protomer. However, our knowledge regarding the function of the second site remains unknown. Additionally, the mechanism of structural impact of S635 and T690 phosphorylation on Rad50 structure and global conformation of MRN complex is also elusive. In this study we produced a central 182-aa fragment of human Rad50 with phosphomimetic mutation T690E residue which was subjected to UV-Vis spectroscopy and spectropolarimetric studies with Zn(II) in order to determine the stability of non- and phosphomimetic states. N-terminally fluorescently labeled proteins, were subjected to examine conformational changes of Zn(II) complex under phosphorylated and dephosphorylated states. Our study indicates that phosphorylation of Rad50 at T690 decreases affinity of zinc hook to Zn(II) ion and promotes major conformational change in coiled coil region in the homodimer. This work was supported by the National Science Center of Poland under Opus grant no. 2014/13/B/NZ1/00935.

P.18-060-Wed
Effect of crowding on oligomeric state of sHsps at elevated temperatures

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Protein aggregation is a universal and unfavorable process for all cells leading to the production of non-native protein structures. It is known that protein aggregates are a hallmark of an increasing number of human diseases including neurodegenerative disorders. Small heat shock proteins (sHsps), as a class of molecular chaperones, form a large family of ubiquitous proteins, which act to prevent protein aggregation. As a rule, sHsps tend to form highly dynamic assemblies of different size and composition, which exchange subunits constantly. It is supposed that the polydispersity and quaternary structure dynamics play an important role in cellular sHsp chaperone function. The detailed mechanism of sHsps chaperone function remains debatable; however, it is often supposed that the large assembly of sHsps undergo reversible dissociation followed by interaction with unfolded proteins and subsequent reassociation to large chaperone-substrate complexes. Unfortunately, there are no data on oligomeric states of sHsps collected either directly in vivo or under conditions realistically mimicking the cell interior. Here, we present a few studies on assembly/disassembly and oligomeric distributions of several sHsps at elevated temperatures in vitro in the presence of agents that mimic crowded conditions. We showed by analytical ultracentrifugation that α-crystallin and αB-crystallin dissociated at elevated temperatures (40 and 48°C) in dilute buffer solutions. However, under crowded conditions sHsps tend to form large assemblies at elevated temperatures. For example, sedimentation coefficient, $s_{20,w}$, of HspB5 increases from 11 S in dilute solution to 20 S and 40 S in the presence of crowded agents and molecular mass of HspB5 increases from 480 kDa to 2 MDa. This study was funded by the Russian Foundation for Basic Research (grant 16-04-00560-a).

P.18-061-Mon
Physico-chemical properties of the chimeric tobamovirus coated with hordeivirus capsid protein with the deleted C-terminal region

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We replaced the CP gene of turnip vein cleaning tobamovirus (TVCV) by the mutant CP gene of Barley stripe mosaic hordeivirus (BSMV) with deletion of 22 C-terminal amino acid residues (TVCV ΔC-CP BSMV). Previously we demonstrated that the infectious cDNA clone of the mutant chimeric virus agroinfiltrated into N. benthamiana plants efficiently accumulated in infected and systemic leaves. Here we studied the physico-chemical characteristics of TVCV (ΔC-CP BSMV) isolated from the systemic symptomatic leaves. The virus preparation was characterized by transmission electron microscopy (TEM) and atomic force microscopy (AFM). The TEM data demonstrated that the preparation contained a heterogeneous set of filamentous structures with width of 5–7 nm, variable in length forming network clusters of a weak electron density. Similar images were obtained by AFM. Measurement of the hydrodynamic diameter of TVCV (ΔC-CP BSMV) particles by dynamic laser light scattering showed the presence of two peaks with sizes of about 100 nm and 800 nm indicating that the virus particles also form aggregates in the solution. However the removal of the C-terminal fragment of the CP BSMV does not significantly affect either the protein structure or its surface properties according the data of circular dichroism spectroscopy in the near ultraviolet range and the measurement of the surface zeta potential. It is known that the C-terminal disordered fragment of the CP is not involved in the formation of intersubunit interactions in the mature virion but we can not ruled out that it participates in the initial stages of the virion assembly. Our data indicate the importance of the integrity of the CP C-terminal region for the correct assembly of virions, and possibility of effective systemic transport of the tobamovirus genome in form of chimeric atypical virions (assumed ribonucleoprotein complexes). This work was supported by the Russian Science Foundation project No 14-24-00007.

P.18-062-Tue
Structural characterization of transferrin-bound ruthenium(II) terpyridine complexes

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Human serum transferrin (Tf) is 80 kDa protein that readily binds and transports Fe^{3+} throughout bloodstream and tissues. Transferrin contains two Fe^{3+} binding sites where two Tyr, one Asp and one His residues are included in Fe^{3+} binding. Also, Tf is believed to transport various metals and metal-based drugs, including Ru anticancer drugs. Since majority of tumor cells overexpress Tf receptor, delivery of Ru drugs via Tf cycle increases drug selectivity. Although some data on Ru(III) drug binding to Tf exists, data on Ru(II) drugs binding to this protein is scarce. In this work, binding of two Ru(II) drugs of general formula mer-[Ru(L3)(N-N)Cl][Cl] (where L3 = 4′-chloro-2,2′:6′,2″-terpyridine (Cl-tpy); N-N = 1,2-diaminoethane (en) or 1,2-diaminocyclohexane (dach)) to Tf has been confirmed using liquid chromatography (LC) and matrix-assisted laser desorption

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