



# RNA and the Link to Motor Neuron Disease

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Wexner  
Medical  
Center



# “Final Common Pathway”

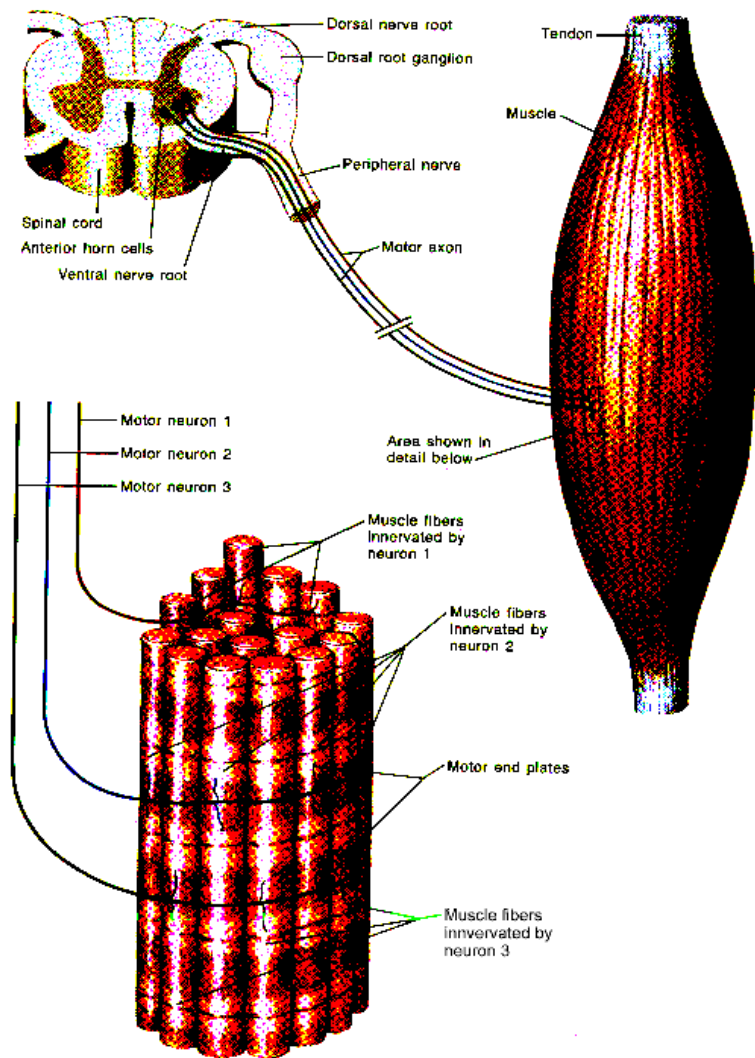
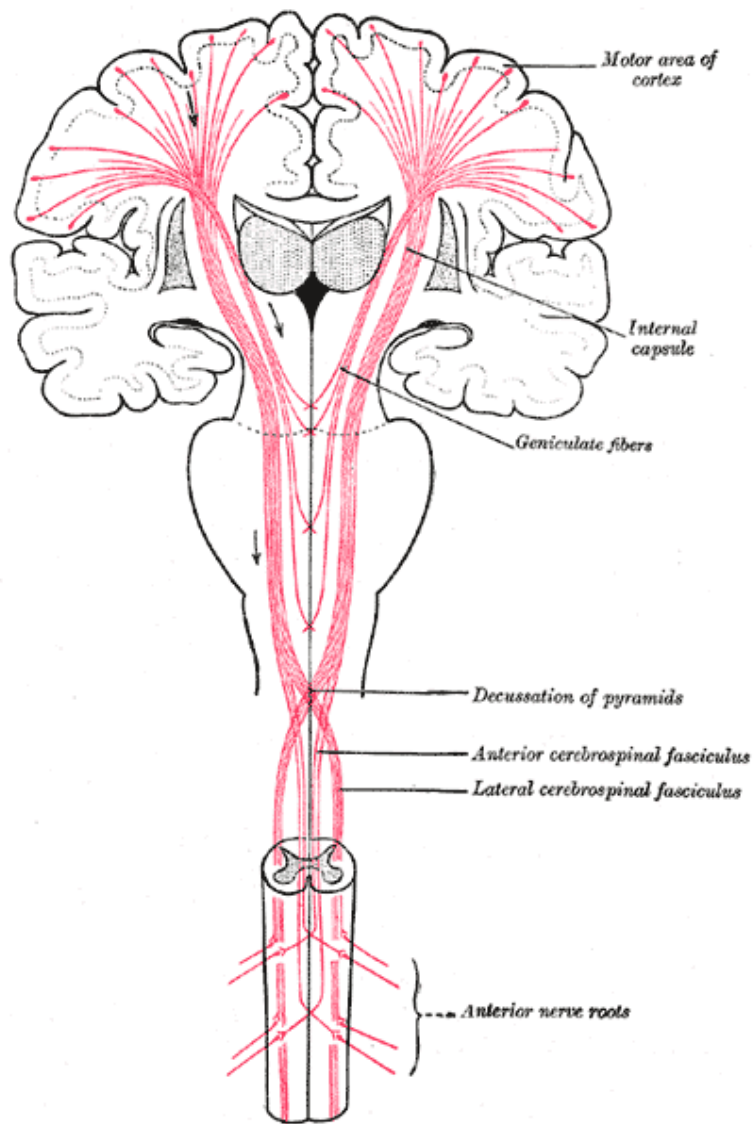
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“...to move things is all that mankind can do, for such the sole executant in muscle, whether in whispering a syllable or felling a forest.”

- Charles Sherrington, 1924



Charles Scott Sherrington 1857-1952



# RNA processing is a Big Deal

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Human Genome  
< 20,000 protein encoding transcripts

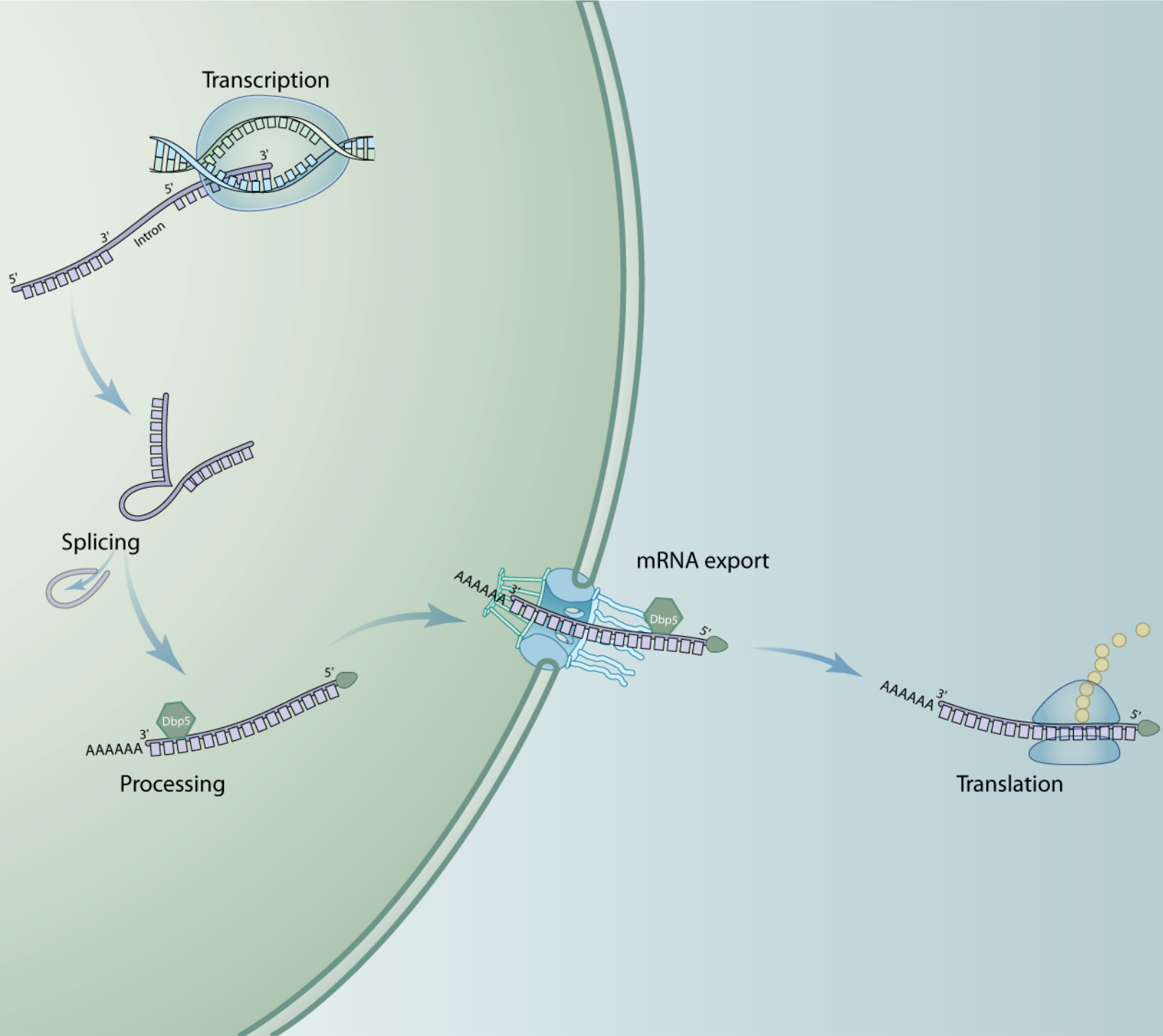


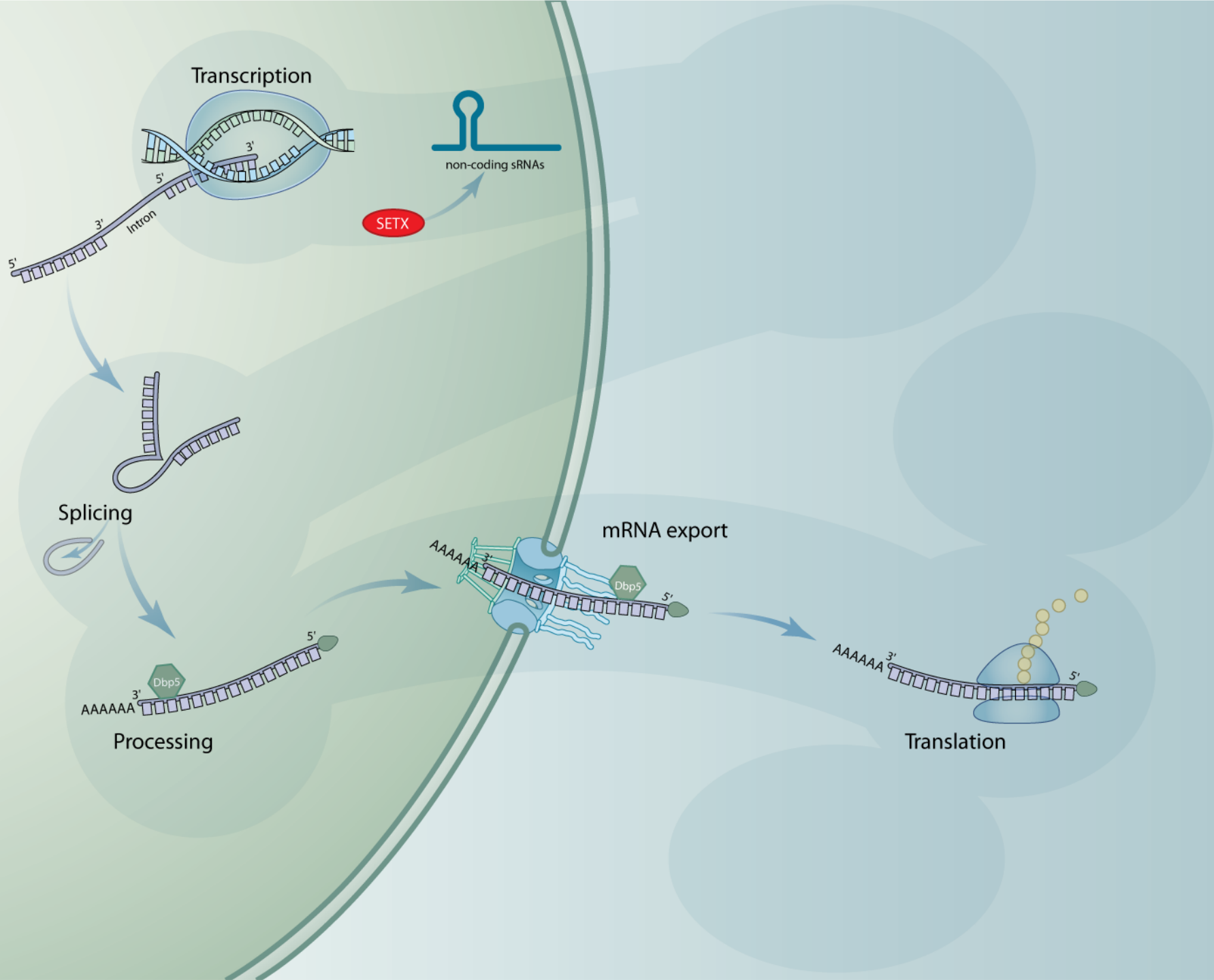
Human Transcriptome  
> 80,000 protein encoding transcripts

