



Atypical translation mechanism of selenoprotein mRNPs

Anne-Sophie Gribling-Burrer, Laurence Wurth, Michael Leichter, Séverine Massenet, Franck Martin, Gilbert Eriani, Christine Allmang

► To cite this version:

Anne-Sophie Gribling-Burrer, Laurence Wurth, Michael Leichter, Séverine Massenet, Franck Martin, et al.. Atypical translation mechanism of selenoprotein mRNPs. Colloque SifrARN 2016, Mar 2016, Toulouse, France. hal-03550134

HAL Id: hal-03550134

<https://hal.science/hal-03550134>

Submitted on 3 Feb 2022

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Atypical translation and maturation mechanism of selenoprotein mRNPs

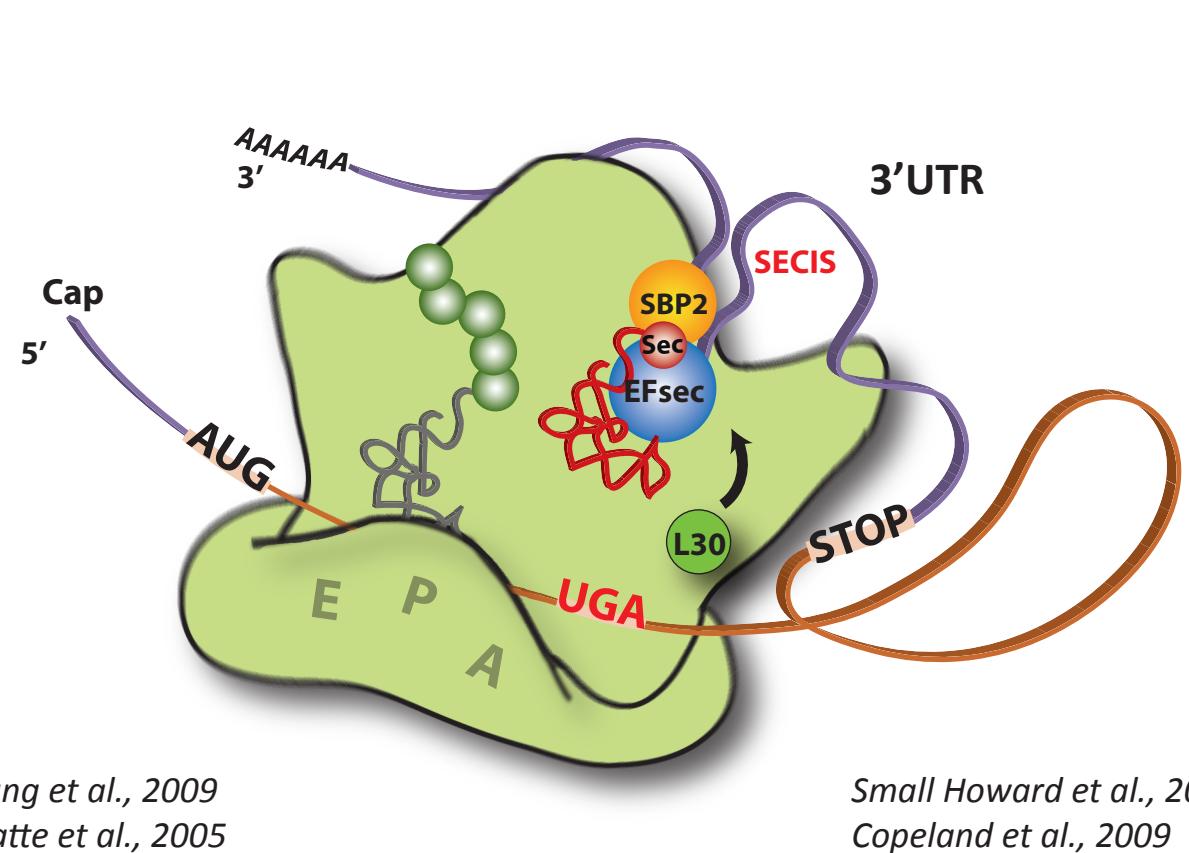


Gribling AS, Wurth L, Leichter M, Massenet S*, Martin F, Eriani G and Allmang C



University of Strasbourg, CNRS, Architecture and Reactivity of RNA, Strasbourg, France ;
*University of Lorraine, CNRS, Ingénierie Moléculaire et Physiopathologie Articulaire (IMoPA), Vandoeuvre-lès-Nancy, France
c.allmang@ibmc-cnrs.unistra.fr

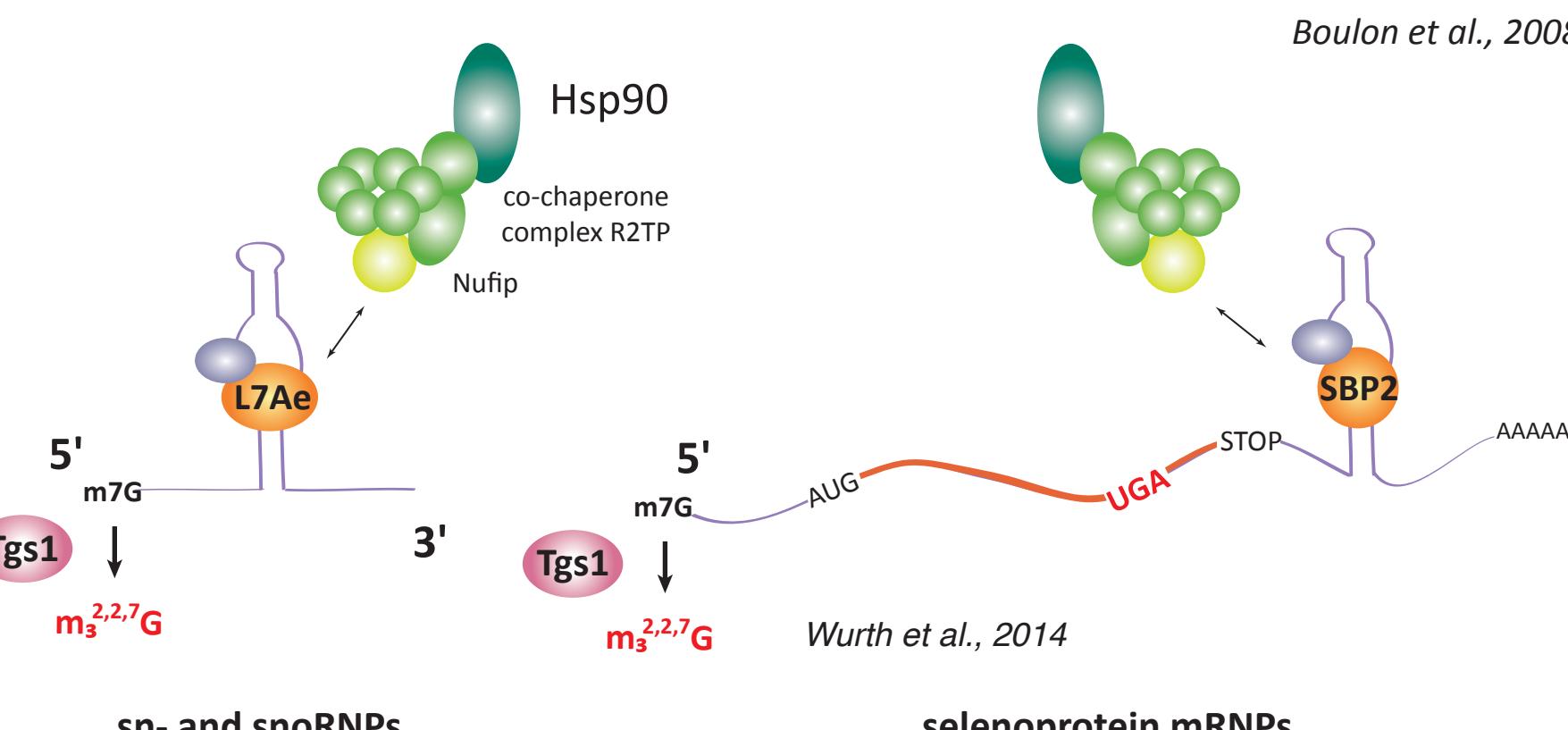
Selenoprotein synthesis, a complex mechanism of co-translational recoding



