROSINE KINASES IN REGULATION OF CELL MOTILITY: ROLE OF FILAMIN A AND PKB/Akt, Velling Teet

- Ettevõtluse Arendamise SA

eeluuringud:

arendustoetused:

- SA Archimedesega sõlmitud lepingud

infrastruktuur (nn „mini-infra“, „asutuse infra“):

- AP108, Nukleotiidide metabolismis osalevad ensüümid - võrdlev biokeemia, molekulaarbioloogia ja evolutsioonilised aspektid, Kelve Merike
- AP145A, Allteema A:Tuumorprogressiooni molekulaarbioloogia ja immunoloogia: molekulaarsed mehhanismid ja biomeditsiinilised rakendused, Kogerman Priit

- AP055, Struktuurne ja meditsiiniline metalloproteoomika , Palumaa Peep
- AP066, Tsirkoviiruse bioloogia ja vaktsinoloogia, Sirje Rüütel-Boudinot
- AP143, Geeniregulatsioon ja signaaliülekanne närvisüsteemis, Timmusk Tõnis
- AP106, Taim-patogeen molekulaarsed interaktsioonid, Truve Erkki
- ÜLTAP63A, Loodusteaduste Maja infrastruktuuri edasiarendus, Andres Veske

Eesti tippkeskused:

- TAR11058, Keskkonnamuutustele kohanemise tippkeskus, Erkki Truve

riiklikud programmid:

- AR11121, Põllukultuuride resistentsusaretus, Erkki Truve

muud T&A lepingud:

- SA Keskkonnainvesteeringute Keskusega sõlmitud lepingud:
- Siseriiklikud lepingud:
- EL Raamprogrammi projektid:
- Välisriiklikud lepingud:

2.8 Struktuuriüksuse töötajate poolt avaldatud sihtfinantseeritava teadusteema taotlemisel arvestatavad eelretsenseeritavad teaduspublikatsioonid *(ETIS klassifikaatori alusel 1.1, 1.2, 1.3, 2.1, 2.2, 3.1, 3.2, 3.3, 4.1 ja 5.1).*

1.1

Paredez, Alexander; Assaf, Zoe; Sept, David; Timofejeva, Ljudmilla; Dawson, Scott; Wang, Rachel; Cande, Zacheus. (2011). An actin cytoskeleton with evolutionarily conserved functions in the absence of canonical actin-binding proteins. PNAS, 108(15), 6151 - 6156.

Kask, M.; Pruunsild, P.; Timmusk, T. (2011). Bidirectional transcription from human LRRTM2/CTNNA1 and LRRTM1/CTNNA2 gene loci leads to expression of N-terminally truncated CTNNA1 and CTNNA2 isoforms. Biochemical and Biophysical Research Communications, 411, 56 - 61.

Kulp, M.; Bragina, O.; Kogerman, P.; Kaljurand, M. (2011). Capillary electrophoresis with led-induced native fluorescence detection for determination of isoquinoline alkaloids and their cytotoxicity in extracts of Chelidonium majus L. . Journal of Chromatography A, 1281(31), 5298 - 5304.

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Vallmann, Kerli; Aas, Nele; Reintamm, Tõnu; Lopp, Annika; Kuusksalu, Anne; Kelve, Merike (2011). Expressed 2-5A synthetase genes and pseudogenes in the marine sponge Geodia barretti. Gene, 478, 42 - 49.

Sarapik, A; Velthut, A; Haller-Kikkatalo, K; Faure, GC; Béné, MC; de Carvalho Bittencourt, M; Massin, F; Uibo, R; Salumets, A. (2011). Follicular Proinflammatory Cytokines and Chemokines as Markers of IVF Success. Clinical and Developmental Immunology, 2012, x - x.

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Pruunsild, P.; Sepp, M.; Orav, E.; Koppel, I.; Timmusk, T. (2011). Identification of cis-elements and transcription factors regulating neuronal activity-dependent transcription of human BDNF gene. Journal of Neuroscience, 31, 3295 - 3308.