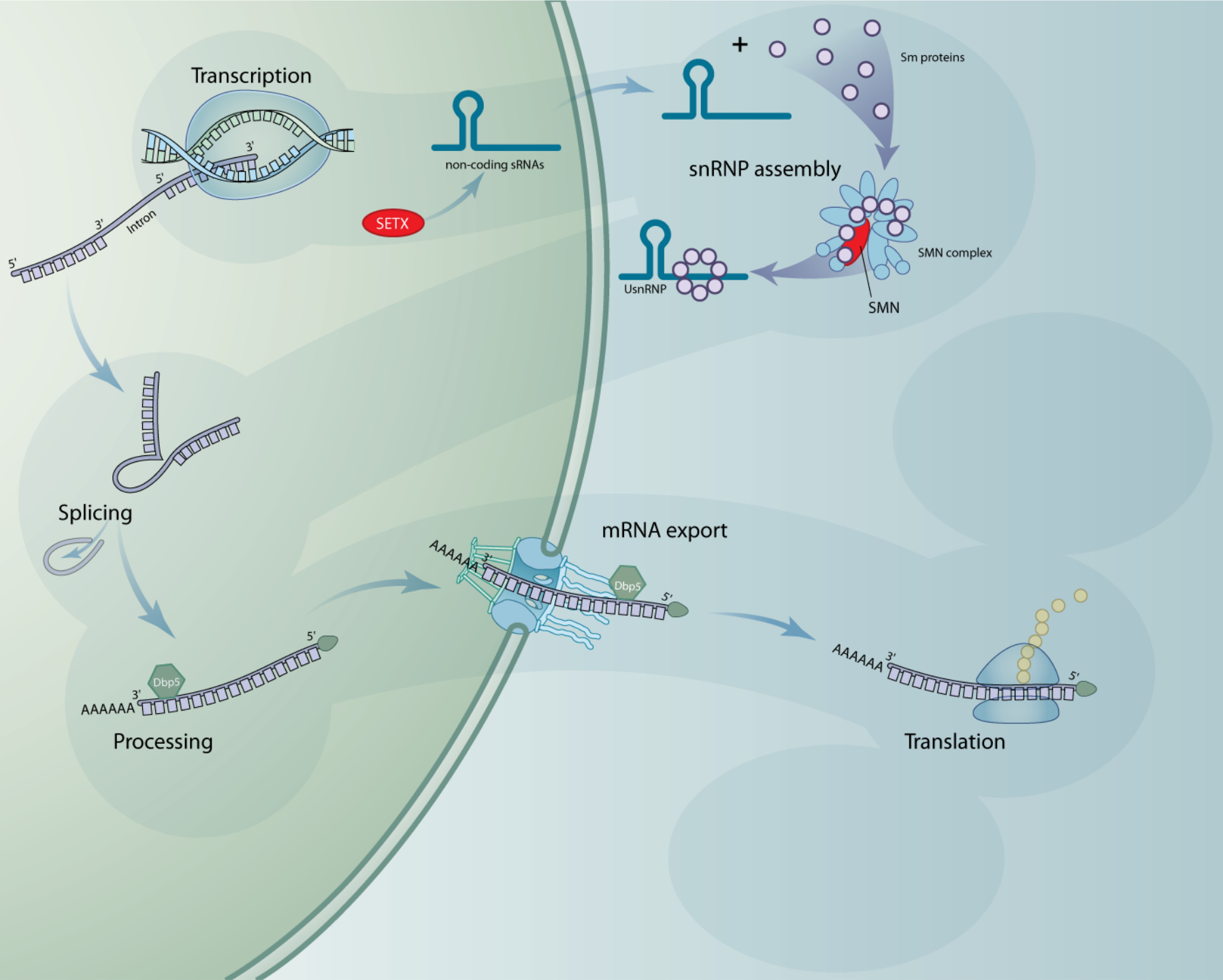


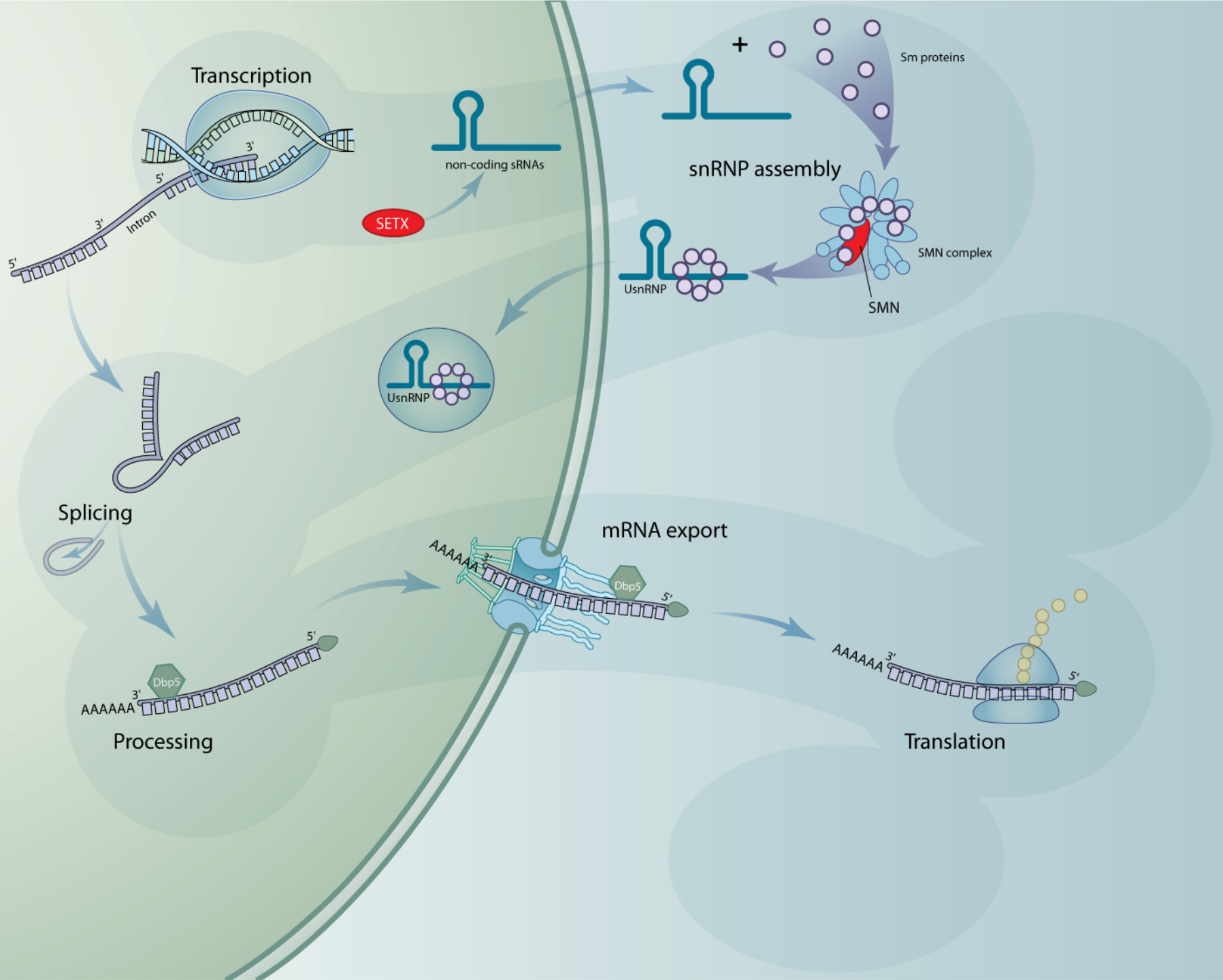
Human Proteome  
250,000 – 1,000,000 distinct proteins