Allmang et al., 2009
Chovatte et al., 2005
Small Howard et al., 2006
Copeland et al., 2009

Selenoproteins, key players of oxidative stress protection, are synthesized by co-translational recoding mechanisms of in-frame UGA codons. In mammals, this process is governed by the recruitment of dedicated factors to a hairpin structure, called Selenocysteine Insertion Sequences (SECIS), in the 3'UTR of selenoprotein mRNAs. Essential in this process is the SECIS binding protein 2 (SBP2) that binds the SECIS RNA and recruits translation and assembly factors to the mRNP.

Selenoprotein mRNA assembly and processing : similarities with sn(o)RNPs

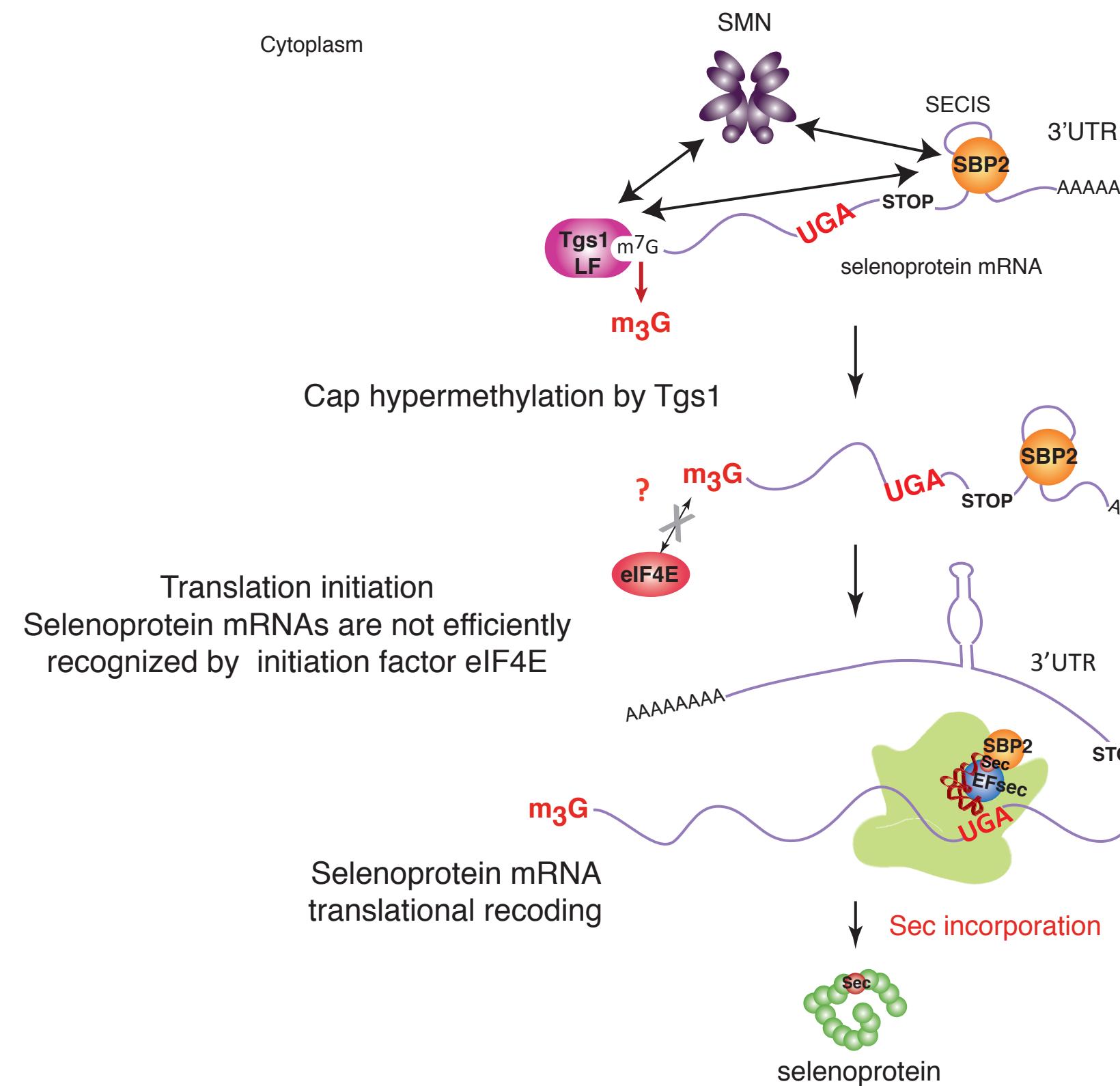


Boulon et al., 2008
Wurth et al., 2014

SBP2 shares a common RNA binding domain with core proteins of small non-coding RNPs. Selenoprotein mRNP assembly in the 3'UTR is similar to that of snRNPs (splicing) or snoRNPs (ribosome biosynthesis) and involves a complex linked to the HSP90 chaperone (Boulon et al., 2008).

