[5] Fermani, S.; Falini, G.; Ripamonti, A.; Bolognesi, A.; Polito, A.; Stirpe, F., *Acta Cryst. D* 2003, 1227
[6] Fermani, S.; Tosi, G.; Farini, V.; Falini, G.; Polito, L.; Ripamonti, A.; Roveri, N.; Barbieri, L.; Chambery, A.; Bolognesi, A. *J. Biol. Chem.* 2007, submitted.

MS04 P12

Ribosomal protein L1 in complex with the rRNA and mRNA: regulation of L1 translation. Alexey Nikulin[a], Svetlana Tishchenko[a], Natalia Nevskaya[a], Ekaterina Nikonova[a], Vladislav Kljashtorny[a], Oleg Nikonov[a], Sergei Volchkov[a,b], Wolfgang Piendle[c], Maria Garber[a], Stanislav Nikonov[a] [a]*Institute of Protein Research RAS, Pushchino, Moscow Region, 142290, Russia.* [b]*Institute of Cell Biophysics RAS, Pushchino, Moscow Region, 142290, Russia,* [c]*Institute for Medical Chemistry and Biochemistry, A-6020 Innsbruck, Austria.*
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Keywords: RNA-protein complexes, RNA-protein interactions, ribosome structure and function

A typical example of regulation on the level of translation is coordinated synthesis of ribosomal components during ribosome biogenesis. When synthesized in excess over rRNAs, some primary rRNA binding ribosomal proteins interact with their mRNA and inhibit translation of their own genes and the other genes in their operons. A serial works on the structures of complexes between ribosomal protein L1 and its targets on 23S rRNA and mRNA have been carried out by our group [1, 2, 3, 4]. The structures of the ribosomal protein L1 protuberance and two regulatory complexes have been determined and analyzed. Both binding sites on the RNAs share a conserved consensus structure, however, the protein binds to its 23S rRNA target site with at least 10-fold higher affinity than to its regulatory site on the mRNA. A structural analysis of L1-rRNA and L1-mRNA complexes revealed structurally invariant regions of the RNA-protein interfaces presumably responsible for the RNA-protein recognition. This region belongs exclusively to domain I of the protein. We conclude that domain II of the protein does not contribute to the RNA recognition but increased the stability of the ribosomal complexes in comparison with the L1-mRNA one. To confirm experimentally that domain I of the L1 protein recognizes targets for the protein on the both RNA molecules, truncated L1 variant has been prepared and RNA-binding ability of the isolated domain I was tested. This work was supported by the Russian Academy of Sciences, the Russian Foundation for Basic Research (grants №№04-04-49634, 03-04-48327) and the PCB RAS program. The research of M.G. was supported in part by International Research Scholar's award from HHMI.

[1] Nikulin A., Eliseikina I., Tishchenko S., Nevskaya N., Davydova N., Platonova O., Piendl W., Selmer M., Liljas A., Drygin D., Zimmermann R., Garber M. and Nikonov S. *Nature Struct. Bio,l.* 2003, 10, 104
[2] Nevskaya N., Tishchenko S., Gabdoulkhakov A., Nikonova E., Nikonov O., Nikulin A., Platonova O., Garber M., Nikonov S., Piendl W. *Nucleic Acids Res.,* 2005, 33, 478.
[3] Nevskaya N., Tishchenko S., Volchkov S., Kljashtorny V., Nikonova E., Nikonov O., Nikulin A., Kohrer C., Piendl W., Zimmermann R., Stockley P., Garber M., Nikonov S. *J Mol Biol.* 2006, 355, 747.
[4] Tishchenko S., Nikonova E., Nikulin A., Nevskaya N., Volchkov S., Piendl W., Garber M., Nikonov S. *Acta Crystallogr D,* 2006, 62, 1545.

MS04 P13

The Electron Transfer Complex Rubredoxin – Rubredoxin Reductase from *P. aeruginosa*. Gregor Gregor Hagelüken[a], Dirk W. Heinz[b], Burkhard Tümmler[c], Wolf-Dieter Schubert[a] [a]*Molecular Host Pathogen Interactions,* [c]*Structural Biology, Helmholtz Centre for Infection Research, Braunschweig,* [c] *Hannover Medical School, Hannover, Germany.*
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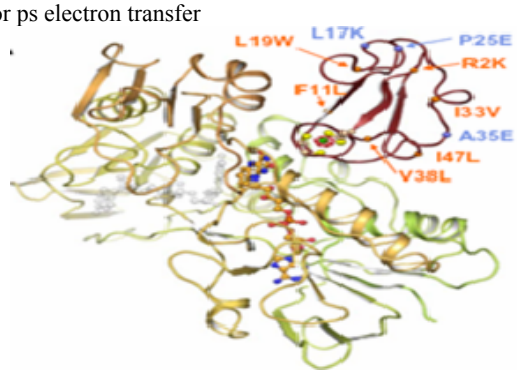
Keywords: Protein-Protein Recognition, Electron Transfer, Pathogenic Bacteria

Crude oil spills represent a major ecological threat due to the chemical inertness of the constituent n-alkanes. The Gram-negative bacterium *Pseudomonas aeruginosa* is one of the few bacterial species able to metabolize such compounds. Three chromosomal genes, *rubB*, *rubA1* and *rubA2* coding for an NAD(P)H:rubredoxin oxidoreductase (RdxR) and two rubredoxins (Rdxs) are required for this ability. They constitute an electron transport (ET) pathway shuttling reducing equivalents from carbon metabolism to the membrane-bound alkane hydroxylases AlkB1 and AlkB2. The RdxR/Rdx system is also crucial as part of the oxidative stress response in archaea or anaerobic bacteria, and has been analyzed in detail as a model system for ET processes. We have solved the structure of RdxR of *P. aeruginosa* both alone and in complex with Rdx, without the need for crosslinking at 2.3 and 2.4 Å resolution, respectively.
RdxR consists of two cofactor-binding domains and a C-terminal domain essential for the specific recognition of Rdx. Only a small number of favorable interactions govern mutual recognition of RdxR and Rdx, corroborating the transient nature of the complex. The shortest distance between the redox centers is 7.5 Å, allowing for ET rates in the picosecond range.

Fig. 1 The complex of Rubredoxin:NADH oxidoreductase (orange-green) with rubredoxin (red). The distance from FAD of RdxR to the Fe^{3+} of rubredoxin is 7.5 Å allowing for ps electron transfer



[1] Hagelueken G, Tümmler B, Heinz DW, Schubert W-D, *Submitted for publication.*