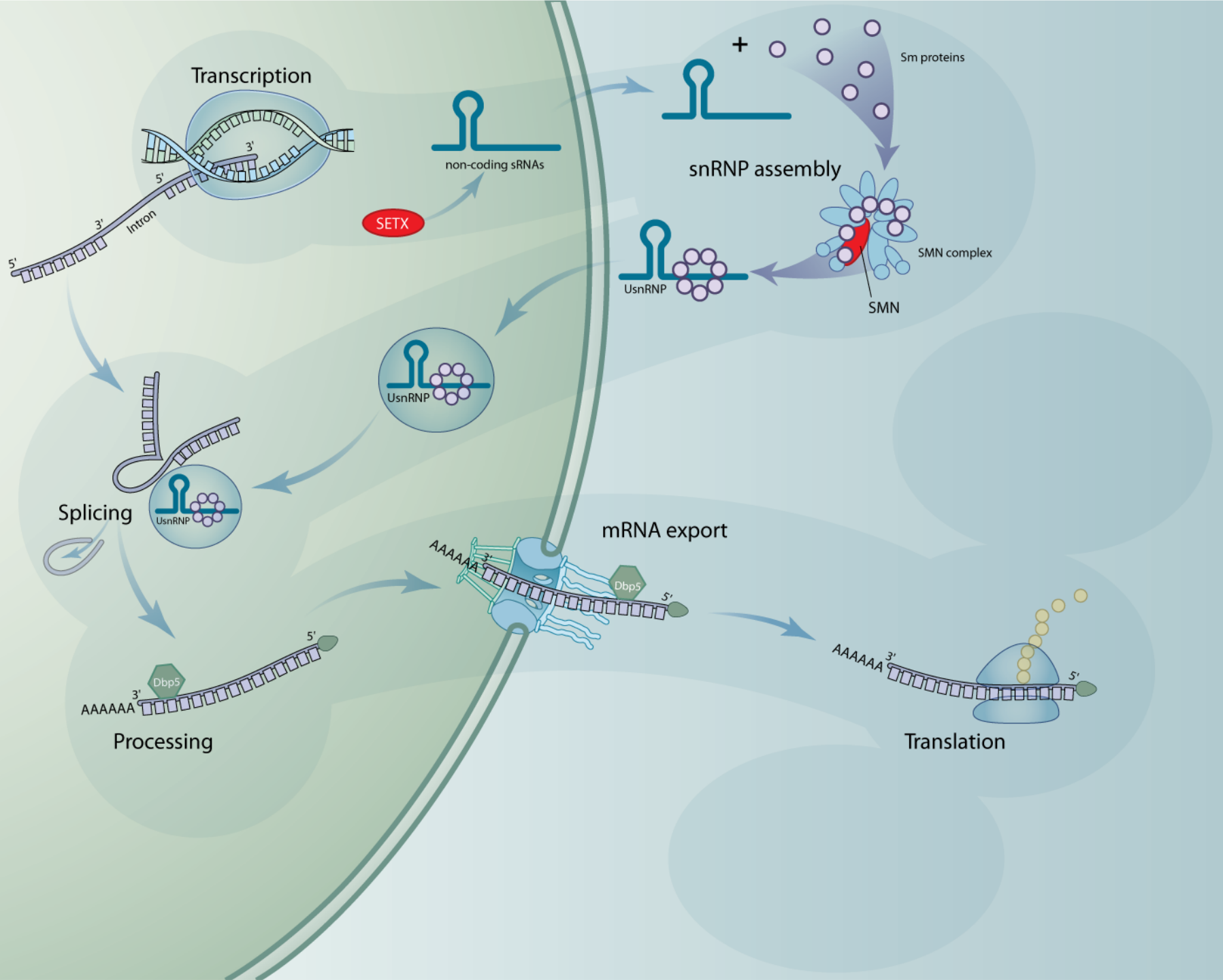


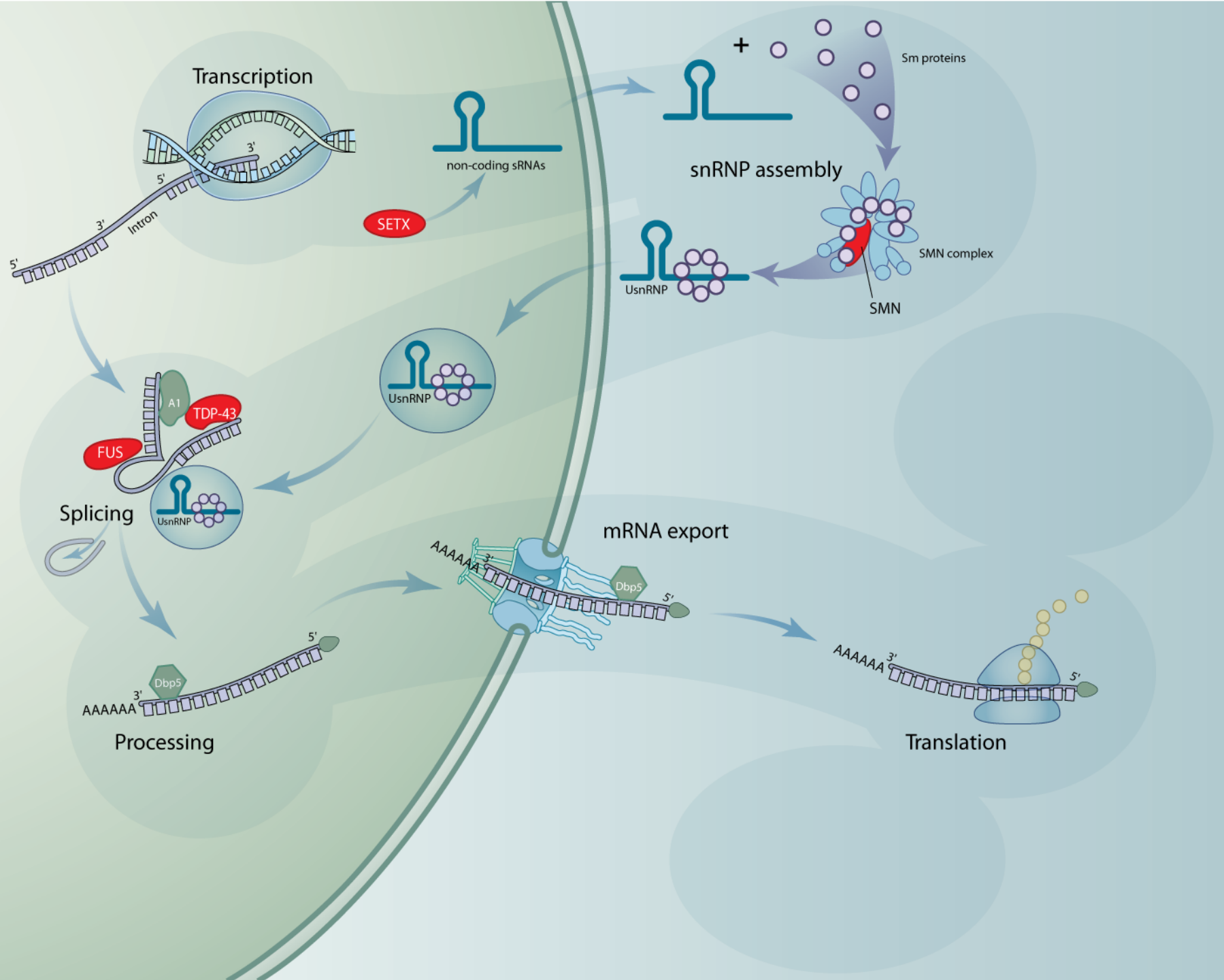


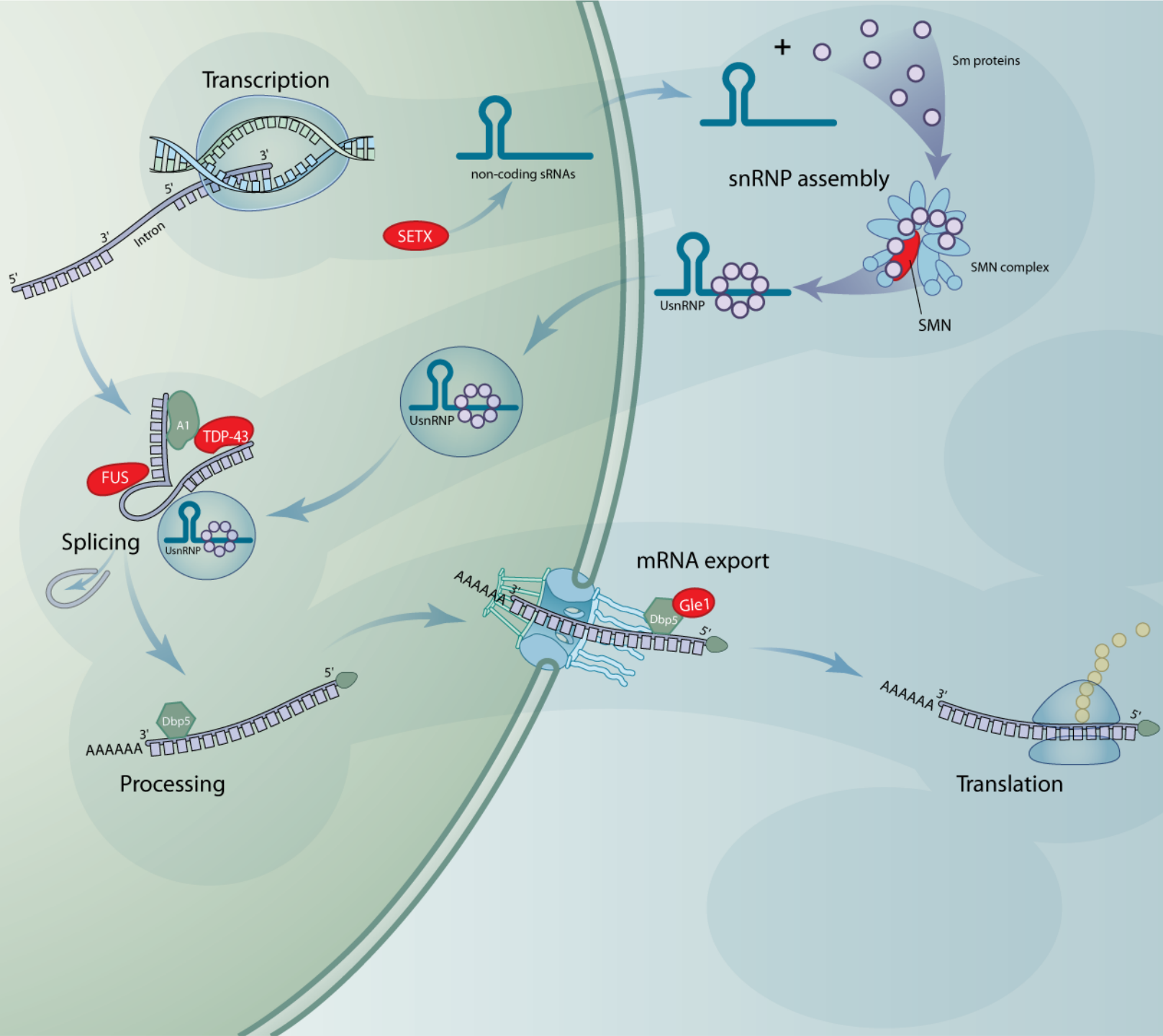




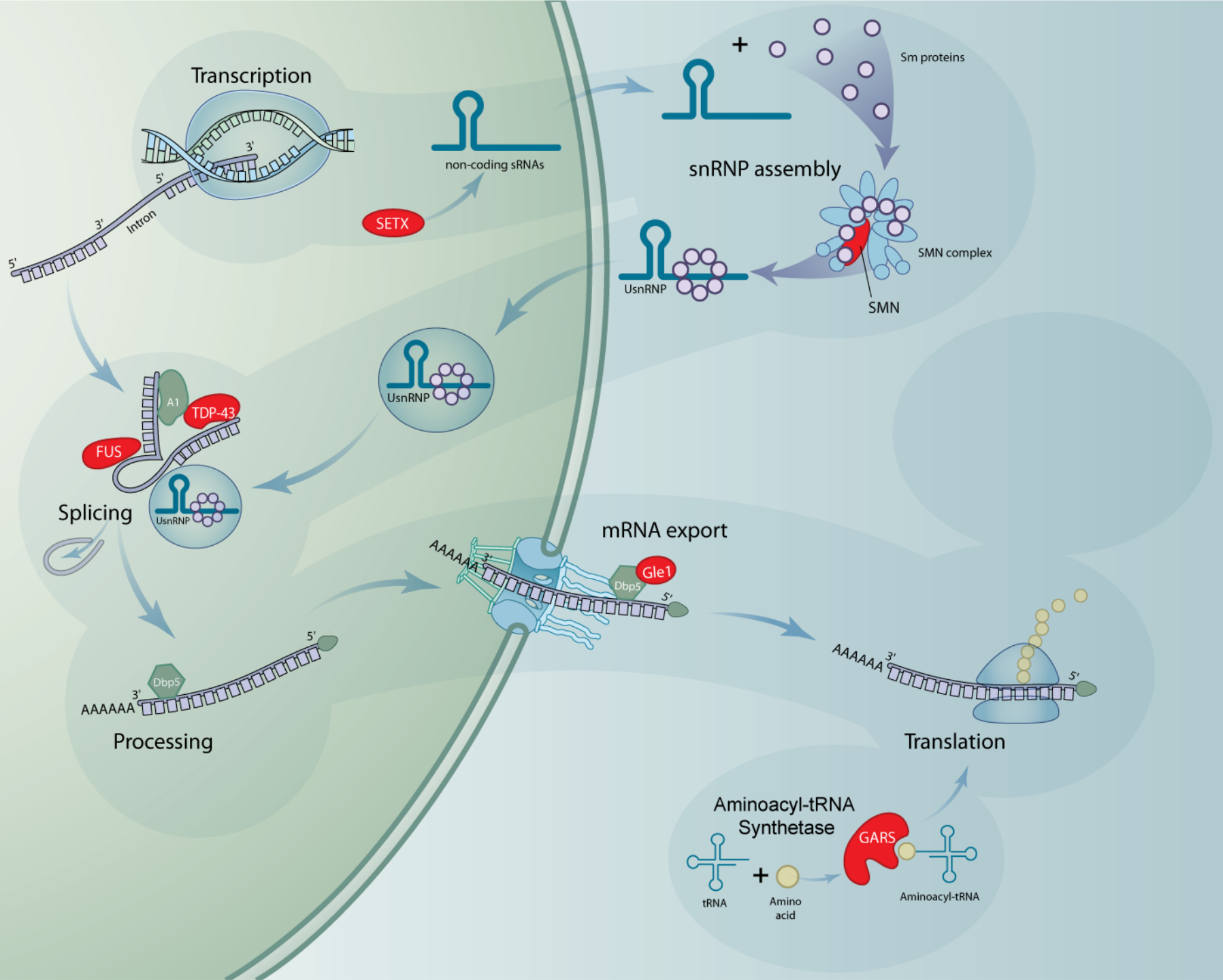




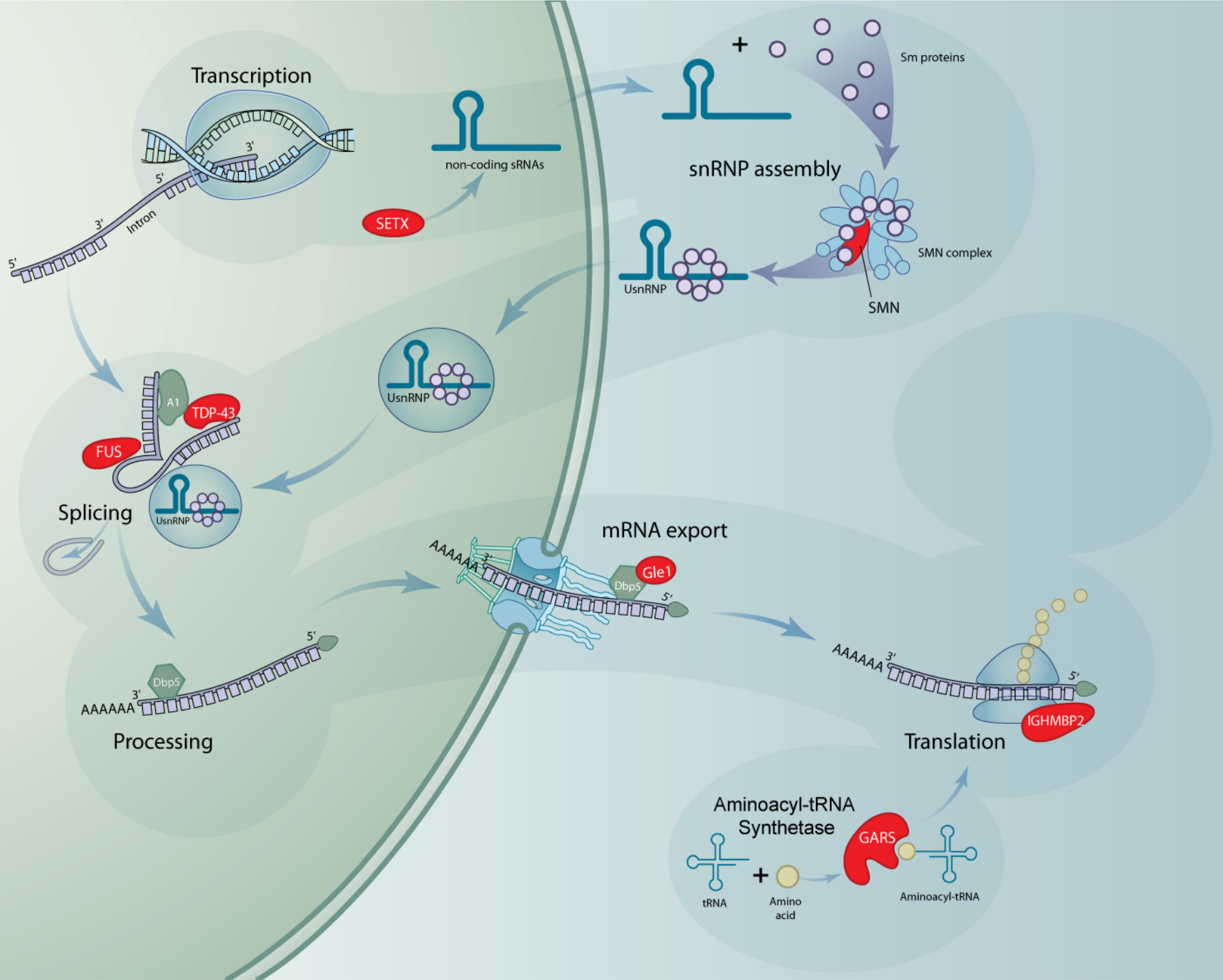


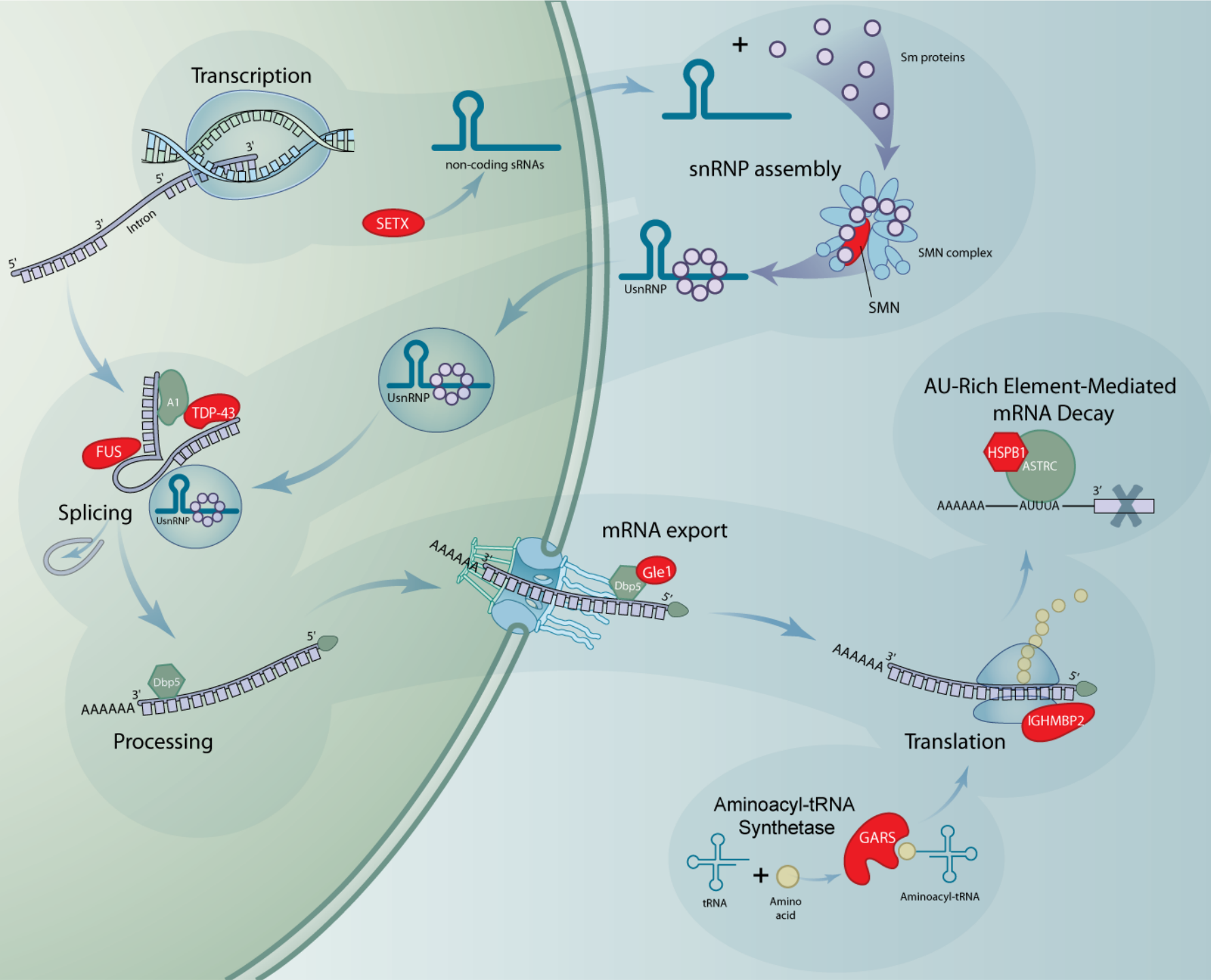




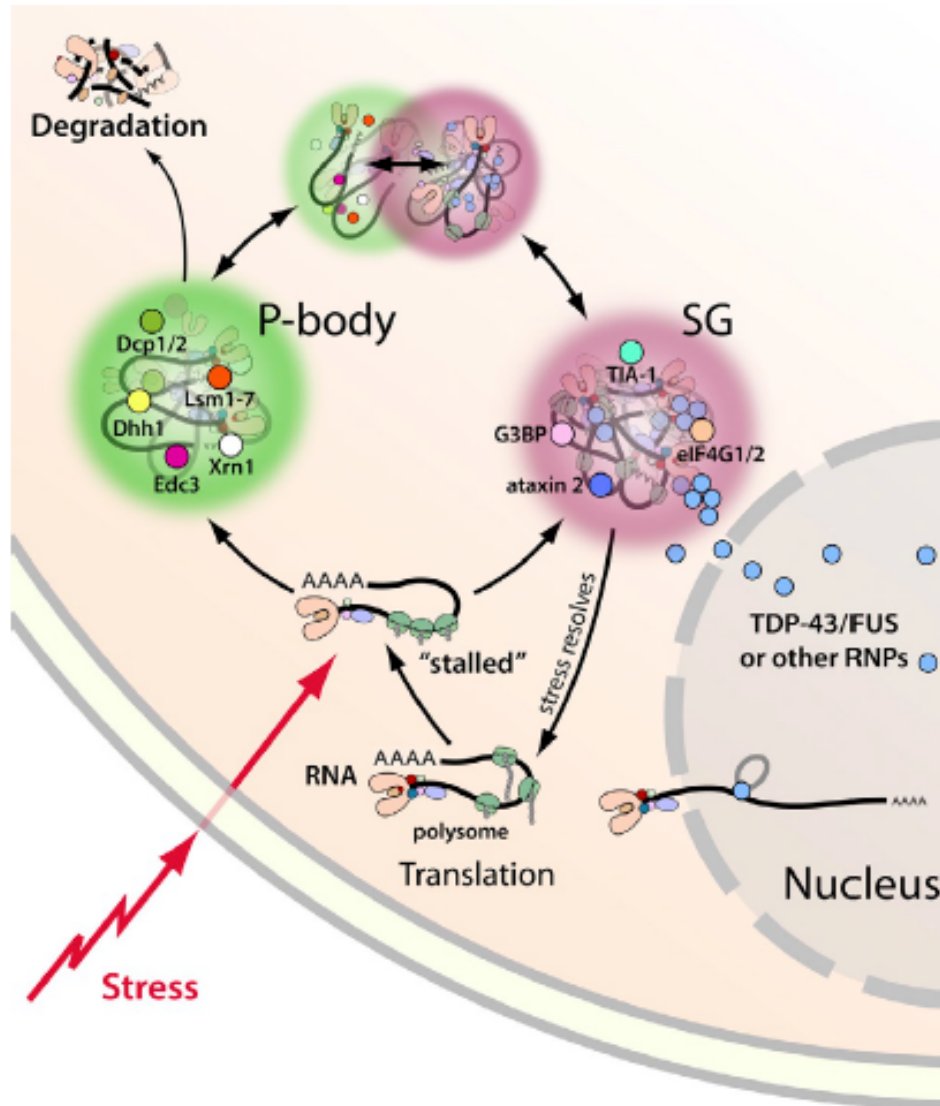






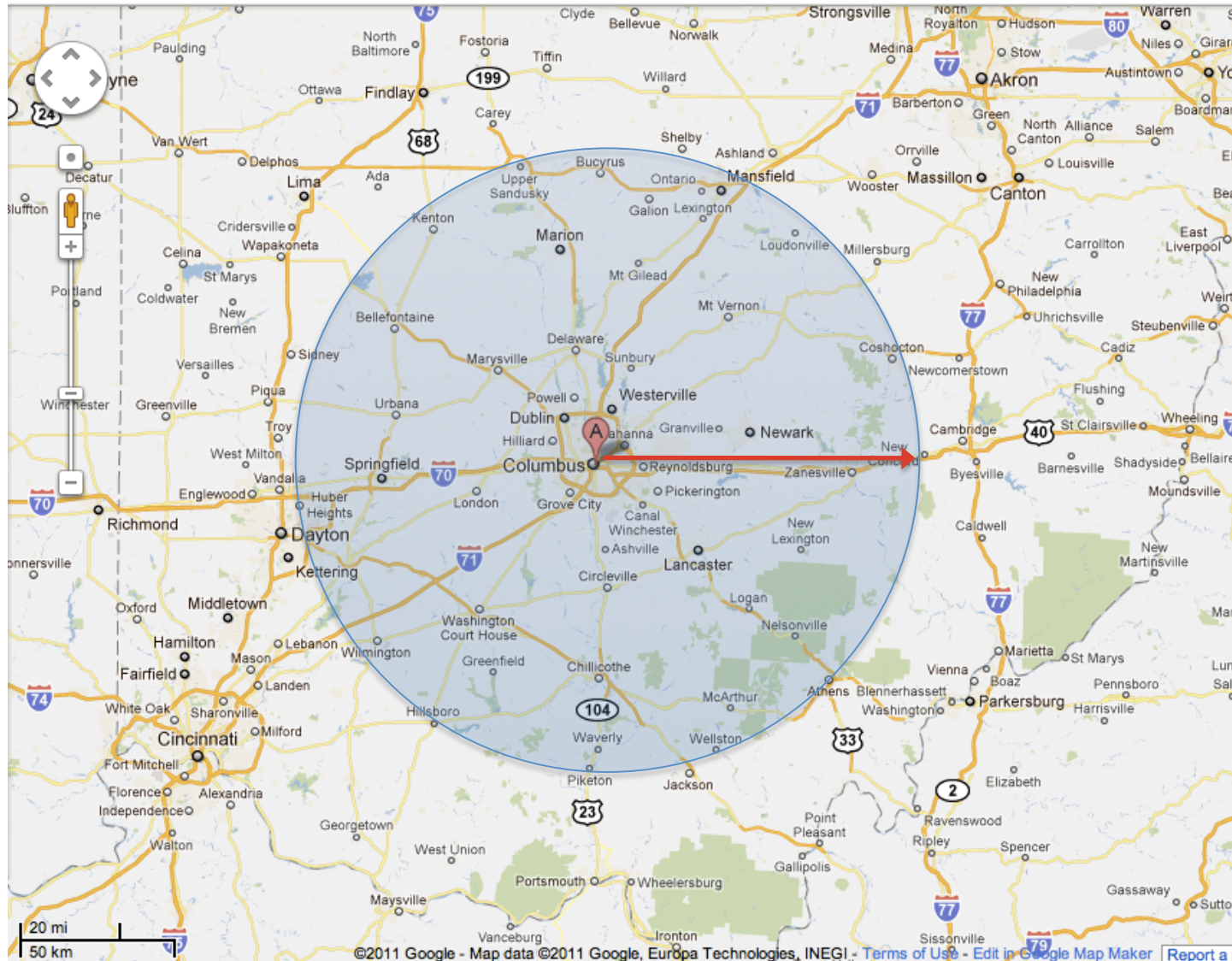


# P-bodies and Stress Granules



- Decapping and degradation of unwanted mRNAs
- Storing of mRNA until needed
- Involved in translational suppression by miRNAs
- Involved in the transport of mRNAs in neurons in response to stimulation

# Axon length is 20,000 x soma diameter



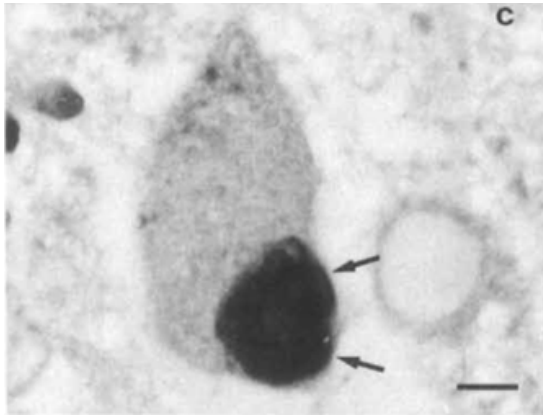


# Gene Variants in ALS genes (Feb, 2015)

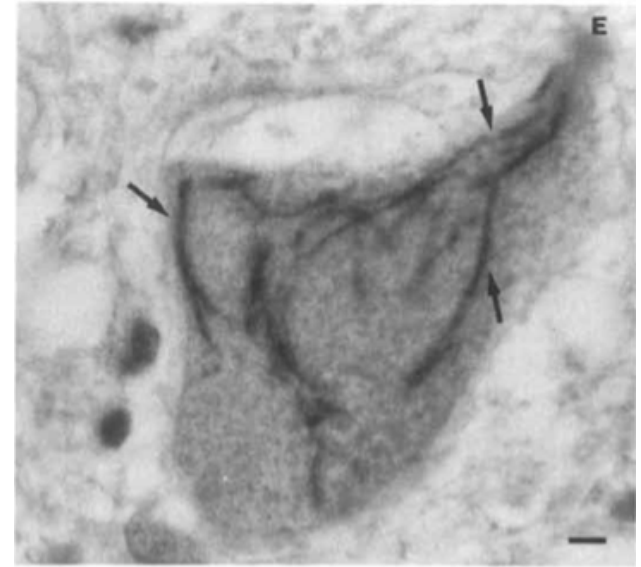
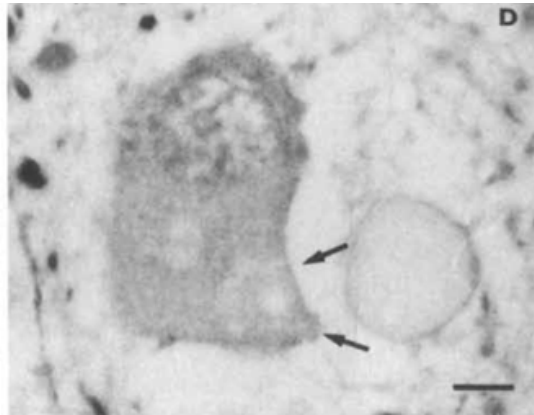
Gene	Reported inheritance model	Reported FALS explained	Reported SALS explained	Best model with case enrichment in present study (p-value)	Cases with variant in best model	Controls with variant in best model	Potential ALS cases explained
TBK1	N/A	N/A	N/A	Dom not benign ( $D = 1.13 \times 10^{-5}$ ; $R = 5.78 \times 10^{-7}$ ; $C = 3.63 \times 10^{-11}$ )	$D = 23$ (0.8%); $R = 23$ (1.745%); $C = 46$ (1.097%)	$D = 12$ (0.187%); $R = 5$ (0.211%); $C = 17$ (0.194%)	0.904%