We have demonstrated that several selenoprotein mRNAs, unlike most mammalian mRNAs, bear a hypermethylated $m_3^{2,2,7}G$ cap instead of a classical 7-methylguanosine (m_7G) cap and undergo a similar 5' end maturation pathway than non-coding RNAs (Wurth et al. 2014).
The trimethylguanosinesynthase 1 (Tgs1) hypermethylates the cap of selenoprotein mRNAs and is recruited by the assembly chaperone Survival of Motor Neuron (SMN) devoted to sn- and snoRNP maturation.

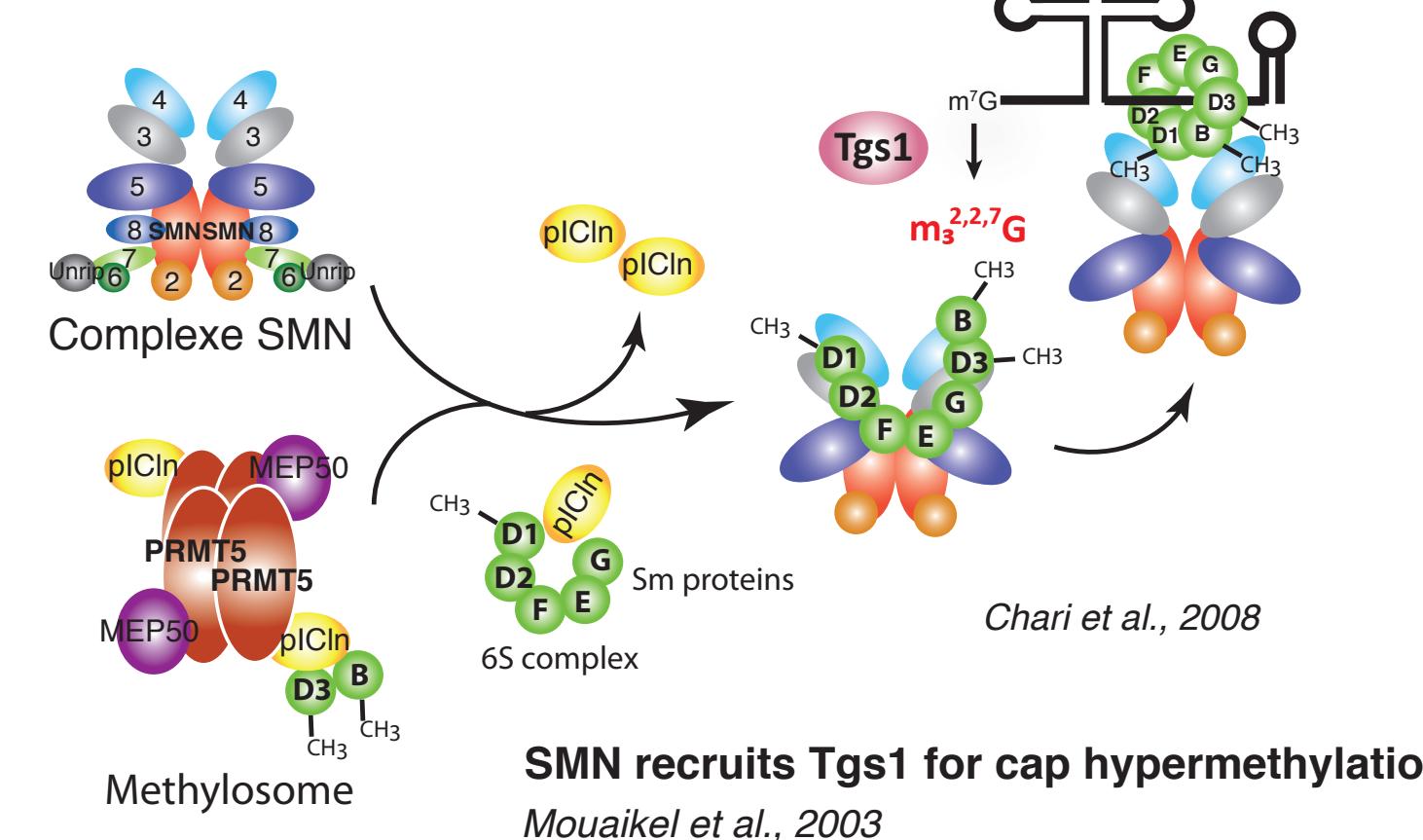
The cap of selenoprotein mRNAs is hypermethylated



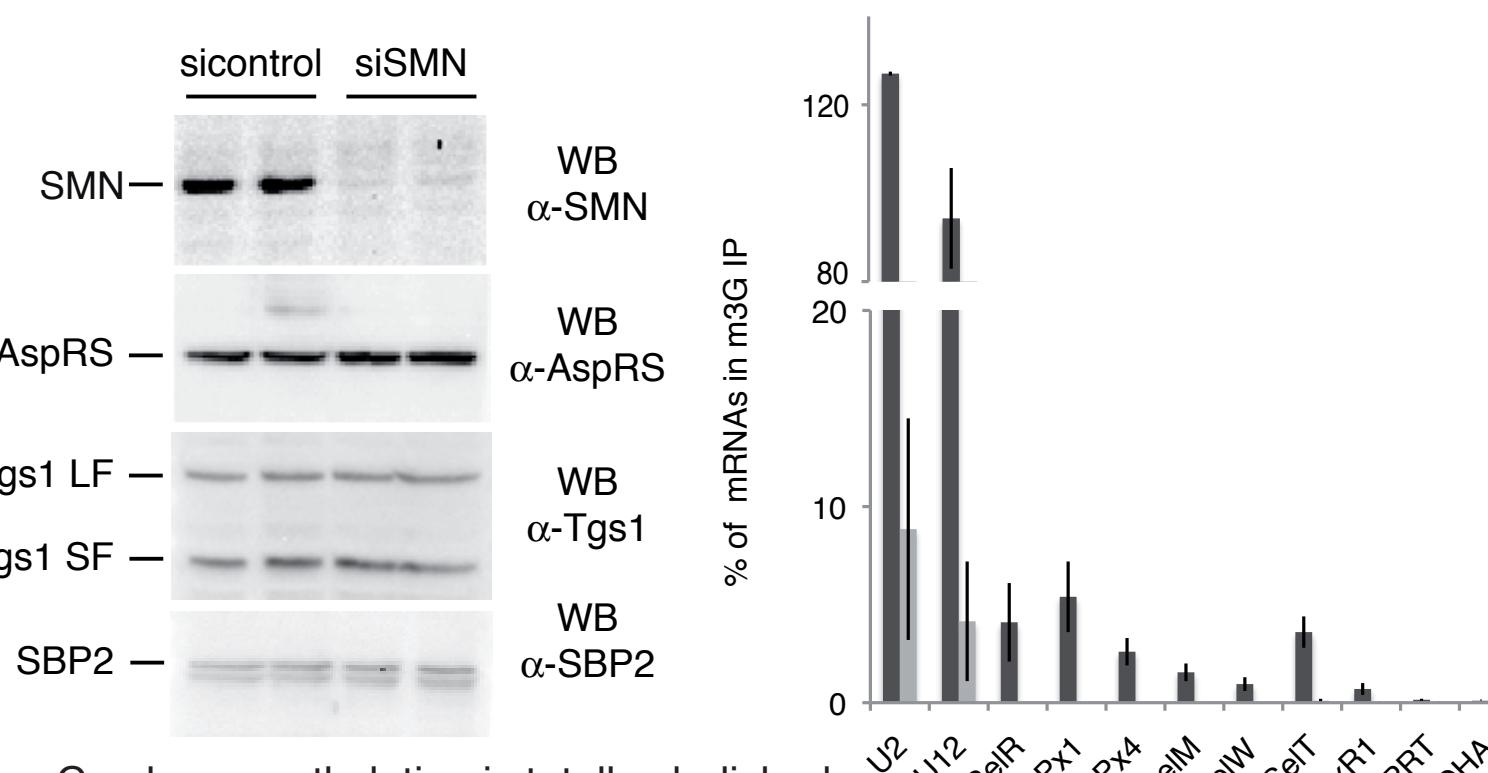
Wurth L (1), Gribling-Burrer A.S (1), Verheggen C, Leichter M, Takeuchi A, Baudrey S, Martin F, Krol A, Bertrand E and Allmang C. Nucleic Acids Res. 2014, 42, 8663-8677. (1) Contributed equally.