Tõugu, Vello; Tiiman, Ann; Palumaa, Peep (2011). Interactions of Zn(II) and Cu(II) ions with Alzheimer’s amyloid-beta peptide. Metal ion binding, contribution to fibrillization and toxicity. Metallomics, 3, 250 - 261.

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Olspert, Allan; Peil, Lauri; Hébrard, Eugénie; Fargette, Denis; Truve, Erkki (2011). Protein-RNA linkage and post-translational modifications of two sobemovirus VPgs. Journal of General Virology, 92, 445 - 452.

Olspert, Allan; Arike, Liisa; Peil, Lauri; Truve, Erkki (2011). Sobemovirus RNA linked to VPg over a threonine residue. FEBS Letters, 585(19), 2979 - 2985.

Päll, Taavi; Pink, Anne; Kasak, Lagle; Turkina, Marina; Anderson, Wally; Valkna, Andres; Kogerman, Priit (2011). Soluble CD44 Interacts with Intermediate Filament Protein Vimentin on Endothelial Cell Surface. PLoS ONE, 6(12), e29305

Kaer Kristel, Branovets Jelena, Hallikma Anni, Nigumann Pilvi and Speek Mart (2011). Intronic L1 retrotransposons and nested genes cause transcriptional interference by inducing intron retention, exonization and cryptic polyadenylation. PLoS ONE, 6(10):e26099. Epub 2011 Oct 13

1.2

1.3

2.1

2.2

3.1

Truve, Erkki; Fargette, Denis (2011). Genus Sobemovirus. Andrew King, Eric Carstens, Mike Adams and Elliot Lefkowitz (Toim.). Ninth Report of the ICTV on Taxonomy of the Viruses (xxx).Elsevier [ilmumas]

3.2

3.3

4.1

5.1

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2.9 Struktuuriüksuses kaitstud doktoriväitekirjade loetelu *(NB! struktuuriüksus lisab struktuuriüksuse töötaja juhendamisel mujal kaitstud doktoriväitekirjade loetelu)*

Priit Pruunsild, geenitehnoloogia instituut
Teema: *Neuronal Activity-DependentTtranscription Factors and Regulation of Human BDNF Gene* (Närvitalitlusest sõltuvad transkriptsioonifaktorid ja inimese BDNF geeni avaldumise regulatsioon)
Juhendaja: prof Tõnis Timmusk
Kaitses: 7.01.2011
Omistatud kraad: filosoofiadoktor (geenitehnoloogia)

Olga Katargina, geenitehnoloogia instituut
Teema: *Tick-Borne Pathogens Circulating in Estonia (Tick-Borne Encephalitis Virus, Anaplasma Phagocytophilum, Babesia Species): Their Prevalence and Genetic Characterization* (Eestis tsirkuleerivate puukide abil ülekantavad patogeenid (Puukentsefaliidiviirus, Anaplasma phagocytophilum, Babesia liigid): nende levik ja geneetiline iseloomustus)
Juhendaja: prof Lilian Järvekülg
Kaasjuhendaja: vanemteadur Irina Golovjova
Kaitses: 21.06.2011
Omistatud kraad: filosoofiadoktor (geenitehnoloogia)

Kairit Zovo, geenitehnoloogia instituut
Teema: *Functional Characterization of Cellular Copper Proteome* (Rakulise vase proteoomi funktsionaalne iseloomustamine)
Juhendaja: prof Peep Palumaa
Kaitses: 12.08.2011
Omistatud kraad: filosoofiadoktor (geenitehnoloogia)

Allan Olspert, geenitehnoloogia instituut
Teema: *Properties of VPg and Coat Protein of Sobemoviruses* (Sobemoviiruste VPg ja kattevalgu omadused)
Juhendaja: prof Erkki Truve
Kaitses: 2.12.2011
Omistatud kraad: filosoofiadoktor (geenitehnoloogia)