NEK1	N/A	N/A	N/A	Dom LoF ( $D = 1.08 \times 10^{-6}$ ; $R = 0.001$ ; $C = 3.20 \times 10^{-9}$ )	$D = 25$ (0.870%); $R = 10$ (0.759%); $C = 35$ (0.835%)	$D = 6$ (0.094%); $R = 2$ (0.084%); $C = 8$ (0.091%)	0.744%
SOD1	AR/AD	12%	1.50%	Dom coding ( $7.23 \times 10^{-8}$ )	25 (0.870%)	5 (0.078%)	0.792%
TARDBP	AD	4%	1%	Dom coding ( $2.97 \times 10^{-6}$ )	19 (0.661%)	6 (0.094%)	0.567%
OPTN	AR/AD	<1%	<1%	Dom not benign ( $D = 0.023$ ; $R = 0.002$ ; $C = 0.002$ )	$D = 18$ (0.626%); $R = 8$ (0.607%); $C = 26$ (0.620%)	$D = 16$ (0.25%); $R = 4$ (0.169%); $C = 20$ (0.228%)	0.392%
SPG11	AR	<1%	<1%	Dom LoF ( $D = 0.015$ ; $R = 0.183$ ; $C = 0.017$ )	$D = 21$ (0.731%); $R = 5$ (0.379%); $C = 26$ (0.620%)	$D = 20$ (0.312%); $R = 7$ (0.295%); $C = 27$ (0.308%)	0.313%
VCP	AD	1%	1%	Dom coding (0.022)	8 (0.278%)	4 (0.062%)	0.216%
HNRNPA1	AD	<1%	<1%	Dom coding (0.103)	6 (0.209%)	5 (0.078%)	0.131%
ATXN2*	AD	<1%	<1%	Rec coding (0.206)	4 (0.139%)	2 (0.031%)	0.108%
ANG	AD	<1%	<1%	Dom LoF (0.217)	2 (0.070%)	1 (0.016%)	0.054%
CHCHD10	AD	<1%	<1%	Dom coding (0.226)	2 (0.070%)	0 (0%)	0.070%
SIGMAR1	AR	<1%	<1%	Dom LoF (0.226)	1 (0.035%)	0 (0%)	0.035%
FIG4	AR/AD	<1%	<1%	Dom LoF (0.233)	9 (0.313%)	12 (0.187%)	0.126%
SS18L1	AD	<1%	<1%	Dom LoF (0.241)	1 (0.035%)	0 (0%)	0.035%
GRN	AD	<1%	<1%	Dom not benign (0.357)	14 (0.487%)	24 (0.375%)	0.112%
SETX	AD	<1%	<1%	Rec not benign (0.380)	3 (0.104%)	4 (0.062%)	0.042%
HNRNPA2B1	AD	<1%	<1%	Dom not benign (0.423)	3 (0.104%)	4 (0.062%)	0.042%
