catalyze poly(ADP-ribosyl)ation, constitute a large family of 17 proteins, but only PARP1 and PARP2 can be immediately activated by DNA damage. Whereas the role of PARP1 in response to DNA damage has been widely illustrated, the contribution of PARP2 has not been studied in detail. To find out specific DNA targets we evaluated affinity of PARP2 to several DNAs mimicking intermediates of different DNA metabolizing processes, and tested these DNA as 'activators' of PARP1 and PARP2. The influence of PARP2 (in comparison with PARP1) on several base excision repair (BER) proteins (Polβ and FEN1) has been investigated. As a whole, both PARPs negatively regulate the activity of the BER enzymes. The FEN1 influence on PARPs is differential: the PARP1 activity is inhibited while the PARP2 one is enhanced. Interplay between PARP1, PARP2, XRCC1 and polβ was also studied. The capability of PARP2 to interact with a key DNA intermediate of BER, abasic sites has been demonstrated for the first time. Therefore, our results testify to the complicated multilevel regulation of DNA synthesis during BER pathways under coordinated action of PARP1 and PARP2.This work was partially supported by RFBR projects 10-04-01083, 11-04-00559.

P20-105
How to determine the size of nuclei of protofibrils from the concentration dependence of lag-time duration of amyloid formation?

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The question about the size of nuclei of protofibrils formed by different proteins and peptides is yet open. By the nucleation mechanism, the formation of protofibrils begins from the thermodynamic unfavorable steps resulting in the formation of a critical nucleus consisting of n monomers. The kinetic model of the process of formation of amyloid fibrils is suggested in our work allowing us to calculate the size of the nucleus using kinetic data. In addition to the stage of nucleation, the given model includes both a linear growth of protofibrils (proceeding only at the cost of attaching of monomers to the ends) and an exponential growth of protofibrils at the cost of branching and fragmentation. Theoretically, only the exponential growth is compatible with the existence of a lag-period in the fibril formation kinetics. The obtained analytical solution and computer modeling allow us to determine the size of the nucleus from the experimentally obtained concentration dependences of the relationship between the lag-time duration and the time of growth of amyloid fibrils. In the case of insulin this relationship does not depend on the protein concentration. According to the elaborated theory it means that the size of the nucleus corresponds to that of the monomer. This study was supported in part by the Russian Foundation for Basic Research (grant 11-04-00763), Russian Academy of Sciences (programs ''Molecular and Cell Biology'' (01200959110 and 01200959111) and ''Fundamental Sciences to Medicine'').

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Functional and structural interactions of Nb, V, Mo and W oxometalates with the sarcoplasmic reticulum $Ca2^{+}$ -ATPase reveal new insights into inhibition processes: a combination of NMR, Raman, AA and EPR spectroscopie with kinetic studies

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Oxometalates, in particular decavanadate, is a potent inhibitor (IC_{50} 15 μM) of the hydrolytic activity of sarcoplasmic reticulum Ca^{2+}-ATPase, a transmembrane protein involved in calcium translocation and responsible for muscle contraction relaxation [1]. Here, we further investigate the interaction of niobate, vanadate, molybdate and tungstate oxometalates with the sarcoplasmic reticulum Ca^{2+}-ATPase in order to reveal new insights into the metal inhibition mechanisms, by combining NMR, AAS, Raman and EPR spectroscopie with kinetic studies. The decavanadate calcium pump interaction is promoted by ATP, and prevented by the iso-structural and iso-electronic decaniobate, as observed by NMR spectroscopy. On the other hand, atomic absorption spectroscopy (AAS), indicatest that decavanadate (V_{10}) binds in the same extent to all protein conformations occurring during the process of calcium translocation, namely E1, E1P, E2 and E2P. Decavanadate ATPase activity inhibition is shown to be competitive at lower concentrations (10 μM) and non-competitive for higher concentrations (50 μM), whereas decaniobate shows a non-competitive inhibition at all concentrations. Although only vanadate and decavanadate induces protein cystein oxidation, gluthatione – a known intracelullar antioxidant – does not revert the inhibition promoted by any of the oxometalates analysed. Finally, the Raman studies suggested that decavanadate, decaniobate and vanadate induce similar Ca^{2+}-ATPase conformational changes – different from E1 or E2 – that differ from those observed upon molybdate and tungstate interaction. In conclusion, decavanadate shows a specific interaction with the calcium pump, as opposed to the other oxometalates, and induces cysteine oxidation and multiple inhibition types. The ATPase inhibition is not reverted by antioxidants and shows a specific mode of interaction between the decavanadate and the Ca^{2+}-ATPase which is not affected by any of the protein conformations that occurs during the process of calcium translocation.
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P20-107
Conformational studies of human leukocyte antigens: when infrared spectroscopy meets immunology

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Human leukocyte antigen (HLA) class I molecules consist of a polymorphic heavy chain (HC), non-covalently associated β_2-microglobulin (β_2m), and a peptide. Certain HLA-B27 subtypes,