Experiments have also demonstrated that several other cytokine receptor
Another miRNA, miR-141, is also predicted to interact with the same region.
structure, ultimately resulting in an increased fraction of paused ribosomes.
with miR-1224. Such interactions can increase the stability of the whole
mRNA – 1 PRF signals are controlled via miRNAs. Altogether these results indi-
1201-Pos Board B152
Exploring RNA Condensation
Suzette A. Pabit, Andrea M. Katz, Lois Pollack.
Applied and Engineering Physics, Cornell University, Ithaca, NY, USA.
DNA and RNA molecules both serve as genetic material inside viruses but the
sequence-specific miRNA interactions. Funded in part by HHSN261200800001E.

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U4 snRNA Regulates Formation of the U6 Telestem within the U4/U6 Di-snRNA
Margaret L. Rodgers1, Allison L. Didychuk2, Samuel E. Butcher1, David A. Brow2, Aaron A. Hoskins1.
1Biochemistry, University of Wisconsin - Madison, Madison, WI, USA,
2Biomolecular Chemistry, University of Wisconsin - Madison, Madison, WI, USA.
Many of the splicedosomal small nuclear RNAs (snRNAs) undergo large-scale structural rearrangements during splicedosome assembly, activation and catalysis. This is exemplified by the highly conserved U6 snRNA which can exist in isolation in the U6 small nuclear ribonucleoprotein (snRNP); basepaired with U4 in the U4/U6 di-snRNP, U4/U6/U5 tri-snRNP, and splicedosomal B complex; or basepaired with the pre-mRNA intron and the U2 snRNA in the catalytic splicedosome. Through genetic evidence and structure probing (1, 2), it was previ-ously proposed that the U4/U6 di-snRNA consisted of a three-helical junction core domain nucleated by the U6 stranded regions. Using single-molecule Förster resonance energy transfer (smFRET), we discovered a dynamic equilibrium be-
tween RNA conformations formed by the flanking single stranded regions. Our
smFRET data is consistent with the presence of two mutually exclusive struc-
tures: (1) a U4/U6 di-snRNA containing both basepaired U4/U6 and the U6 tele-
stem and (2) a U4/U6 di-snRNA with extended basepairing located near U4/U6 stem I. These data show that the U6 telestem persists in the U4/U6 di-snRNA and that its formation can be regulated by novel basepairing interactions with U4. This suggests conservation of mechanism between the yeast and human U4/U6 di-snRNAs. Finally, we speculate that telestem formation can be dynami-
cally regulated by splicedosomal proteins to aid in tri-snRNP disassembly and splicedosome activation. Rationalizing previous observations concerning the mechanism of the U4/U6 RNA helicase Brr2.
References
Direct probing of RNA structure and RNA-protein interactions in purified
HeLa cell’s and yeast splicedosomal U4/U6.U5 tri-snRNP particles. Journal of

1200-Pos Board B151
A Ribosomal Frameshifting Structure in the CCR5 mRNA Leads to
Mirna-Stimulated Simultaneous-Mediated mRNA Decay
Wejcieczech Kasparkiewicz1, Jonathan D. Dinman1, Bruce A. Shapiro3.
1Basic Research Program, Leidos Biomedical Research, Inc., Frederick, MD, USA,
2Department of Cell Biology and Molecular Genetics, University of
Maryland, College Park, College Park, MD, USA, 3Basic Research Laboratory,
National Cancer Institute, Frederick, MD, USA.
RNA structure-based signals are used by viruses to affect programmed ribo-
somal frameshifting (PRF) yielding extended fusion protein products in a frac-
tion of translation processes. Computational tool identified – 1 PRF signals in
cellular mRNAs have been predicted to lead to premature termination of trans-
lation in the vast majority of cases. We found that a -1 PRF signal predicted in
the mRNA of the human CCR5 cytokine receptor is a pseudoknotted structure
that is responsible for redirecting translation toward a premature termination
codon (PTC), ultimately destabilizing the mRNA via the nonsense mediated
mRNA decay pathway (NMD) and possibly another decay pathway. A chemo-
kine receptor, CCR5 is also a co-receptor used by HIV-1 to enter its target CD4+
T-cells. We built a 3D model of the -1 PRF structure and validated its stability in
molecular dynamics simulations (MD). The structure is a two-stemmed pseudo-
knot, with the larger of the two stem domains consisting of multiple half-turn hel-
ical segments, separated by asymmetric single strands, which enable bending of
the larger stem region and bridging of the two stems. MD predicted this larger
region and the pseudo-knot to be stable, which is consistent with the experimen-
tal results indicating that it may form triple base interactions with miR-1224. Such interactions can increase the stability of the whole – 1 PRF structure, ultimately resulting in an increased fraction of paused ribosomes. Another miRNA, miR-141, is also predicted to interact with the same region. Experiments have also demonstrated that several other cytokine receptor

Membrane Physical Chemistry 1

1203-Pos Board B154
Influence of Ether Bronds and Branched Lipid Tails on Stability of Mem-
brates to Pore Formation
Petr V. Panov1,2, Sergey A. Akimov1,3, Pavel E. Volynsky4, Oleg V. Batsichev5,6,7.
1A.N. Frumkin Institute of Physical Chemistry and Electrochemistry of RAS (IPCE RAS), Moscow, Russia Federation, 2Moscow Institute of Physics and
Technology, Dolgoprudny, Russian Federation, 3National University of
Science and Technology “MISiS”, Moscow, Russian Federation, 4M.M. Shemyakin and Yu.A. Ovchinnikov Institute of Bioorganic Chemistry of
RAS, Moscow, Russian Federation.
Archaeal lipid membranes have a number of unique structural features that distinguish them from those of bacteria and eukaryotes allowing archaea to sur-
vive in harsh environments, such as high temperature, increased acidity and
pressure. To date the data on the impact of certain peculiarities of archaeal
lipids on its membrane properties are fragmentary and insufficient for the
understanding of their functioning. In general, archaea contain diether and tet-
rather lipids with chemically stable ether bond. Archaeal lipid tails are fully
saturated (with rare exceptions) isoprenoid chains and sometimes contain