the long run, the transfection efficiency of pegylated liposomes increases in comparison with the unmodified particles. The most effective transfection was achieved with the insertion of 4–6 mol % PEG in the liposomes. It should be also noted that the structure of thehydrophobic anchor in PEG-derivatives does not affect the physico-chemical and biological properties of the particles.

This work was supported by the Russian Science Foundation (grant № 17-74-10111).

Modeling of ATP synthase rotor ring protein-lipid complex

Novitskaia O.S., Buslaev P., Gushchin I.
Research center for molecular mechanisms of aging and age-related diseases, Moscow Institute of Physics and Technology, Dolgoprudny, Russia
e-mail: olga.novitskaya@phystech.edu, ivan.gushchin@phystech.edu

ATP synthases are large multiprotein complexes found in all kingdoms of life and in cell membranes of prokaryotes as well as in mitochondria and chloroplasts of eukaryotes [1]. Generally, the complexes consist of two subunits, one of which is soluble and another is embedded in the membrane. The membrane part includes a so-called c-ring formed by 8 to 15 *c* subunits, which is rotating in the membrane during ATP synthesis. Highly detailed atomistic structures of isolated c-rings and whole ATP synthases have recently become available [2]. Here, we present a computational approach for obtaining models of c-ring-lipid complexes. The resulting models are stable in simulations, and positions of lipid molecules correspond well to those observed in experimental structures.

1. Walker J.E. The ATP synthase: the understood, the uncertain and the unknown. *Biochem. Soc. Trans.* (1-16). **41** (2013).
2. Kühlbrandt W. & Davies K.M. Rotary ATPases: a new twist to an ancient machine. *Trends Biochem. Sci.* (106–16) **41** (2016).

Comparison of various substitution matrices for amino acid alignment and homology search of microbial rhodopsins

Novoseletsky V.N.[1], Kudriavtsev A.V.[1,2], Armeev G. A.[1], Shaitan K.V.[1], Kirpichnikov M.P.[1,3]
[1]Lomonosov Moscow State University, Biological Faculty, Moscow, Russia; [2]Emanuel Institute of Biochemical Physics, RAS, Moscow, Russia; [3]Shemyakin–Ovchinnikov Institute of Bioorganic Chemistry, RAS, Moscow, Russia
e-mail: valeryns@gmail.com

Alignment of amino acid sequences by means of dynamic programming is one of the popular sequence comparison methods. This work is focused on the finding of microbial rhodopsin family-specific scoring functions for global similarity matrix-based sequence alignment. We constructed a set of substitution matrices based on sequence (RHOD1, RHOD2) and structure (RHODS) alignment of microbial rhodopsins using methods described elsewhere [1]. We examined performance of developed substitution matrices along with several popular (BLOSUM, VTML) and rare (JTT, PHAT, PFASUM) substitution matrices for pairwise amino acid alignment of microbial rhodopsins in two kind of tests. First, we compared alignments obtained with the particular matrix with a reference alignment obtained from structural superposition of corresponding proteins. We found that all matrices demonstrate similar performance which was slightly better for family-specific matrices RHOD1, RHOD2, and RHODS. Second, we checked an ability of matrices under consideration to detect similarity between type-1 rhodopsins and novel heliorhodopsin discovered recently [2]. To this end, we tried to find probable heliorhodopsin homologues in SwissProt and PDB databases. In this test, matrices showed very different performance. While BLOSUM and VTML matrices were able to detect similarity with halorhodopsin in both databases, PFASUM matrices did it only in PDB and the rest matrices (RHOD1, RHOD2, RHODS, JTT, PHAT) failed the test.
The research is carried out using the equipment of the shared research facilities of HPC computing resources at Lomonosov Moscow State University [3]. The work is ongoing with the support of RFBR grant 17-00-00167K (KOMFI 17-00-00166).

1. Kuznetsov I.B., Protein sequence alignment with family-specific amino acid similarity matrices BMC Res. Notes 4 (2011).
2. Pushkarev A., et al. A distinct abundant group of microbial rhodopsins discovered using functional metagenomics. Nature 558 (2018).
3. Sadovnichy V., et al. "Lomonosov": supercomputing at Moscow State University in:, Contemp. High Perform. Comput. From Petascale Towar. Exascale (2013).

The role of acetylcholine in P2X7-gated mast cells activation

Nurkhametova D.F.[1,2], Koroleva K.S.[1,2], Sinyavin A.E.[3], Tsetlin V.I.[3], Giniatullin R.G.[1,2]
[1]Kazan Federal University, Laboratory of Neurobiology, Kazan, Russia; [2]University of Eastern Finland, A.I. Virtanen Institute, Kuopio, Finland; [3]Shemyakin-Ovchinnikov Institute of Bioorganic Chemistry, Moscow, Russia
e-mail: d.nurkhametova@gmail.com

Emerging evidence suggest implication of immune system and inflammation in migraine. Thus, patients with migraine revealed signs of systemic inflammation, such as elevated levels of several pro-inflammatory cytokines including interleukin-1β (IL-1β), IL-6, and tumor necrosis factor-alpha (TNFα) [1, 2]. In the frame of the cholinergic anti-inflammatory pathway (CAP) theory, it has been shown that acetylcholine (ACh) via nicotinic receptors inhibited ATP-triggered release of the pro-inflammatory interleukin-1β [3]. However, it remains unclear whether it was inhibited at the P2X7 receptor level or at following stages.
To address this issue, in this project, we investigated ATP-induced activation of P2X7-gated channels on peritoneal mast cells and tested effect of ACh on opening of P2X7-gated channels. Freshly isolated mast cells were stimulated with ATP alone, or in the presence of ACh. To assess mast cells activation, we used a fluorescent dye YO-PRO1, which penetrates the cell membrane through opened P2X7-gated ion channels. Samples were analyzed using flow cytometry.
We found that ATP largely increased P2X7 receptor-mediated uptake of YO-PRO1 in mast cells. ACh also slightly increased YO-PRO1 uptake but this cholinergic agonist did not reduce ATP-induced dye uptake via P2X7 channels. Obtained data indicate that ATP efficiently opens P2X7 receptor large pore associated with activation of inflammasome. The lack of inhibitory effect of ACh suggests that its anti-inflammatory action is realized downstream of active P2X7-receptors.
This work was supported by RFBR KOMFI grant 17-00-00053 and performed in the framework of the Russian Government Program of Competitive Growth of Kazan Federal University. DN was supported by EDUFI fellowship.

1. Wang, F. *et al*. Association of serum levels of intercellular adhesion molecule-1 and interleukin-6 with migraine. *Neurol Sci*. (2015) 36:535-540. https://doi.org/10.1007/s10072-014-2010-3.
2. Khaiboullina, S. *et al*. Cerebellar atrophy and changes in cytokines associated with the CACNA1A R583Q mutation in a Russian familial hemiplegic migraine type 1 family. *Front Cell Neurosci*. (2017) 11:263. https://doi.org/10.3389/fncel.2017.00263.
3. Hiller, S. et al. β-Nicotinamide adenine dinucleotide (β-NAD) inhibits ATP-dependent IL-1β release from human monocytic cells (2018) 19: 1-21. https://doi.org/10.3390/ijms19041126