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Loss of alpha-e-catenin in embrionic heart leads to dramatic malformation of adult heart

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Aim. In our work we have focused on the embryonic cardiospecific ablation of alpha-E-catenin and its reflection on heart adult heart formation. **Methods.** We studied the significance of embryonic cardiospecific ablation of alpha-E-catenin for heart aging using the conditional knockout approach. We analyzed how alpha-E-catenin haploinsufficiency and homozygotic deletion affected the postnatal heart development and adult heart formation. For this we used measurement of the heart weight/body weight (HW/BW) and heart weight/tibia length (HW/TL) indices, hematoxylin-eosin staining, van Gieson staining, qPCR. **Results.** The alpha-E-catenin deletion leads to a shortened lifespan of the mutant mice. The mice with homozygotic deletion of alpha-E-catenin had mean survival 36.44 ± 2.62 weeks, haploinsufficiente mice – 38.11 ± 2.39 weeks, controls – 66.2 ± 4.1 weeks. The maximal lifespan in homozygotic mice was 48 weeks, in haploinsufficiente – 44 weeks, whereas in the control we observed more than 78 weeks. In our experiment we revealed the increasing of HW/BW and HW/TL indices in the homozygotic and haploinsufficiente mice compared to the control mice. Using histological staining we found that the full ablation and deficiency of alpha-E-catenin led to the growing of interstitial fibrosis and cardiomiocyte disintegration. We analyzed the expression of target genes of the canonical WNT signaling and HIPPO-signaling. **Conclusions.** We have shown that embryonic cardiospecific deletion of one as well as both alleles of the alpha-E-catenin gene leads to the disorders of heart structure, which are typical for the dilated cardiomyopathy, ischemic heart disease, accompanied by fibrosis. As a result this violation of the heart tissue structure causes an early death of animals. We assume that the loss of alpha-E-catenin leads to such dramatic consequences not only due to the violation of cells interactions, but to the deregulation of signalling pathways in cardiomyocytes, that should be clarified by further molecular genetics and physiological studies.

Assessing the relationship between enhancer transcription and activity during embryonic development

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Aim. Although enhancer transcription has been discovered and extensively studied in mammals, it remains largely unexplored in *Drosophila*. As a model organism, *Drosophila* offers unique advantages over other organisms for a direct experimental validation of enhancers, including accurate spatio-temporal maps of enhancer activity during the embryonic development. Given the essential role of enhancers in driving the transcriptional programs regulating development, the understanding of enhancer transcription and its contribution to the enhancer activity may offer new insights into the principles of gene regulation, cell identity control, and development. **Methods.** Here, we use the *Drosophila* development as a model system to test the association of initiating and elongating forms of RNA Polymerase II (Pol II) in various phosphorylation states with spatial and temporal enhancer activity, over a time course covering the embryonic mesoderm and nervous system development. We complement our analysis with the strand-specific PRO-cap data, which maps nascent transcripts to their initiation sites. **Resuts and Conclusions.** Our results confirm the existence of enhancer transcription in *D. melanogaster* at comparable levels to the vertebrate genomes. We also provide evidence for a bidirectional pattern of the intergenic enhancer transcription similar to the vertebrate enhancers, along with the presence of initiating Pol II at enhancers. Considering the density of *Drosophila* genome, we show that many enhancers are associated with active transcription as a consequence of their genomic location, are the result of transcriptional read through, or are possible alternative transcription start sites. We also identified an association between the experimentally defined enhancer activity and enhancer transcription, and showed that this association was weaker than the vertebrate studies suggest.

mTOR-signaling network in paracryne regulation of HeLa cancer cell motility by NIH 3T3 fibroblasts