SQSTM1	AD	1%	<1%	Dom LoF (0.546)	1 (0.035%)	2 (0.031%)	0.004%
TAF15	AR/AD	<1%	<1%	Rec not benign (0.555)	2 (0.070%)	1 (0.016%)	0.054%
FUS	AR/AD	4%	1%	Dom LoF (0.612)	2 (0.070%)	3 (0.047%)	0.023%
ALS2	AR	<1%	<1%	Rec coding (0.655)	2 (0.070%)	4 (0.062%)	0.007%
VAPB	AD	<1%	<1%	Dom not benign (0.688)	3 (0.104%)	5 (0.078%)	0.026%
NEFH	AD	<1%	<1%	Dom coding (0.777)	22 (0.765%)	37 (0.578%)	0.188%
C9orf72*	AD	40%	7%	Dom not benign (1.000)	4 (0.139%)	7 (0.109%)	0.030%
CHMP2B	AD	<1%	<1%	Rec coding (1.000)	1 (0.035%)	1 (0.016%)	0.019%
MATR3	AD	<1%	<1%	Dom coding (1.000)	19 (0.661%)	35 (0.546%)	0.115%
PFN1	AD	<1%	<1%	Rec coding (1.000)	9 (0.313%)	15 (0.234%)	0.079%
PRPH	AD	<1%	<1%	Dom LoF (1.000)	1 (0.035%)	2 (0.031%)	0.004%
SPAST	AD	<1%	<1%	Dom coding (1.000)	6 (0.209%)	12 (0.187%)	0.021%
TUBA4A+	AD	1%	<1%	Dom coding (0.743)	3 (0.104%)	7 (0.109%)	0%
ELP3+	Allelic	<1%	<1%	Rec coding (1.000)	0 (0%)	0 (0%)	0%
DAO+	AD	<1%	<1%	Rec coding (1.000)	0 (0%)	0 (0%)	0%
DCTN1+	AD	<1%	<1%	Dom coding (0.668)	32 (1.113%)	76 (1.187%)	0%
EWSR1+	AD	<1%	<1%	Dom coding (0.375)	10 (0.348%)	28 (0.437%)	0%
GLE1+	AD	<1%	<1%	Rec LoF (1.000)	0 (0%)	0 (0%)	0%
UBQLN2+	XD	<1%	<1%	Dom LoF (1.000)	0 (0%)	0 (0%)	0%

# Ubiquitin-positive inclusions

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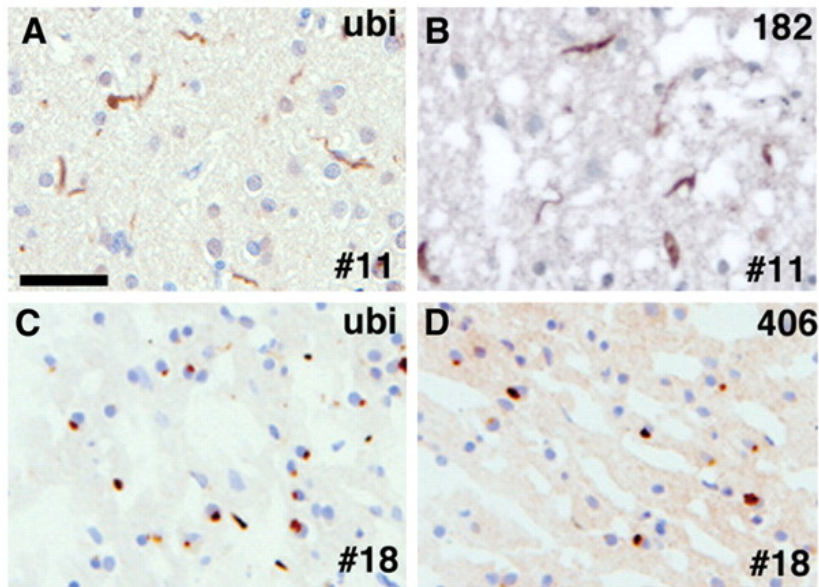
Dense anti-ubiquitin positive deposit