Aim: Determine the implication of the SMN complex and the methylosome in the cap maturation and expression of selenoprotein mRNAs

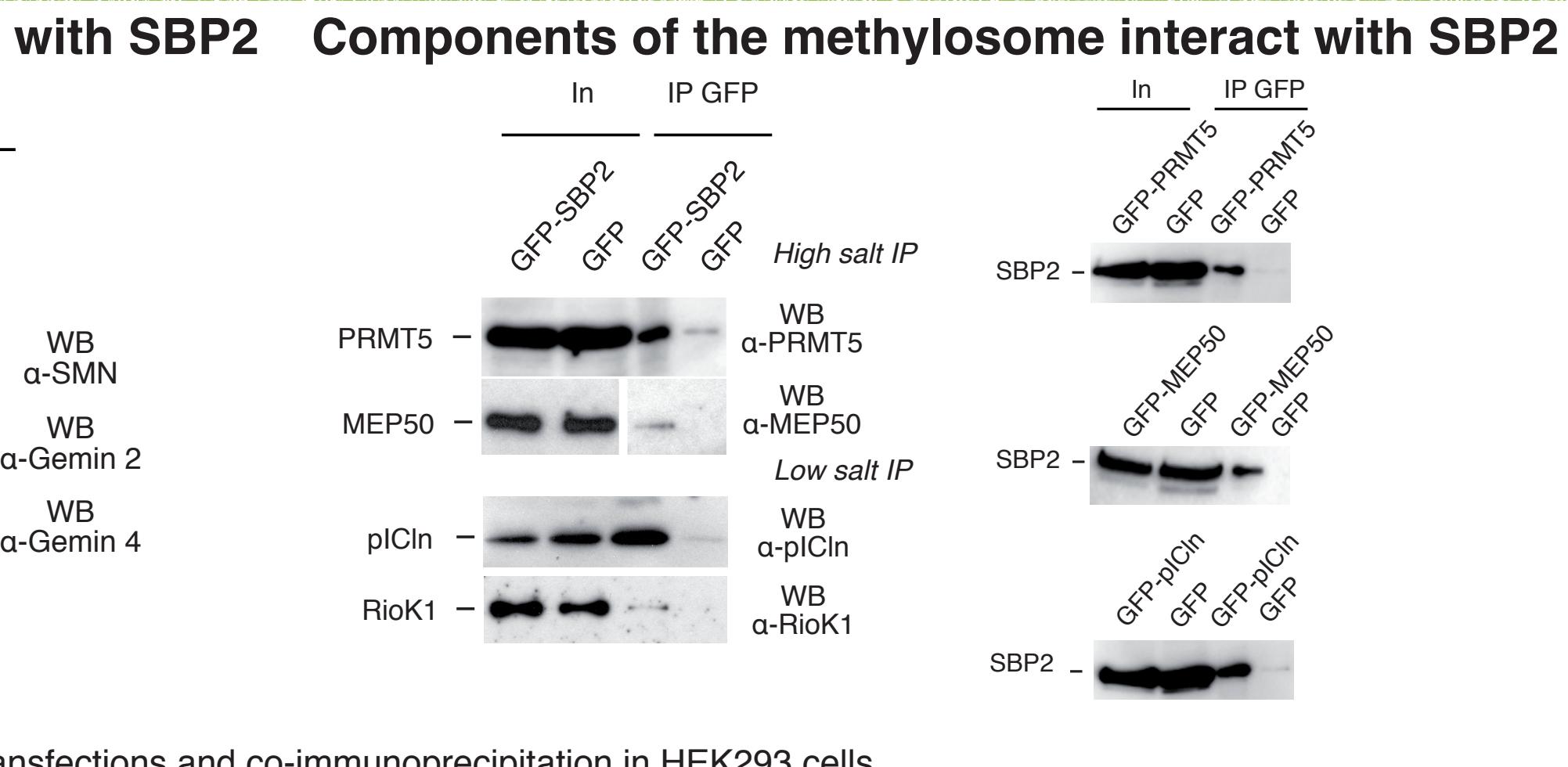
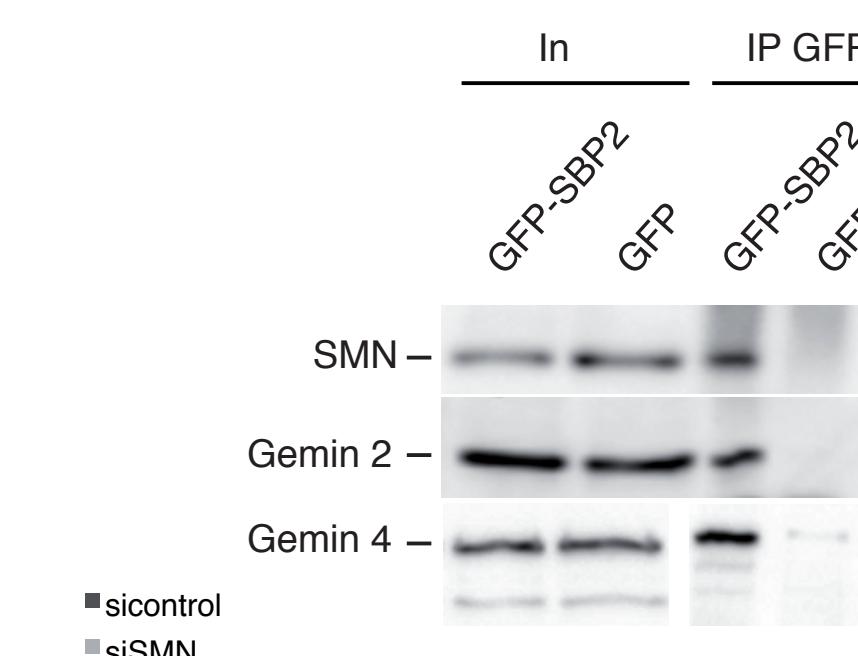
Role of the SMN complex and the methylosome in snRNP assembly