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Aim. The main aim of this work was to evaluate the involvement of mTOR signaling in paracrine regulation of HeLa cancer cell motility by NIH 3T3 fibroblasts. **Methods.** Cell culture, immunoblotting, immunocytochemistry, soft agar colony formation, 3D-2D cell culture transformation, confocal microscopy, scratch test assay and Transwell test were used in this study. **Results.** The significant changes were revealed in malignant phenotype of HeLa cells cultivated in the NIH 3T3 fibroblasts conditioned medium (CM). The revealed phenotypic changes caused by this factor are present at the molecular level as well as at the cellular one. It was manifested as an increase in the $mTOR^{S2448}$, $p85\text{-}S6K1^{T389}$, $p70\text{-}S6K1^{T389}$, $p70\text{-}S6K1^{S371}$ and FAK^{Y925} phosphorylation rate and a decrease in the cell migration activity. The alteration in protein expression profile of the above mentioned molecules was not found. Besides, the effects of specific mTOR kinase inhibitor and anticancer drug rapamycine on the CM modified HeLa phenotype were investigated. It was shown that the addition of rapamycin to CM significantly reduced the $mTOR^{S2448}$, $p85\text{-}S6K1^{T389}$ and $p70\text{-}S6K1^{T389}$ phosphorylation induced by CM. Interestingly, a decline of the mentioned kinases phosphorylation level caused by rapamycin was more pronounced in the cells stimulated with CM as compared to the unstimulated cells. At the cellular level, a combined treatment with rapamycine and CM enhanced the inhibitory effect on the HeLa cell migration activity. Moreover, the observed effects of CM, rapamycine and their combination on the cancer cell motility tightly depended on the cell nutrient consumption. The effect of all these factors as well as the migration activity decreased under the starvation conditions. Additionally, we also revealed the cytoskeleton remodeling, namely, a decrease in cytokeratin branching in HeLa cells, exceptionally under the combined action of rapamycin and NIH 3T3. The revealed NIH 3T3 CM induced effects on HeLa cells and their sensitivity to the mTOR inhibition by rapamycine along with the data of other authors give grounds for assuming that mTOR signaling may play an editing role in the cell reactions and facilitate the inhibition of cancer cell motility by NIH 3T3 CM. **Conclusion.** mTOR signaling is involved in the motility regulation of HeLa cells by NIH 3T3 fibroblasts at the molecular, cellular and sub-cellular levels.

Prediction of regulatory motifs for RNA-binding proteins in 3'UTRs of some endocytic genes

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Introduction. The **c**lathrin-mediated endocytosis is fundamental for the neurotransmission, signal transduction and regulation of many plasma membrane activities. In the first step of endocytosis the interaction between FCHO1/2, EPS15 and ITSN1/2 is essential. These proteins have different isoforms (between 2 and 4) encoded by multiple transcripts with variable 3' untranslated regions (3'UTRs) length (between 262 and 11561 bases). **The aim** was to predict the sites for regulatory elements in 3'UTRs of FCHO1/2, EPS15 and ITSN1/2, which may be common for all or the majority of their transcripts and thus may regulate the expression of genes involved into the first step of endocytosis. **Materials and Methods.** The analysis was performed by 'RegRNA 2.0' and 'Scan for Motifs' services. **Results.** The analysis showed 13 types of regulatory elements. As far as the FCHO1 transcript variants have very short 3'UTRs (262-270 nt), there are no regulatory elements predicted for these mRNAs, except 15-LOX-DICE element, which specifically inhibits the 15- Lipoxygenase gene expression ('Scan for Motifs'). It is unknown yet whether it regulates the expression of any other genes. According to 'Scan for Motifs', Pumilio binding element (PBE) is common for all FCHO2, EPS15 and ITSN2 transcript variants and for the ITSN1-L transcript variant. Pumilio is a sequence-specific RNA-binding protein (RBP) that acts as a post-transcriptional repressor by binding the PBE. It mediates the post-transcriptional repression of transcripts by different mechanisms: acts via a direct recruitment of the CCR4-POP2-NOT deadenylase leading to the translational inhibition and mRNA degradation, or mediates the deadenylation-independent repression by promoting an accessibility of miRNAs. According to both sources, Musashi binding element (MBE) is common for all FCHO2, EPS15 ITSN1 and ITSN2 transcript variants (is not predicted only for ITSN1-L isoforms by 'Scan for Motifs'). The Musashi family is an evolutionarily conserved group of RBPs, which have emerged as a key signal that confers and protects the stem cell functions during the development and regenerative processes. Musashi1 acts as a translational repressor through the sequence-specific interaction with the 3′UTR of various target mRNAs. **Conclusion:** The obtained data may be used as a basis for further studies, particularly, for the validation of predicted common sites for RBPs in 3'UTRs of the genes involved in the first step of clathrin-mediated endocytosis.