2.10 Struktuuriüksuses järeldoktorina T&A-s osalenud isikute loetelu *(ETIS-e kaudu esitatud taotluste alusel)*

MJD37, High-throughput screening of inhibitors of A? peptide aggregation, Kumm Tiina
JD155, Cloning, overexpression and labelling of intracellular C-terminal domain of human Smoothened (a receptor protein synthesised from proto-oncogene) in Escherichia coli system for functional and structural studies, Tomson Katrin
MJD121, Studies on function of human RNase L inhibitor (RLI), Toompuu Marina

2.11 Struktuuriüksuses loodud tööstusomandi loetelu

WO2011/100982A2 (PCT/EE2011000003)
Suppressors of RNA silencing as modulators of miRNA levels
Taotlus esitatud: 18.02.2011
Autorid: Maria Cecilia Sarmiento Guerin, Kairi Kärblane, Illar Pata, Pille Pata, Erkki Truve
Omanikud: TTÜ, VTAK
Instituut: YT

EP2304022A1 (EP09761338.4)
The use of extract of selenium-enriched yeast (Se-YE) in mammalian cell culture media formulations
Taotlus esitatud: 10.01.2011
Autorid: Monika Drews, Reet Rumvolt, Karoli Voodla
Omanikud: TTÜ, VTAK, Cambrex Tallinn AS, InBio OÜ, Celecure AS, Kevelt AS, SA PERH
Instituut: YT

US13/124741
Potato virus A coat protein-based vaccine for treating melanoma and its use
Taotlus esitatud: 18.04.2011
Autorid: Lilian Järvekülg, Viiu Paalme, Ave Laas, Sulev Kuuse, Ülo Puurand, Sirje Rüütel Boudinot, Reet Rumvolt
Omanikud: TTÜ, Tartu Ülikool
Instituut: YT

EP2381958A1 (EP09752274.2)
Potato virus A coat protein-based vaccine for treating melanoma and its use
EP faasi esitatud: 16.05.2011
Autorid: Lilian Järvekülg, Viiu Paalme, Ave Laas, Sulev Kuuse, Ülo Puurand, Sirje Rüütel Boudinot, Reet Rumvolt
Omanikud: TTÜ, Tartu Ülikool
Instituut: YT

US2011152346A1
Use of oligonucleotides with modified bases in hybridization of nucleic acids
Taotlus esitatud: 14.02.2011
Autorid: Mati Karelson, Erkki Truve, Allan Olspert, Cecilia Sarmiento, Mart Saarma
Omanik: Balti Tehnoloogiaarenduse AS
Instituudid: YK, YT

US20110251132A1
Treatment with pharmaceutical composition comprising MANF2 nucleic acid
Taotlus esitatud: 15.04.2011

Autorid/Omanikud: Mart Saarma, Juha Lauren, Päivi Lindholm, Tõnis Timmusk, Raimo Tuominen
Instituut: YT

3. Struktuuriüksuse infrastruktuuri uuendamise loetelu

- ELISA aparatuur koos arvuti ja,10.01.2011,7 395 €
- Bioimidzer-IVIS Lumina Imaging,21.01.2011,149 651 €
- Fluorestsentsmikroskoop TILL,14.02.2011,199 822 €
- Reaalaja PCR-i süsteem,7.04.2011,58 123 €
- Lüofilisaatori komplekt,14.04.2011,10 592 €
- Imidžer "ImageQuant LAS 4000",12.05.2011,42 000 €
- Geelelektroforeesi süsteem,19.05.2011,6 857 €
- Geelelektroforeesi süsteem,19.05.2011,6 857 €
- Autom. magnetiline rakusorter,19.08.2011,39 000 €
- DNA amplifitseerimise apara,28.10.2011,11 510 €
- In vitro / in vivo füsioloogia,28.10.2011,36 752 €
- Raku-, koe-, ja organkultuuri,28.10.2011,9 679 €
- Valkude analüüsi aparatuuri,28.10.2011,8 490 €
- Fotokaamera NIKON komplekt,7.12.2011,2 513 €