SMN is required for cap hypermethylation of selenoprotein mRNAs



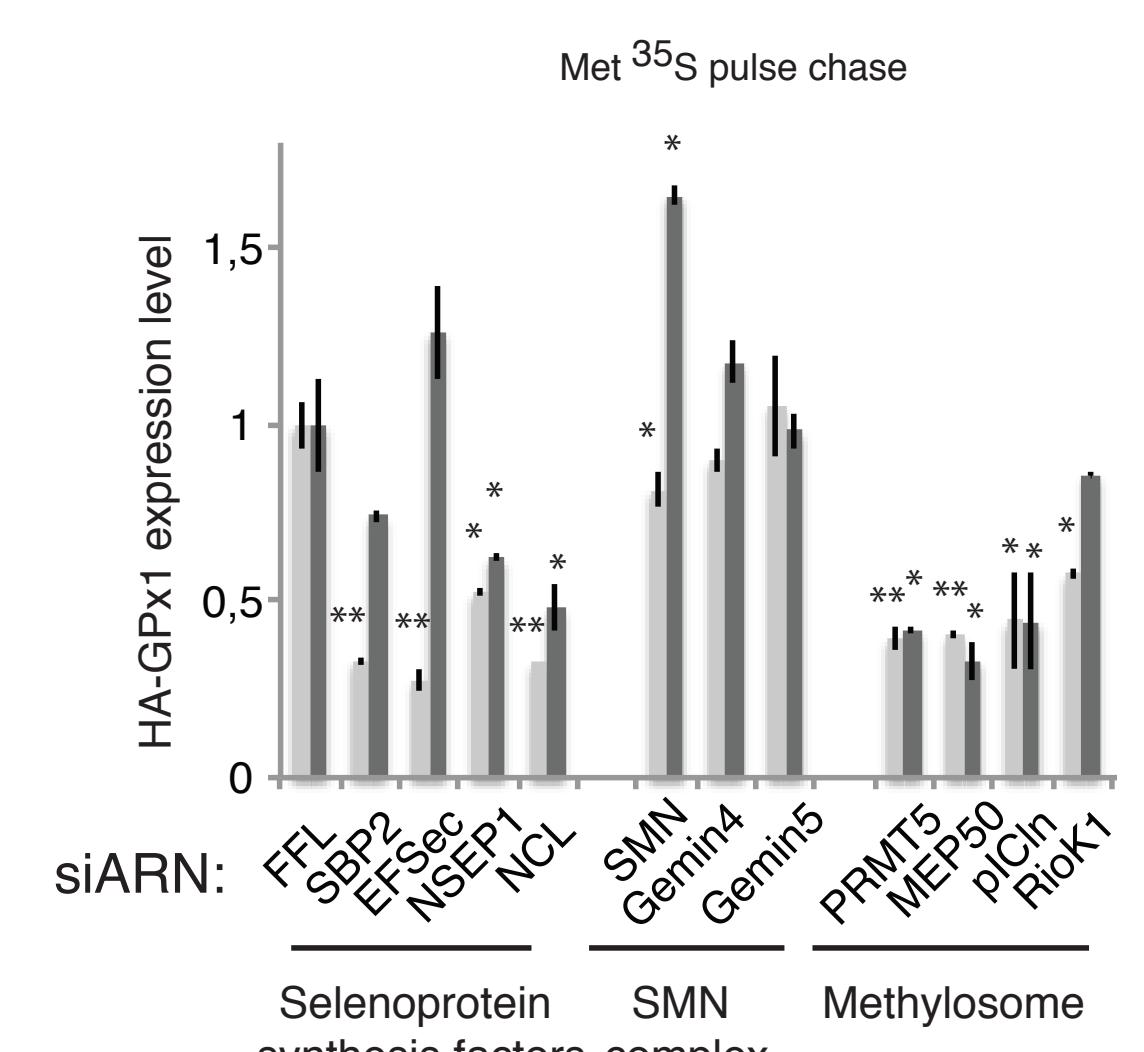
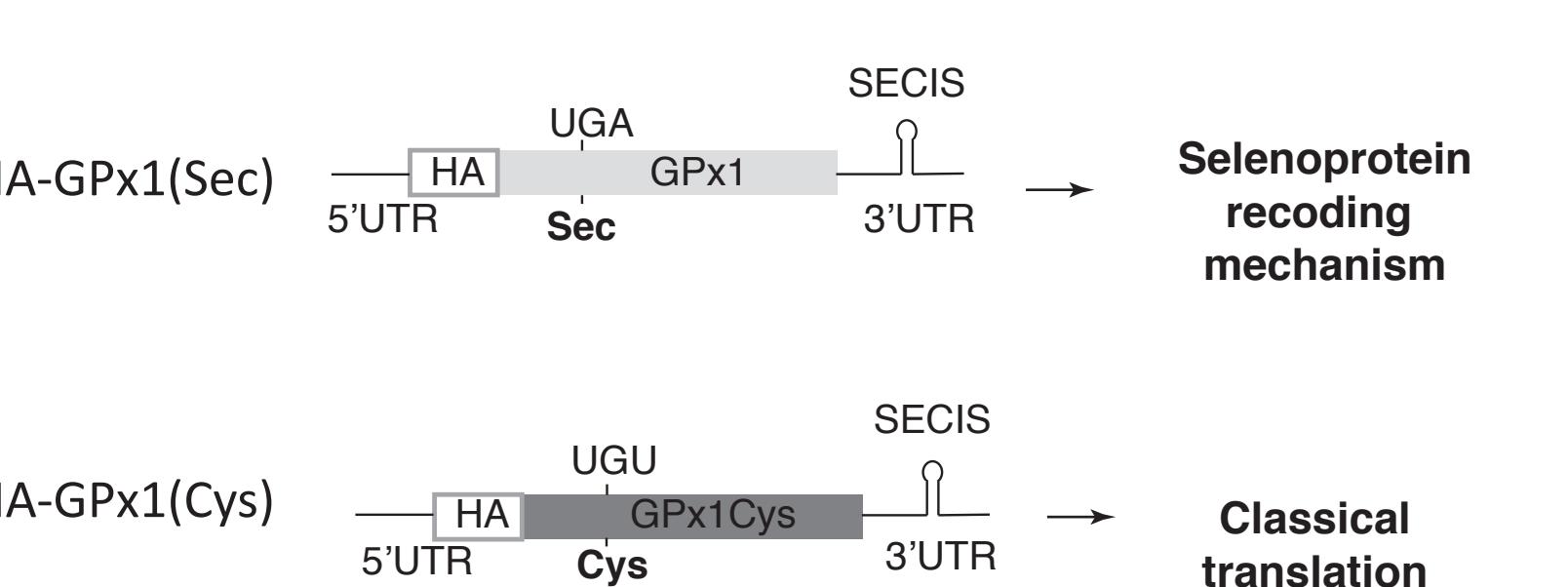
The SMN complex interacts with SBP2