In silico study of the complexes ofB.*taurus* tyrosyl-tRNA synthetase with substrates

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Tyrosyl-tRNA synthetase (TyrRS) is one of the key enzyme of protein biosynthesis. At present, the crystallographic data for the mammalian TyrRS in complexes with the substrates have not been obtained. The structural exploration of this enzyme is not only of fundamental, but also of biomedical significance. However, there are few structural data for mammalian TyrRS compared to those] for bacterial enzymes. **Aim.** In this work, using several computational modeling techniques, we constructed 3D models of *Bostaurus*TyrRS (*Bt*TyrRS) structure corresponding to the different stages of the catalytic reaction. To understand the conformational changes involved in the catalytic mechanism, we performed several 100 ns molecular dynamics (MD) simulations for separate complexes. **Methods.** The previously reported full-length *Hs*TyrRS structure (Savytskyi *et al.*, 2013) was used as a template for the full-length *Bt*TyrRS structure modeling. We constructed the catalytic loop in different conformations with subsequent ligand docking. Modeller 9 and AutoDock 4.2.6 software were used for molecular modeling and docking, respectively. The selected protein-ligand complexes were simulated for 100 ns using all-atom MD simulations with GROMACS 5.0 (CHARMM27 force field). **Results.** It was found that ATP binds at the active site via hydrogen bonds interactions with more than 50 % of simulation time (50–100 ns): Val215 – 96 %, Asn212 – 86 %, Trp40 – 85 %, Lys154 – 78 %, Lys222 – 62 %, and Tyr52 – 56 % whereas the same interactions [of ?] fortyrosyl-adenylate (Tyr-AMP) are following:Ala43 – 99 %, Thr42 – 99 %, Asp173 –98 %, Tyr39 – 97 %, Asn212 – 77 %, Val215 – 73 % and Trp40 – 63 %. For the TyrRS complexes with the Tyr-AMP and the diphosphate ion (PP_i), different catalytic loop conformations were modeled. ThePP_i remained in the active site with the compact form of catalytic loop during 100 ns simulation time, whereas it is rapidly (14 ns) released from the active site with the extended form of catalytic loop. We revealed that both $Mg^{2+}$and K^+ were functionally crucial in each step of the catalytic reaction. **Conclusion.** We performed the modeling of the *Bt*TyrRS complexes with the substrates corresponding to different stages of the catalytic reaction with the following MD simulations. The results obtained are in good agreement with other experimental and modeling data which allows usage of these models for the study on the mechanism of mammalian TyrRS function.

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An iron (II) clathrochelate derivatives and serum albumins: exploration of the binding