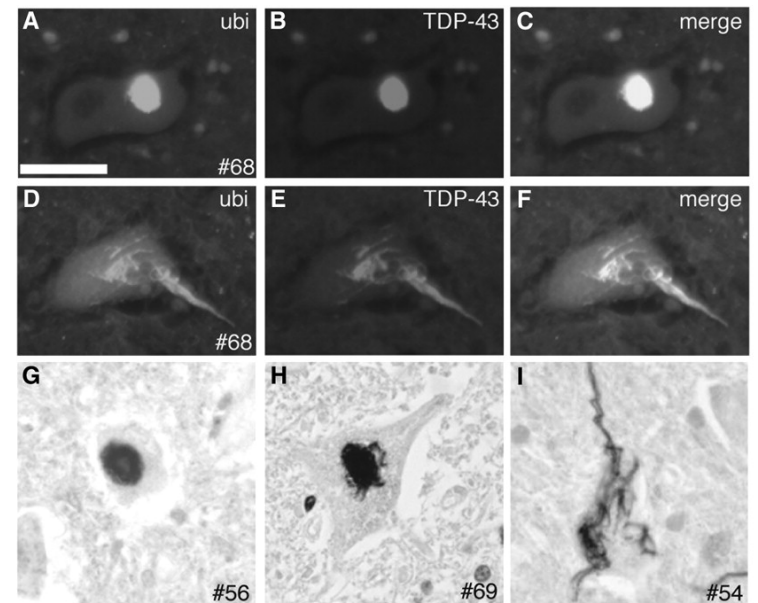
“Skein-like” filamentous arrays

# TDP-43 inclusions in FTD and ALS

## FTLD Ubiquitinated inclusions



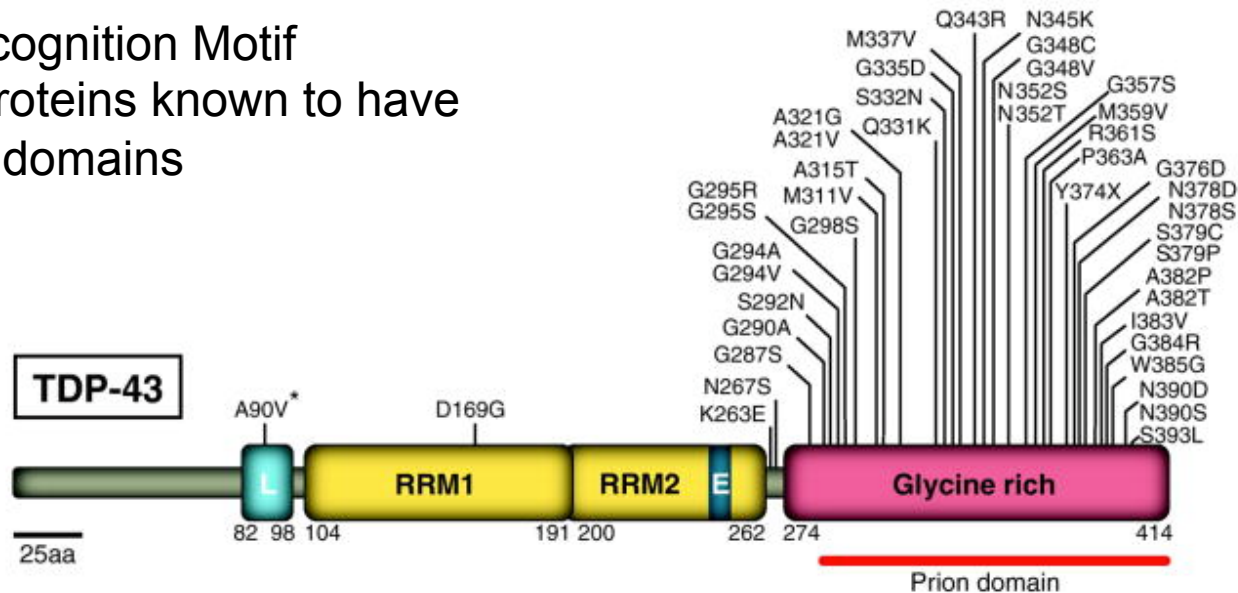
## ALS Ubiquitinated inclusions



# Mutations in TDP-43 result in FTD and ALS

## RNA Recognition Motif

- 210 proteins known to have these domains



**29 RNA binding proteins contain prion-like domains!**

## Prion-like domain:

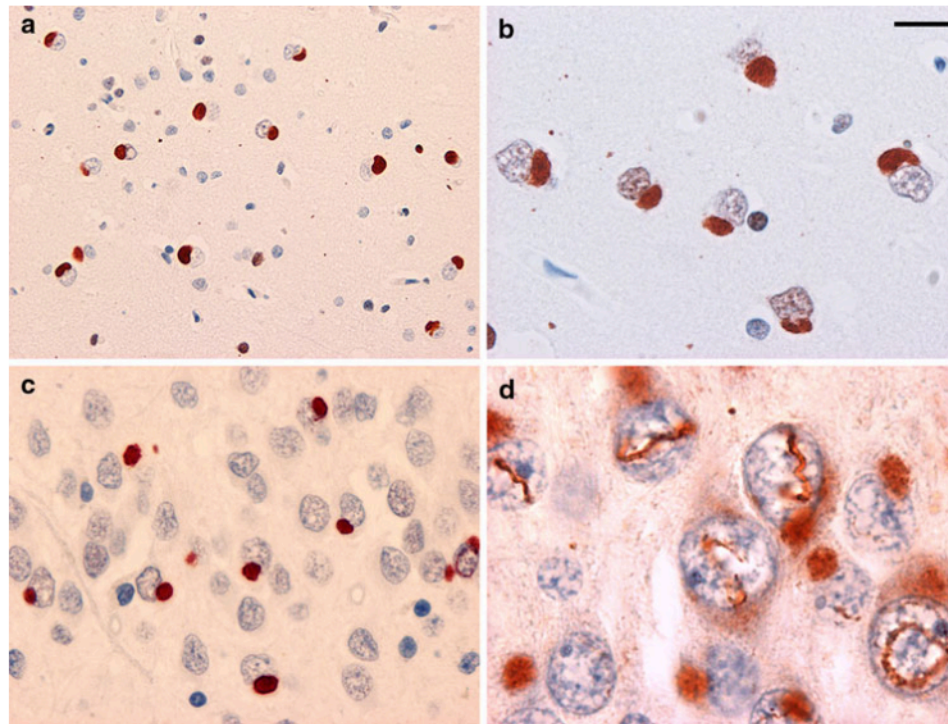
- enriched in polar residues and glycine
- Confer "prionogenicity"



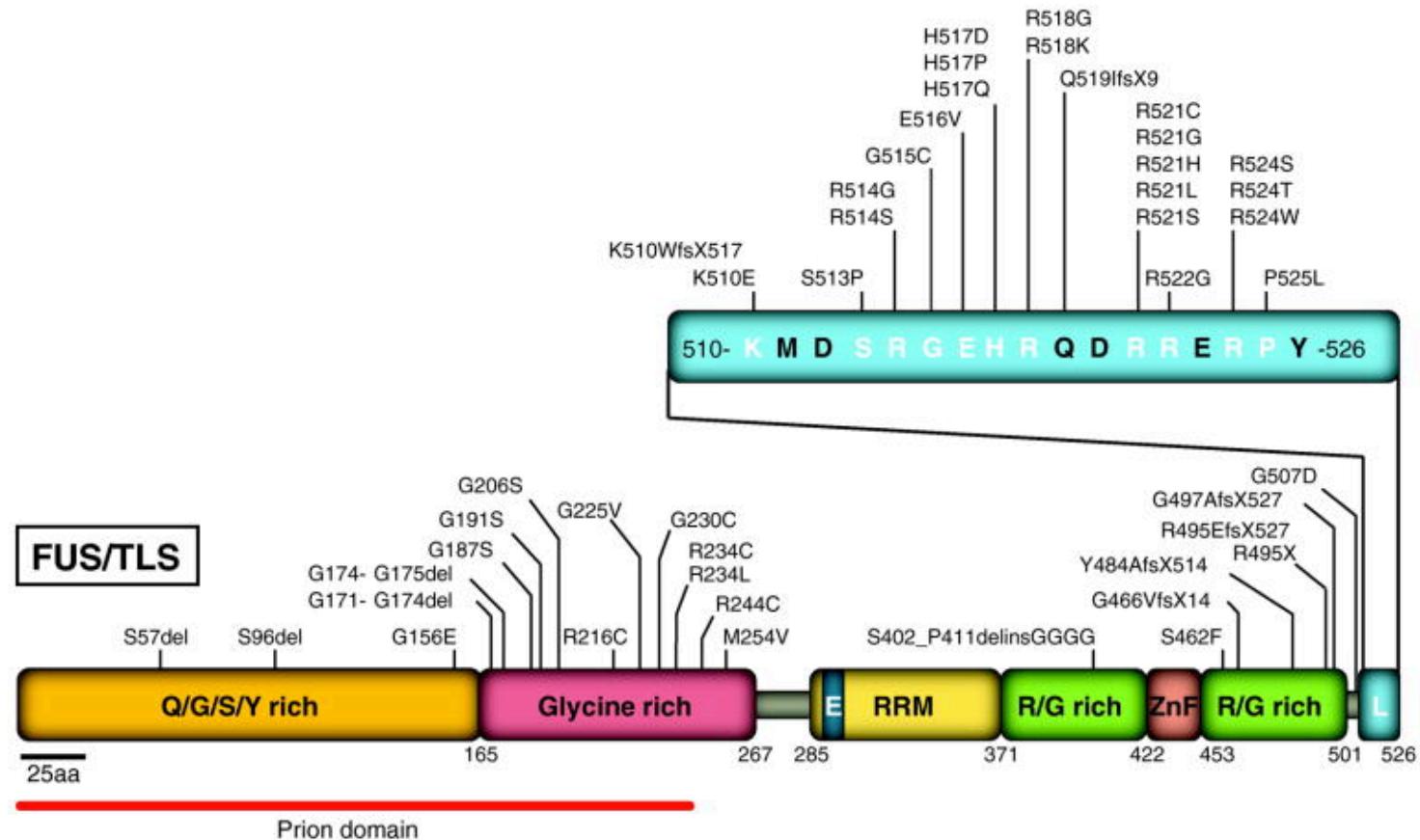
# FUS/TLS inclusions in FTD

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## FTLD Ubiquitinated inclusions