Transfections and co-immunoprecipitation in HEK293 cells

Inhibition of SMN and of methylosome components has a functional impact on HA-Gpx1 selenoprotein synthesis *in vivo*

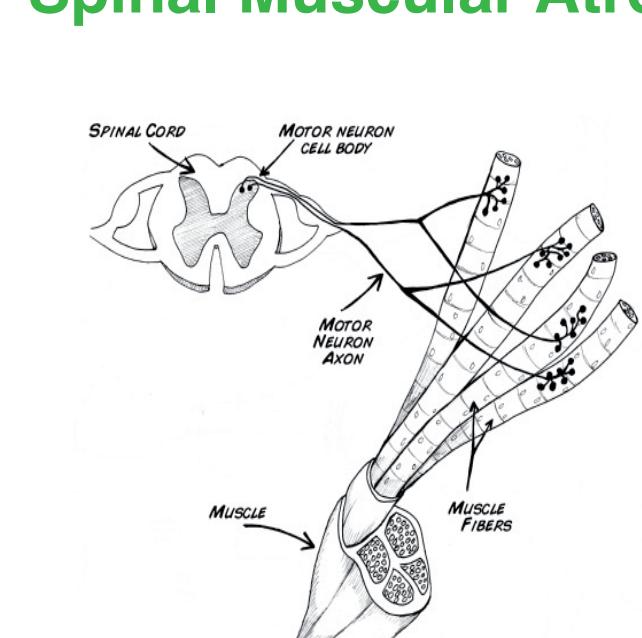
De novo translation assays using stable inducible cell lines (Fip-In T-Rex 293 system)



The inhibition of SMN, but not of Gemin4 and 5, affects the translational recoding of the selenoprotein HA-GPx1(Sec). Inhibition of methylosome components affects both HA-GPx1(Sec) and HA-GPx1(Cys)

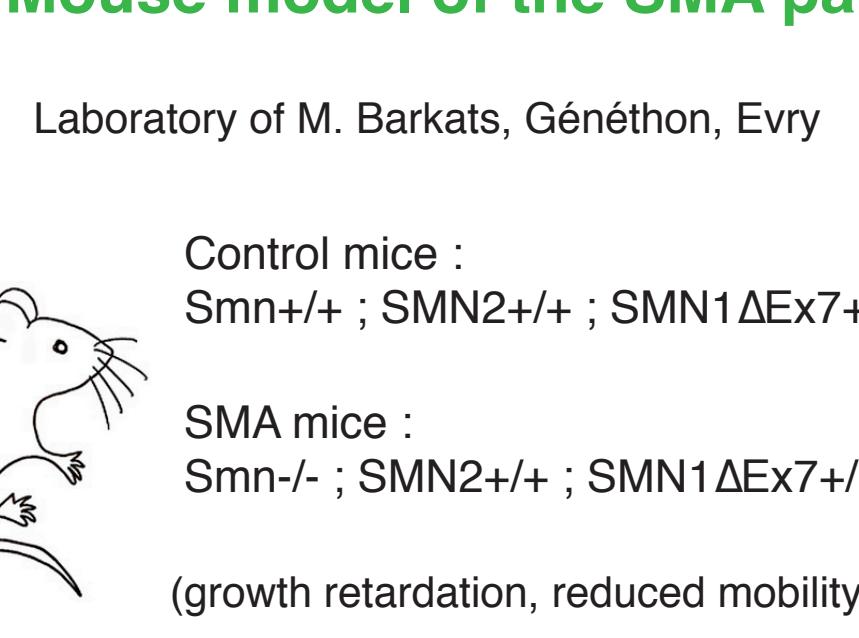
Functional role of SMN in selenoprotein synthesis. The Spinal Muscular Atrophy (SMA) pathology leads to reduced levels of selenoprotein mRNAs in the spinal chord