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The macrocyclic cage metal complexes –iron(II) clathrochelates possess a range of bioactive properties. These compounds are able to inhibit T-7 RNA polymerase, suppress the amyloid fibril formation, display a high toxicity in leukemia cells, bind serum albumins [1]. This provokes interest in studying their interaction with biomolecules, particularly the proteins. **Aim.** To characterize the interactions between clathrochelates, bearing different number of functional groups, with serum albumins (bovine/human, BSA/HSA) by physico-chemical **Methods:** fluorescent and circular dichroism (CD) spectroscopy, isothermal titration calorimetry (ITC). **Results.** The protein fluorescence quenching studies evidenced to the complex formation between the functionalized clathrochelates and albumins. This binding strongly depends on the nature of the ribbed substituents in the clathrochelate framework, an extreme binding affinity is observed for the compounds bearing carboxy groups (quenching of the BSA fluorescence up to 17 times). Upon binding, clathrochelates are able to gain optical activity and induce the pronounced CD-signal in 350-600 nm region. The shape and intensities of these CD-bands are determined by the nature and number of clathrochelate's ribbed substituents and kind of a protein. Only an alteration of isomery of carboxyphenylsulfid substituent results in the variations of their CD-bands intensity upon binding to HSA up to 63 times. In the presence of BSA and HSA, hexa carboxyphenylsulfid substituted clathrochelates evoke the CD-spectra of distinct maxima positions and intensity. Fluorescent studies at different pH and displacement method show the involving of albumins main binding sites I and II in this interaction. According to the ITC data, the thermodynamic parameters of the complex formation between hexa carboxyphenylsulfid clathrochelates and BSA are determined by the isomery of ribbed substituent's of clathrochelates. The binding constants of such complexes are moderate, K_a ranges from 5 to 28 $10^3 M^{-1}$ and the protein-ligand binding ratio is about 1:2 for meta- and ortho- isomers and 1:1 for para- isomer of compound. **Conclusions.** We suggest that the structure of albumin-clathrochelate complex noticeably depends on the spatial geometry of the clathrochelates ribbed substituents. This is reflected in the optical response –the isomers of functionalized clathrochelates differently affect the protein intrinsic fluorescence and the induced CD-signal character. This high structure-sensitivity gives clathrochelate the ability to distinguish the similar proteins (BSA and HSA) by acquiring different CD-bands in their presence.

1. *Blechinger J, Varzackii O, Kovalskaet V et al.*, *Bioorg Med Chem Lett*, V 26, Iss 2, Pp 626–629(2016)

Oligoribonucleotide effects on the influenza virus *in vitro* and expression of the *nos2, arg2*, *xdh, nfkbia*, *nfkb1* genes at the influenza virus infection *in vivo*

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Influenza (flu) virus causes activation of NOS2, Arg2, XOD enzymes involved in the production of free radicals, such as $NO^{\cdot}$, O_2^{-}, $ONOO^{-}$. Free radicals, involved in signal transduction pathways, activate the transcription factors such as NFκB and may lead to the lung tissue damage. It was shown that NFκB induces transcription of the proinflammatory genes in influenza-infected cells and takes part in the flu virus life cycle. Natural and synthetic oligoribonucleotides (ORN) have a wide range of biological effects playing a key role in the antiviral activity. However, the mechanisms underlying ORN effects are not clear for today. **Aim.** To study ORN effects on the influenza virus *in vitro* and the expression of the *nos2, arg2,xdh, nfkbia*, *nfkb1* genes at influenza virus infection *in vivo*. **Methods.** Experimental groups: healthy – healthy mice; prevention with ORN – ORN are injected to the mice 24 hours before the flu virus infection; treatment with ORN – ORN are injected to the mice 24 hours after the flu virus infection; inluenza –the flu-infected mice; control ORN – ORN are injected to the healthy mice. The ORN were modified by D-mannitol. The genes expression in the mouse lung cells was investigated with RT-PCR. The *gapdh* was used as a reference gene. The infectivity of flu virus and hemagglutinin (HA) activity, determined by cytopathic effect and HA assay respectively, were studied after incubation with the ORN. **Results.** The overexpression of all investigated genes was shown in the virus-infected mice compared to the healthy ones. We observed increasing the mRNA expression level of the *xdh*, *arg2, nos2, nfkbia* and *nfkb1* genes in the infected animals by 2.5, 3.5, 10, 3.2 and 1.5 times respectively compared to the healthy animals. A decrease in the mRNA level of the *arg2, nfkbia* and *nfkb1* genes was detected after the prevention and treatment with ORN compared to the virus-infected mice. The ORN injection for prevention and treatment reduced the mRNA expression level of the *arg2 gene* by 50 % and 22 % respectively vs. the virus-infected mice, whereas the mRNA expression of the *xdh* gene remained unchanged. A decrease in the mRNA expression of the *nos2* gene by 36 % occurred when the ORN were injected for prevention and an increase by 73 % at the treatment. The study of ORN influence on the flu virus showed a decrease in the infectious titer of flu virus by 3.0 $lgTCID_{50}$ and a 4-fold decrease in HA activity compared to thecontrol virus (without ORN). **Conclusions:** Our results have shown that the modification of ORN by D-mannitol modulates the expression of the *nos2*, *arg2,xdh,nfkbia*, *nfkb1* genes at the flu virus infection *in vivo* and affects flu virus *in vitro*. We supposed that ORN reduced the flu virus infectivity via decreasing HA activity.