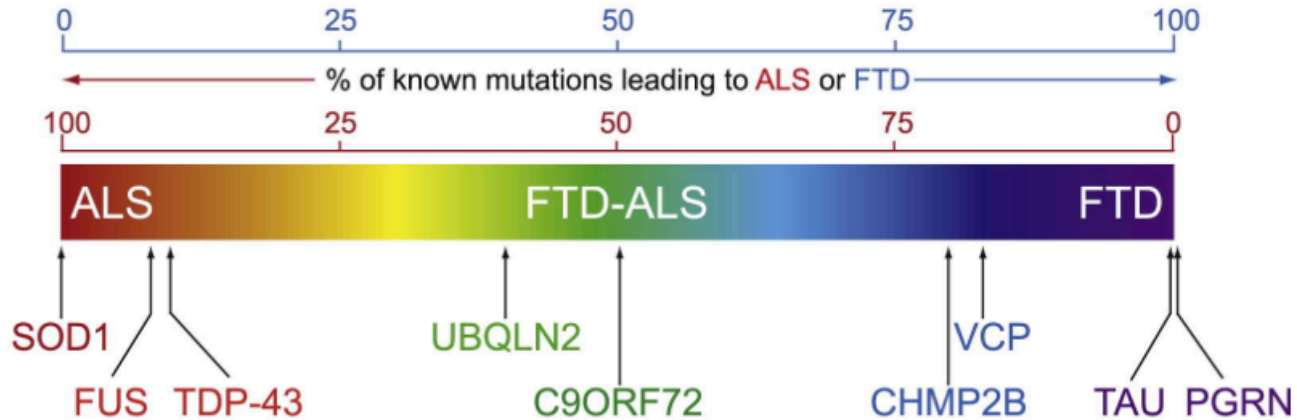


# Mutations in FUS/TLS result in FTD and ALS



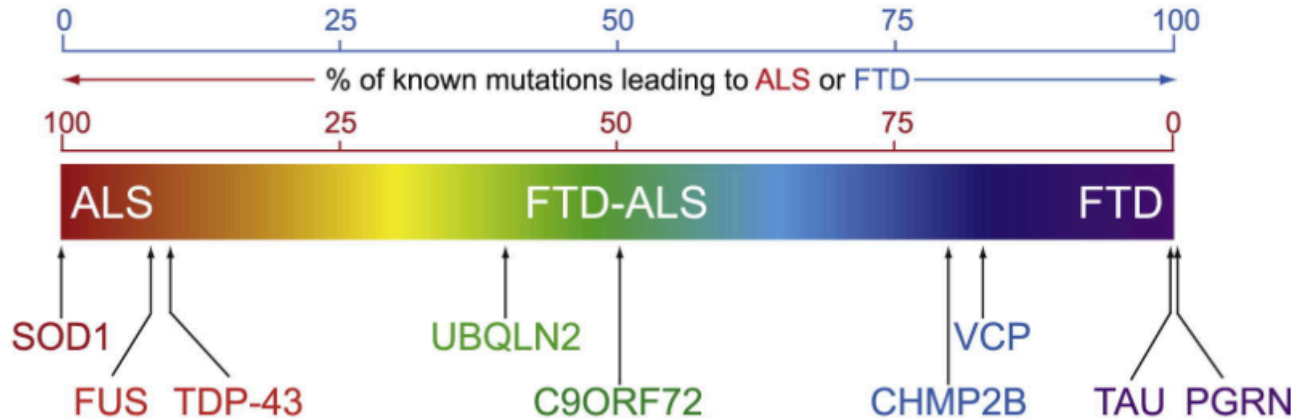
# Link between RNA metabolism and Pathological Inclusions

## A Genetics of ALS and FTD

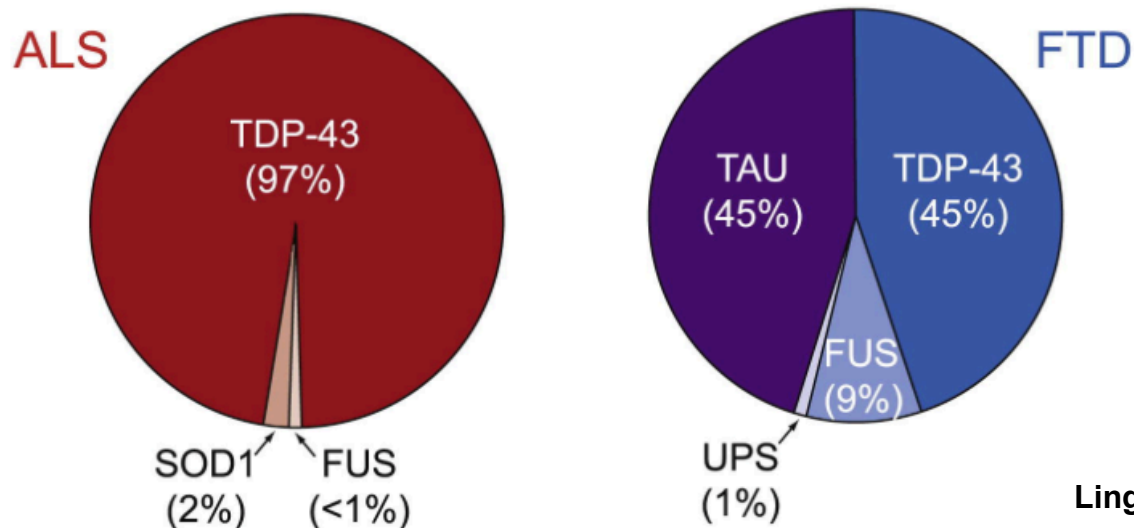


# Link between RNA metabolism and Pathological Inclusions

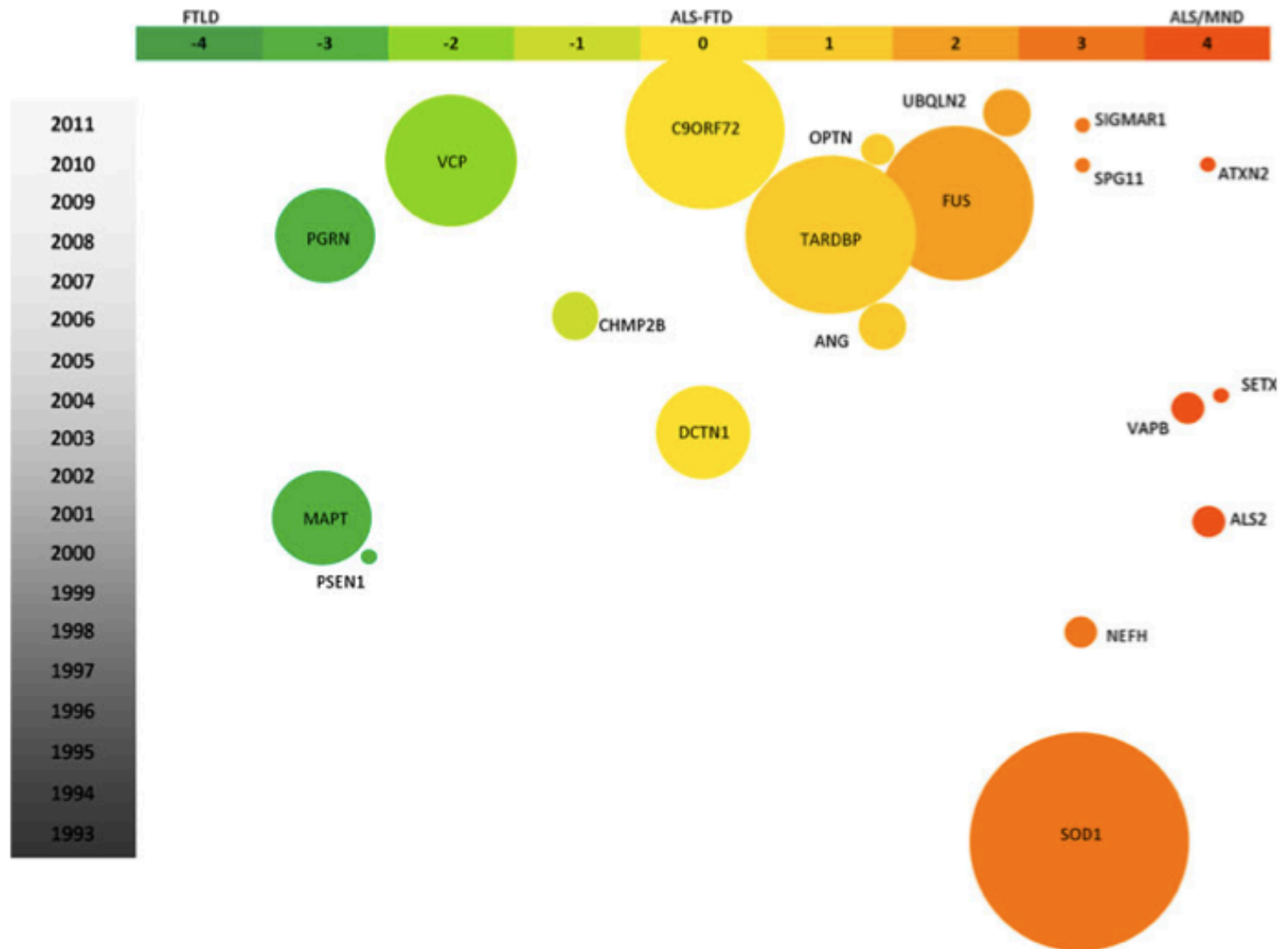
## A Genetics of ALS and FTD



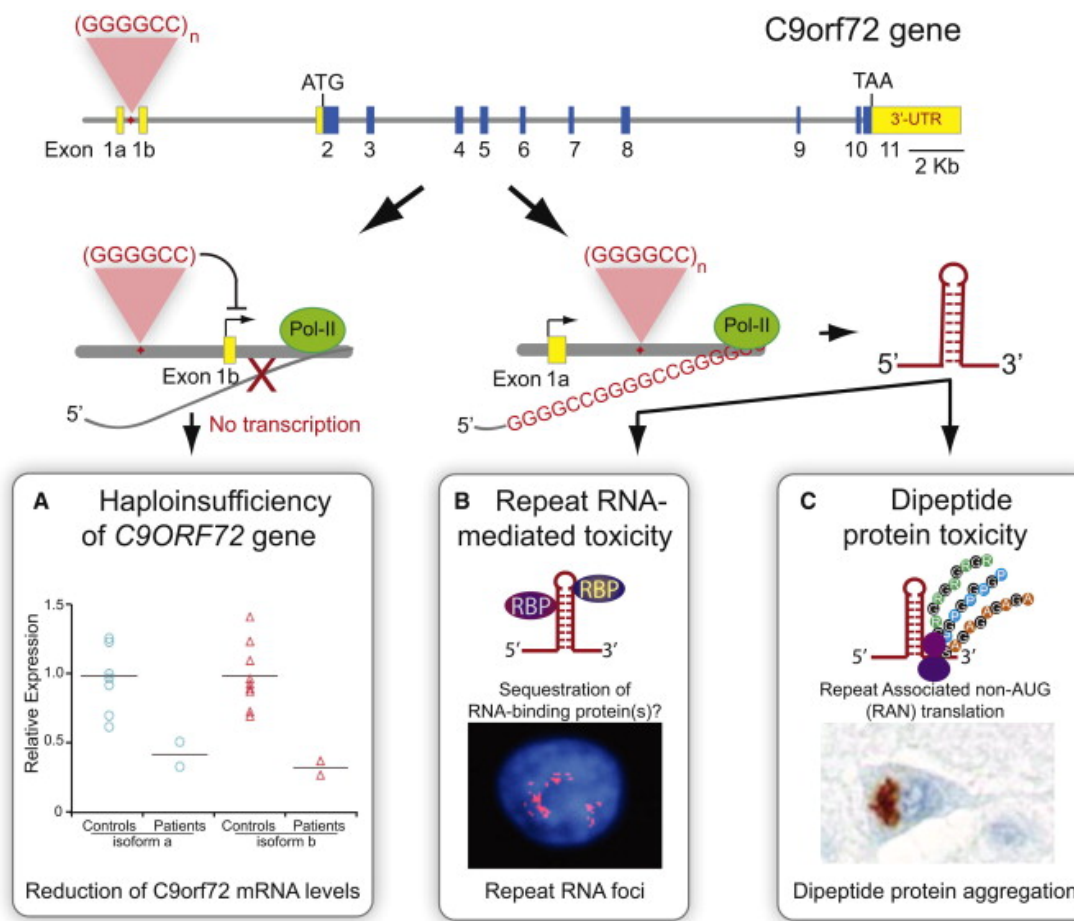
## B Pathological inclusions in ALS and FTD