Spinal Muscular Atrophy



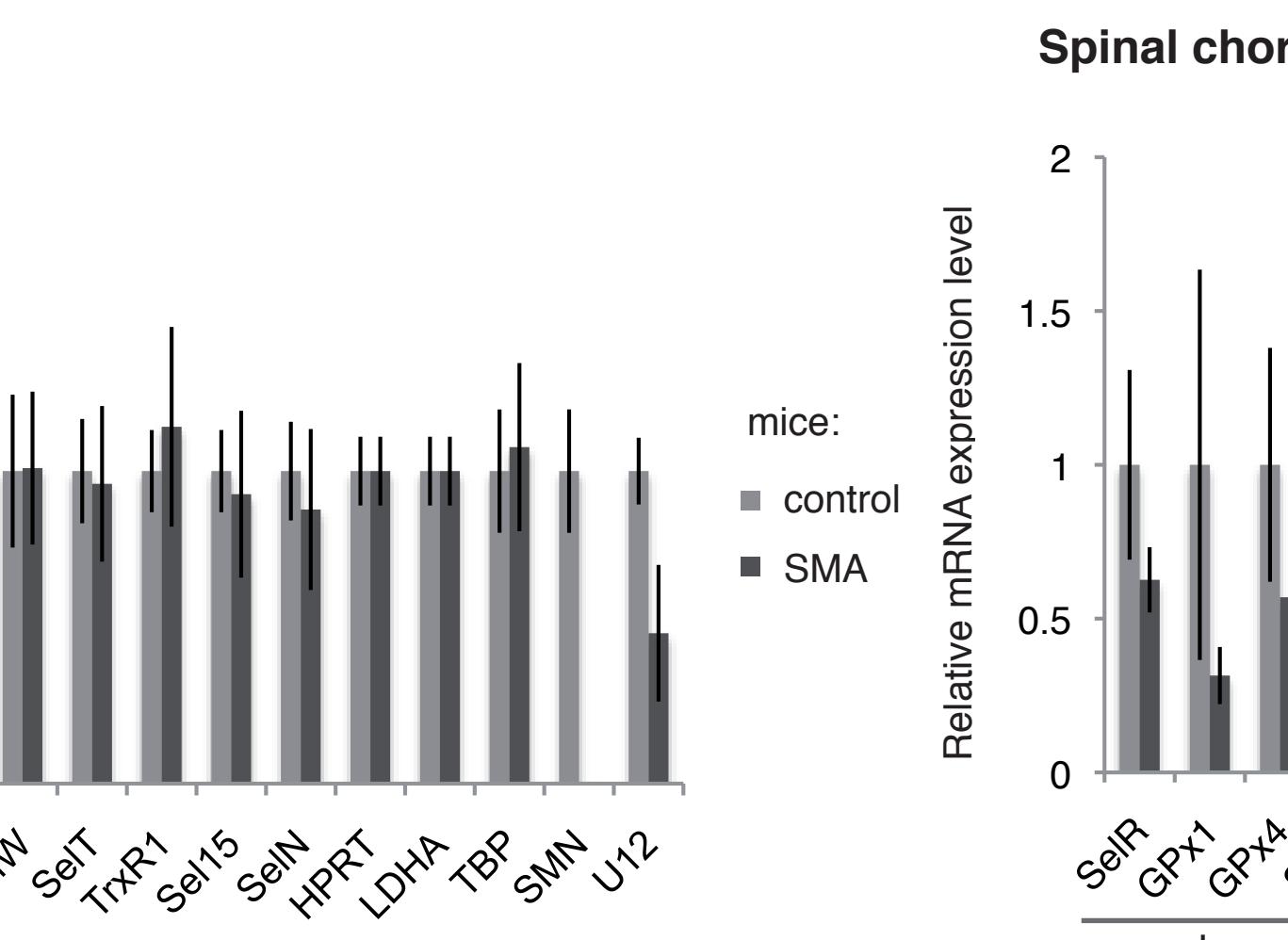
Major cause of neonatal death of genetic origin 1/6000
Increased oxidative stress was observed in motor neurons of the spinal chord (Hayashi et al., 2012)

Mouse model of the SMA pathology

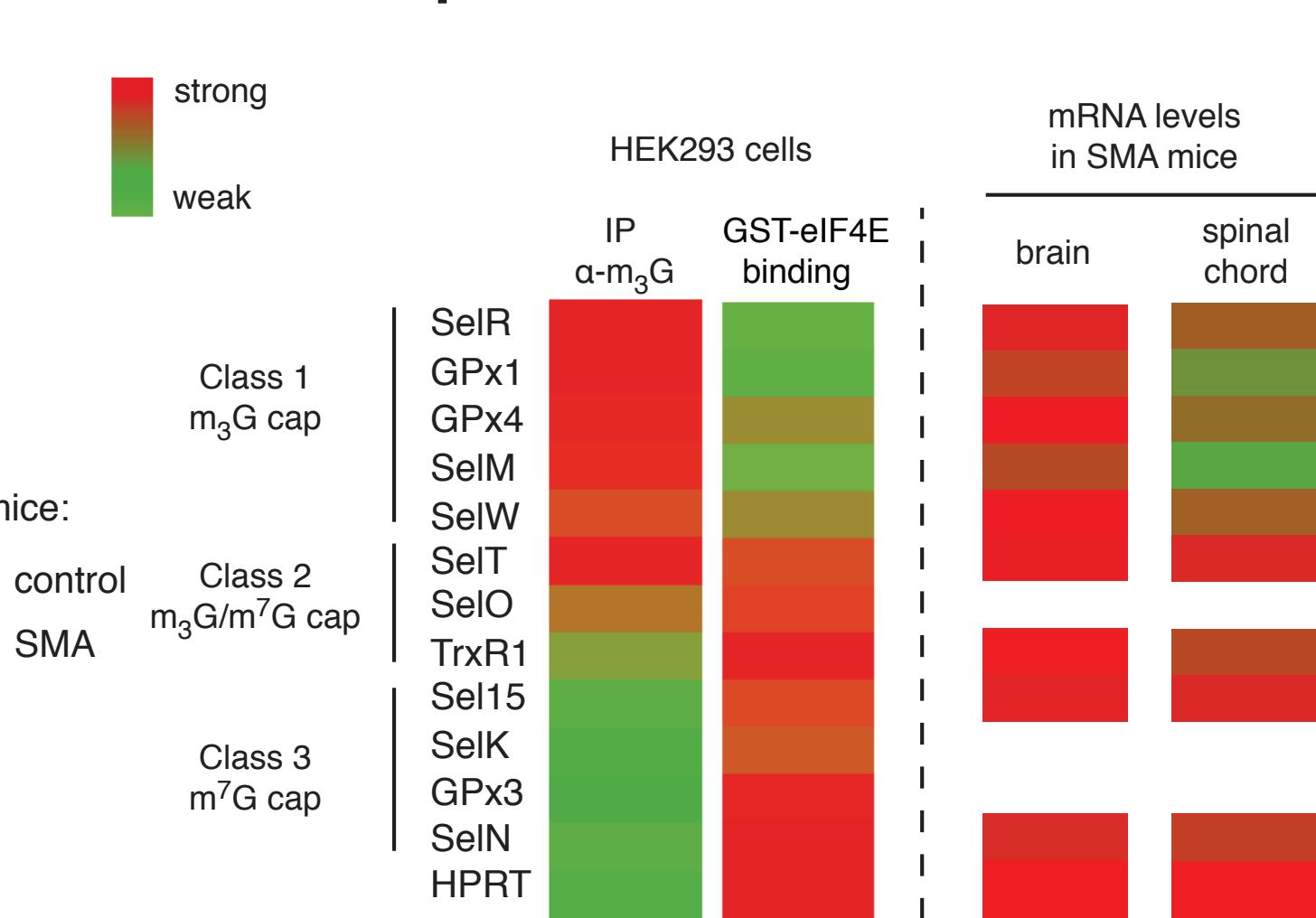
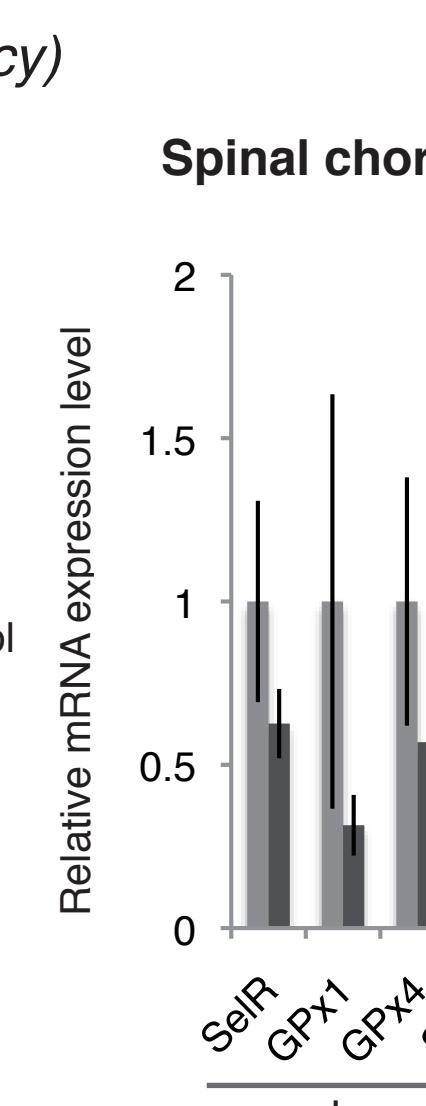