Study of genomic variation in Deschampsia antarctica Desv. (*Poaceae*) from the maritime Antarctic

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Aim. *Deschampsia antarctica* Desv. is a unique species in the family *Poaceae* that occupies the Antarctic Peninsula region and demonstrates adaptation to the local unfavorable environments. It is well known that the stressful environmental factors can influence the plant genome by causing changes in the chromosome number and structure, as well as an increase in the genetic variation. Therefore, our study was aimed at investigating alterations in the genome of *D. antarctica* plants at both chromosomal and molecular levels that may be an important source of adaptive variation within the species. Furthermore, the genome stability was studied in the micropropagated plants and tissue cultures of the species. **Methods.** In the study we used *in vitro* grown *D .antarctica* plants that were derived from the seeds collected in the Argentine Islands region (Darboux, Galindez, Skua, Great Yalour Islands, and Rasmussen Cape) of Maritime Antarctic. The chromosome number of plants was determined in the cells of root apical meristems counterstained by DAPI. The 5S rDNA and 25S rDNA loci were visualized by the dual-color fluorescence *in situ* hybridization (FISH) technique. For cytological analysis the samples of tissue cultures derived from the root explants were fixed in ethanol : acetic acid = 3:1 and stained with 1% aceto-orsein. A molecular-genetic analysis was performed by PCR with polymorphic ISSR-primers. **Results.** Most of *D. Antarctica* plants from the Argentine Islands region have 2n = 26 chromosomes in their karyotypes. Moreover, the mixoploid plants were also found: accessions from Darboux Island (2n =13-27, 2n=26+1-2B) and Great Yalour Island (2n =13–39). FISH analysis revealed ten 5S rDNA sites and four 25S rDNA sites in the plant with the typical chromosome number (2n = 26). However, a greater number of rDNA loci (twelve of 5S rDNA and six of 25S rDNA) were found in the near-triploid plant from Great Yalour Island. The molecular-genetic analysis of *D. antarctica* plants demonstrated that the differences between the normal and mixoploid plants do not exceed the level of within population variation observed in the Argentine Islands region. The cytogenetic analysis revealed that tissue cultures have modal class composed of the cells with diploid and near-diploid chromosome number that indicates the conservation of cytogenetic features of *D. antarctica* genotypes at the early stages of culture irrespective of the karyotype of initial plant (diploid, mixoploid or poliploid). We failed to reveal the genetic changes in the clonally propagated *D. antarctica* plants during prolonged cultivation *in vitro* at both molecular (using ISSR-PCR) and chromosomal levels. The obtained results indicate that *in vitro* conditions used for the plant culture may ensure maintenance of the genome stability of *D. antarcica*. **Conclusions.** The cytogenetic analysis of *D. antarctica* plants revealed the intraspecies chromosomal polymorphism, which was further confirmed by FISH analysis. The molecular genetic analysis of the plants with different chromosome number demonstrated a low genetic diversity. The tissue cultures obtained from *D. antarctica* plants with the different karyotypes have similar cytogenetic structure with a predominance of diploid cells in the proliferative pool.

Molecular basis for proposed mechanism of editing activity by D-amino-acyl-tRNA-deacylase from *Thermus thermophilus*

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Introduction. Quality control during protein biosynthesis (particularly – in translation) provides an accurate flow of genetic information from mRNA to the correct amino acid sequence. This process is controlled by several mechanisms: precise amino acid recognition by aminoacyl-tRNA-synthetases (aaRSs), proofreading mechanisms against appearing mistakes by *cis*- (aaRSs) and *trans*-editing factors (additional enzymes), and discrimination of mischarged substrates by the elongation factors. D-aminoacyl-tRNA-deacylase (DTD) belongs to such *trans*-factors. It is involved in the correction of mischarged tRNAs with D-amino acids by aaRSs, which are deficient in the L-stereospecificity in recognition process. DTD is specific only to D-aminoacyl-tRNA substrates (D-Tyr/D-Phe/D-Trp/D-Asp-tRNA) and does not hydrolyse L-aminoacyl-tRNAs. TyrRS is not able to discriminate the stereospecificy of amino acids, requiring an additional checkpoint before elongation. **Aim.** To investigate the mechanism of aminoacylation by TyrRS from *Thermus thermophilus* (TyrRSTT) and editing misaminoacylated D-Tyr-tRNA^{Tyr}by DTD from *T. Thermophilus* (DTDTT), we used molecular modelling, molecular dynamic (MD) simulations, site-directed mutagenesis of the enzyme and tRNA^{Tyr} modifications. **Methods.** We performed comprehensive site-directed mutagenesis studies, based on molecular modelling and MD simulations of the proposed active site of DTDTT and amino- and deacylation assays with α-[^{32}P]-tRNA^{Tyr} from *T. thermophilus*. The structural model of DTDTT bound to the D-Tyr-A76 was generated by homology modelling using the reported crystal structure of *Plasmodium falciparum* DTD bound to this substrate [Ahmad, eLife, 2013]. MD simulations were used to study the frames where the water molecules formed a necessary angle and distance to perform a nucleophilic attack at a carbonyl group of the ester of the mischarged D-Tyr-tRNA^{Tyr} . The assays with radiolabelled tRNA^{Tyr} were applied as an experimental basement of the proposed catalytic mechanism. **Results.** The kinetic parameters for TyrRSTT aminoacylation reaction were determined from Michaelis-Menten plot by Origin 9.0 software, representing the average values from at least three independent measurements. The results of MD simulations after 5 ns were analysed to perform further in site-directed mutagenesis of the enzyme's active site. DTDTT and its substitution mutants G137A and P138A showed significant differences in the activity, confirming the importance of Gly-Pro motif in the enzyme's selectivity. The role of 3'-OH group of the terminal ribose of tRNA^{Tyr} is also essential for DTDTT' proofreading mechanism of the misaminoacylated substrates. **Conclusions.** In sum, because of the absence of discrimination between L- and D-Tyr by TyrRS (discrimination factor is only 11 against 3300 in the literature data of the ratio cognate/noncognate amino acid), there is the necessity of additional checkpoint of D-aminoacyl-tRNA substrates by DTDTT, the catalytic mechanism of which, based on MD stimulations and primary mutagenesis studies is proposed here.