Lower motor neuron disease caused by loss-of-function mutations in the SMN1 gene
Major cause of neonatal death of genetic origin 1/6000
Increased oxidative stress was observed in motor neurons of the spinal chord (Hayashi et al., 2012)

Collaboration with S. Massenet (Nancy)



Selenoprotein mRNA levels are reduced in the spinal chord of SMA mice but not in the brain
Origin of the oxidative stress detected in Spinal Muscular Atrophy (SMA)?

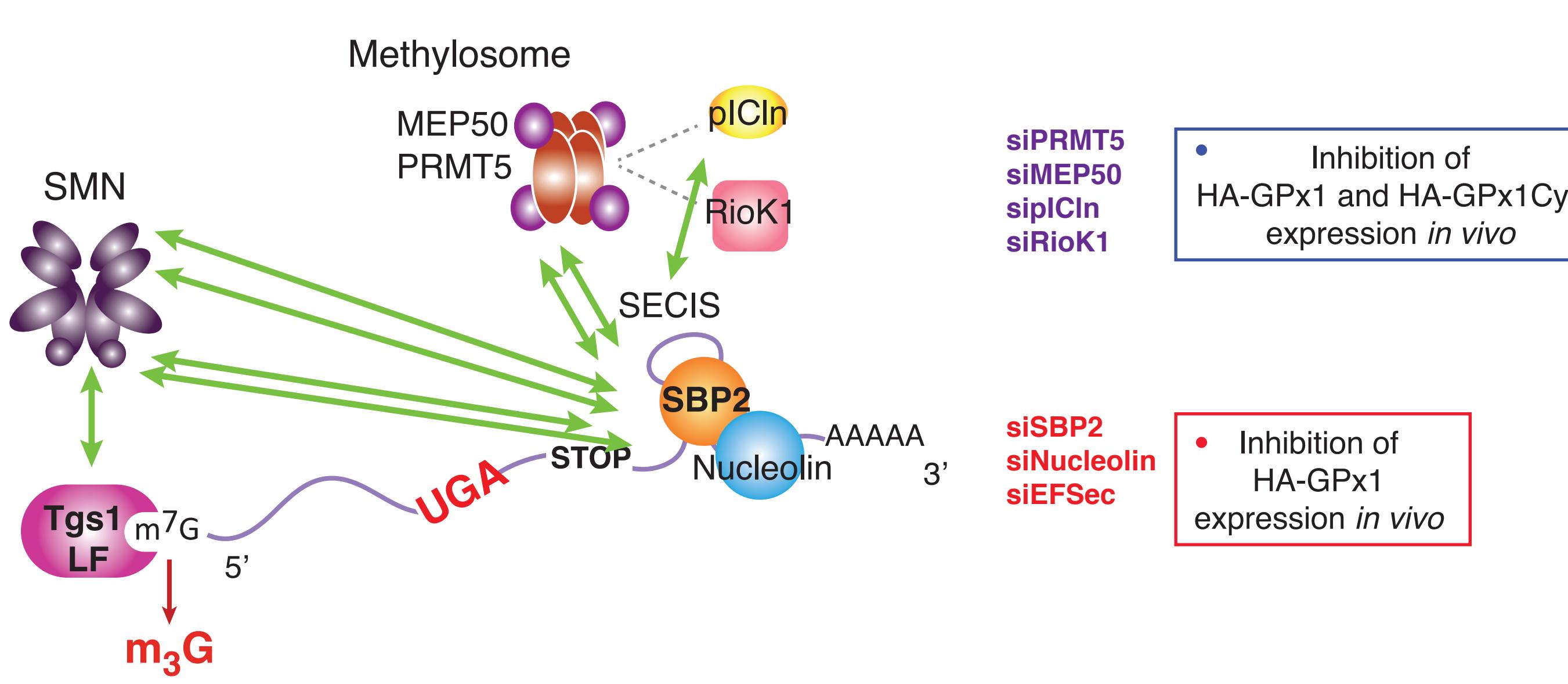


The same selenoprotein mRNAs that bear m3G cap and that are poorly recognized by initiation factor eIF4E in HEK293 cells are also preferentially reduced in the spinal chord of SMA mice

Summary

SMA mice siSMN

- SMA mice : tissue specific perturbation of selenoprotein mRNA levels
- siSMN : inhibition of cap hypermethylation
- Inhibition of HA-GPx1 expression *in vivo*



The entire SMN complex interacts with SBP2 and contributes to the recruitment of Tgs1 for the cap hypermethylation of selenoprotein mRNAs

Inactivation of SMN inhibits cap hypermethylation and reduces selenoprotein synthesis *in vivo*

The methylosome complex acts in concert with the SMN complex and also interacts with SBP2

We revealed that selenoprotein mRNA levels are reduced in the Spinal muscular atrophy pathology