Molecular docking study of oligoribonucleotides with D-mannitol molecule

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Aim. RNA is a pharmacologic target of many drugs currently used in clinical trials. Small molecules that bind RNA have been proven to be effective anticancer, antibiotic, and antiviral therapeutic agents. One of the most effective drugs of this series is an antiviral and anti-inflammatory drug "Nucleks". In our spectrometric studies we have found that RNA, which is part of the drug, forms complex with mannitol. Accordingly, the aim of our research was to model the complex formation between oligoribonucleotides and D-mannitol molecule. Also, we present the application of the flexible ligand docking techniques in order to elucidate the most probable oligoribonucleotide binding mode with D - mannitol molecule. **Methods.** Our investigation was performed using "Autodock", "Hyperchem" and "Chimera" software packages. **Results.** We have studied the interaction of oligoribonucleotides with different nitrogenous bases: adenine, uracil, guanine and cytosine. For complex formation we used oligoribonucleotides with 1, 3, 5 10, 15 nucleotides. We have obtained complex spatial structure of D-mannitol molecule with oligoribonucleotides. We have found that binding energy of single nucleotides is different and lies within the range of -2.0 to -1.9 kcal / mol. For 3 residue-long oligoribonucleotides the binding energy lies in the range of -4.1 to -2.7 kcal / mol. In this case the binding energy for oligoadenilate with D-mannitol is significantly less in comparison to binding energies for other oligoribonucleotides. For 5 residue-long oligoribonucleotides the bindig energy lies in the range of -3.9 to -3.4.For 10 residue-long oligorybonucleotides the binding energy value lies in the range of -4.0 to -3.3 kcal / mol. The lowest binding energy was observed in case of oligoguanilate. For 15 residue-long oligoribonucleotides the binding energy value was in the range of -4.3 to 3.1 kcal / mol. Similarly to previous cases, the biggest binding energy was observed in case of oligoguanilate. Therefore, the molecular docking analysis suggests that the D-mannitol molecule binds to the nitrogenous base within the oligoribonucleotide. **Conclusion.** This study allows us to predict more accurately the nature of the interactions between the molecules D–mannitol and oligoribonucleotides.

Conformational changes of Interferon under the influence of oligoribonucleotides and their derivative

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Aim. RNA-based antiviral drugs are actively implemented in practical medicine during last decades, nevertheless the molecular mechanism of their action is still unclear. As it was shown in our previous work the combination of total yeast RNA with alcohol sugar D-mannitol leads to the changes of the biological activity and efficiency. At this stage of our investigation we studied the ability of total yeast RNA and RNA-D-mannitol complex to affect the conformation and stability of interferon (IFN) α-2b - a key protein of the antiviral cell defense mechanism. **Methods.** To investigate the interaction, conformational changes and stability of IFN protein at the presence and/or absence of the ligands the fluorescence and CD (circular dichroism) spectroscopies were used. All experiments were performed on spectrofluorometer Jasco FP-8200 and CD spectrometer Jasco J-815 with the peltier temperature cell holder. **Results.** The thermal denaturation profiles of IFN α–2b, IFN α–2b (PEG) and IFNα–2b with 100mM NaCl alone and in the presence of RNA and RNA-D-mannitol complex were obtained from their fluorescence spectra at the temperature range of 25-75 ˚C. The analysis of these profiles shows that the addition of ligands leads to the thermal stabilization of protein and could indicate the interaction between IFN α-2b and the mentioned compounds that causes the changes of its conformation. For further confirmation of this assumption we calculated a dissociation constant that appeared to be relatively weak (micromolar) in all cases. CD spectroscopy demonstrated that both RNA and RNA-D-mannitol complex caused tiny alterations in the IFN 3D structure reflected in a small decrease in molar ellipticity within both helical bands. The analysis of IFN secondary structure changes by CDNN software shows that adding RNA or RNA-D-mannitol complex leads to the decreasing of α-spiral components in the protein structure and to the small increasing of β-turn and random coil components. All studied probes demonstrated that RNA-D-mannitol complex affects the IFN α-spiral stronger than RNA itself. **Conclusions.** We suppose that total yeast RNA and RNA-D-mannitol complex act as compounds, altering the secondary structure of interferon and in this way can change its biological activity. Our results are important for revealing a molecular mechanism of the antiviral action of RNA-based compounds.