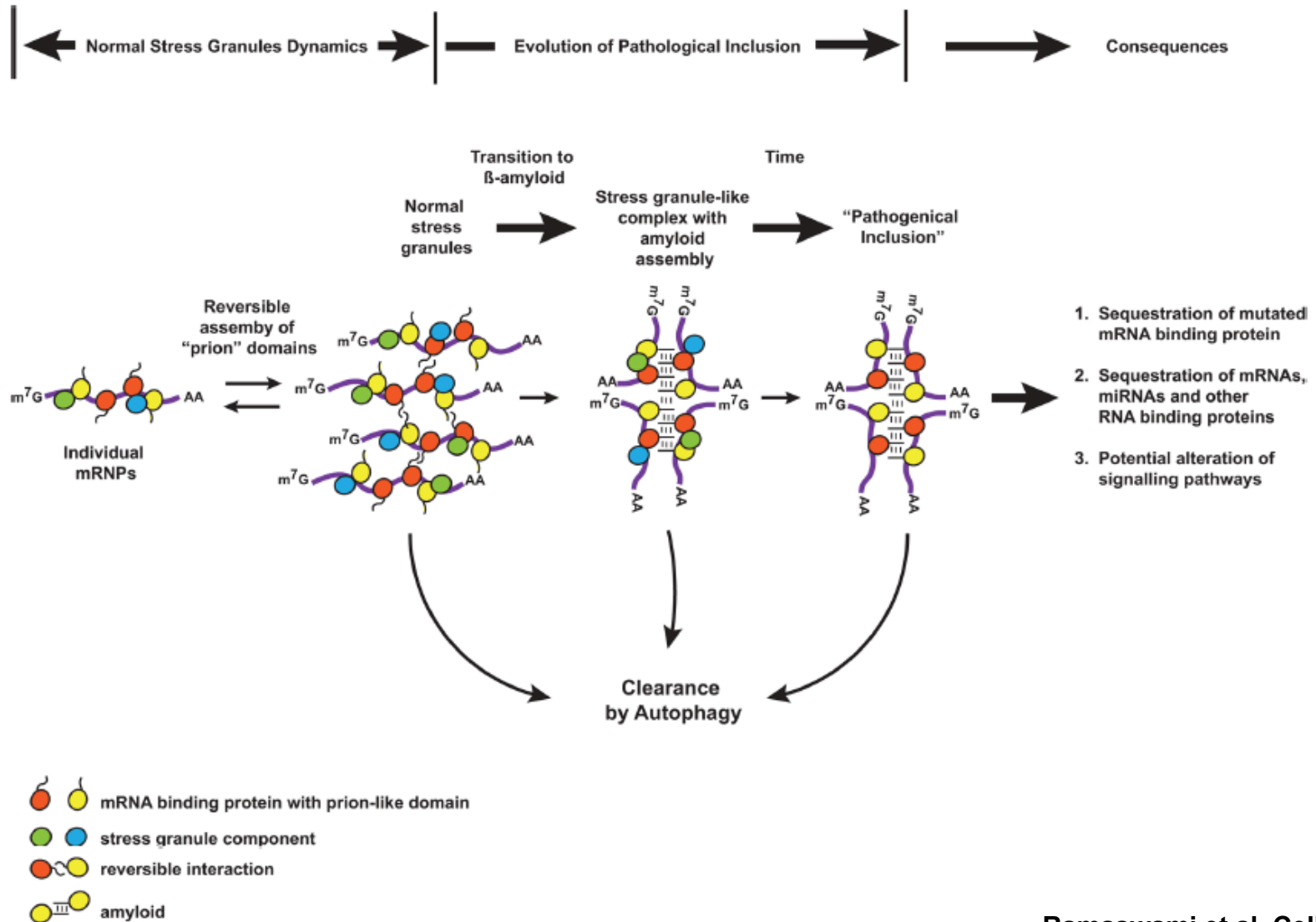
# Clinical - Genetic Spectrum of ALS-FTD



# Another Link between FTD and ALS

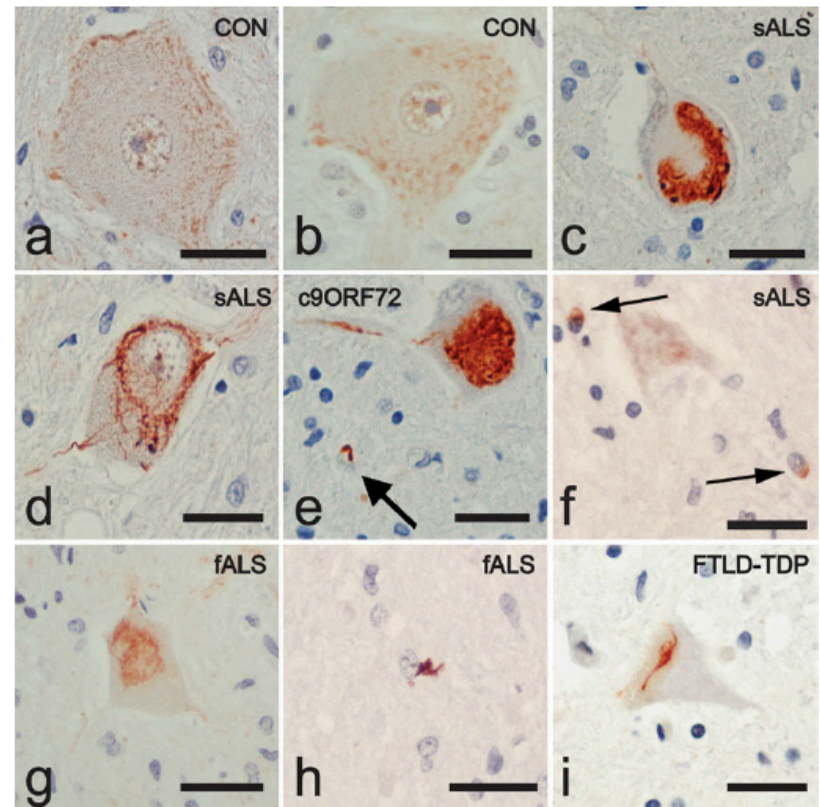
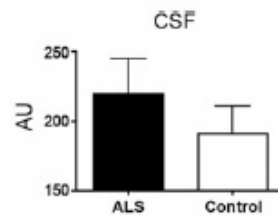
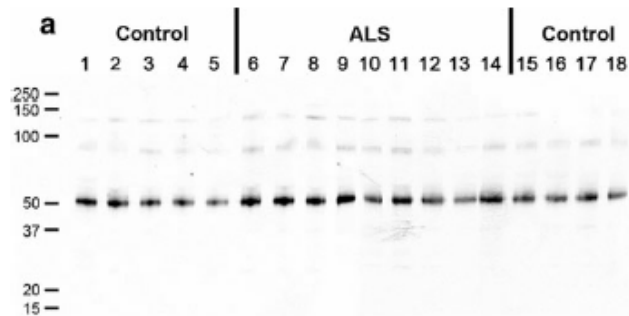


# Why prion-like domains in RNA-binding proteins?



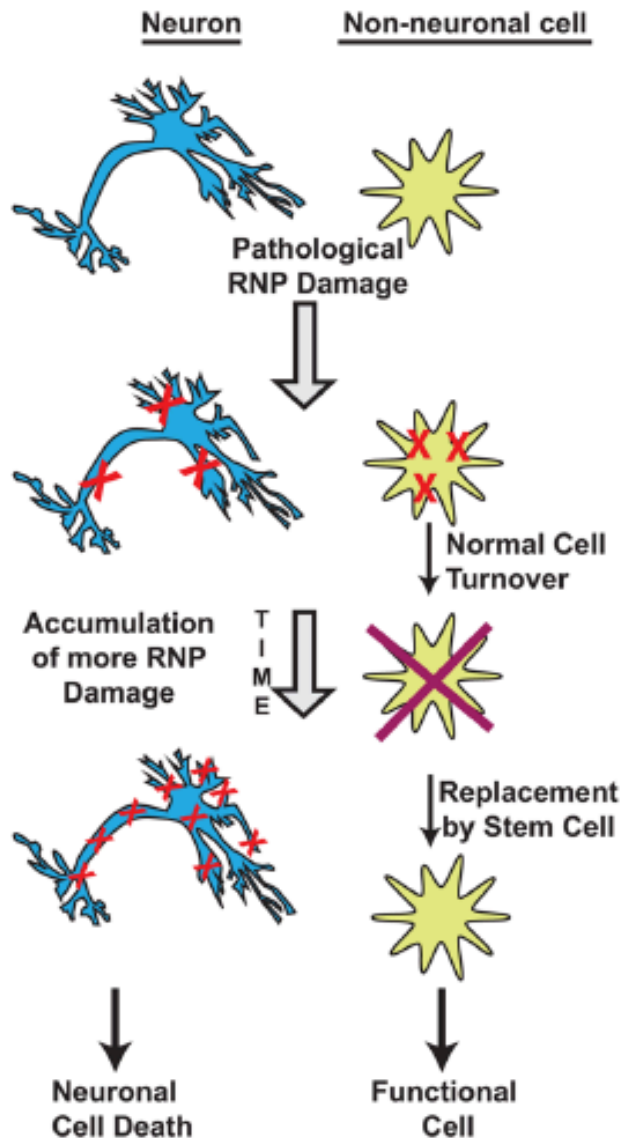


# RNA - binding motif 45 accumulates with TDP-43 inclusions



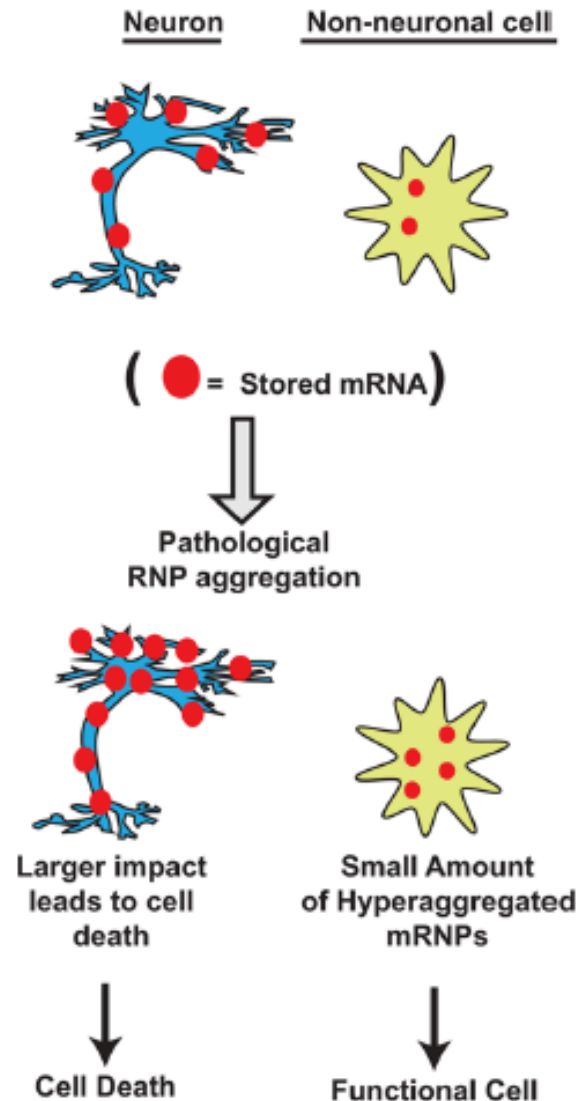


# Why neurons? Why motor neurons?



Longevity of neurons allows accumulation of more damage

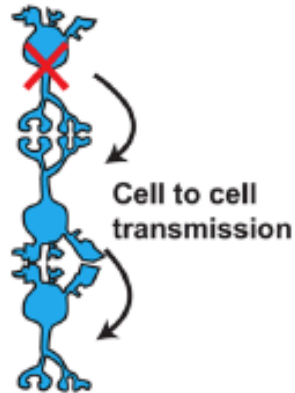
# Why neurons? Why motor neurons?



Higher amount of stored mRNA  
increases sensitivity to  
hyperaggregation

# Why neurons? Why motor neurons?

## Neuronal Circuit

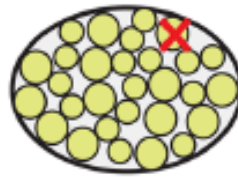


↓ Loss of Neuronal Circuit

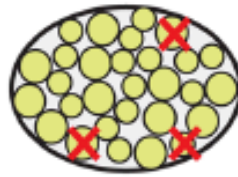


↓ Organism Dysfunction

## Tissue



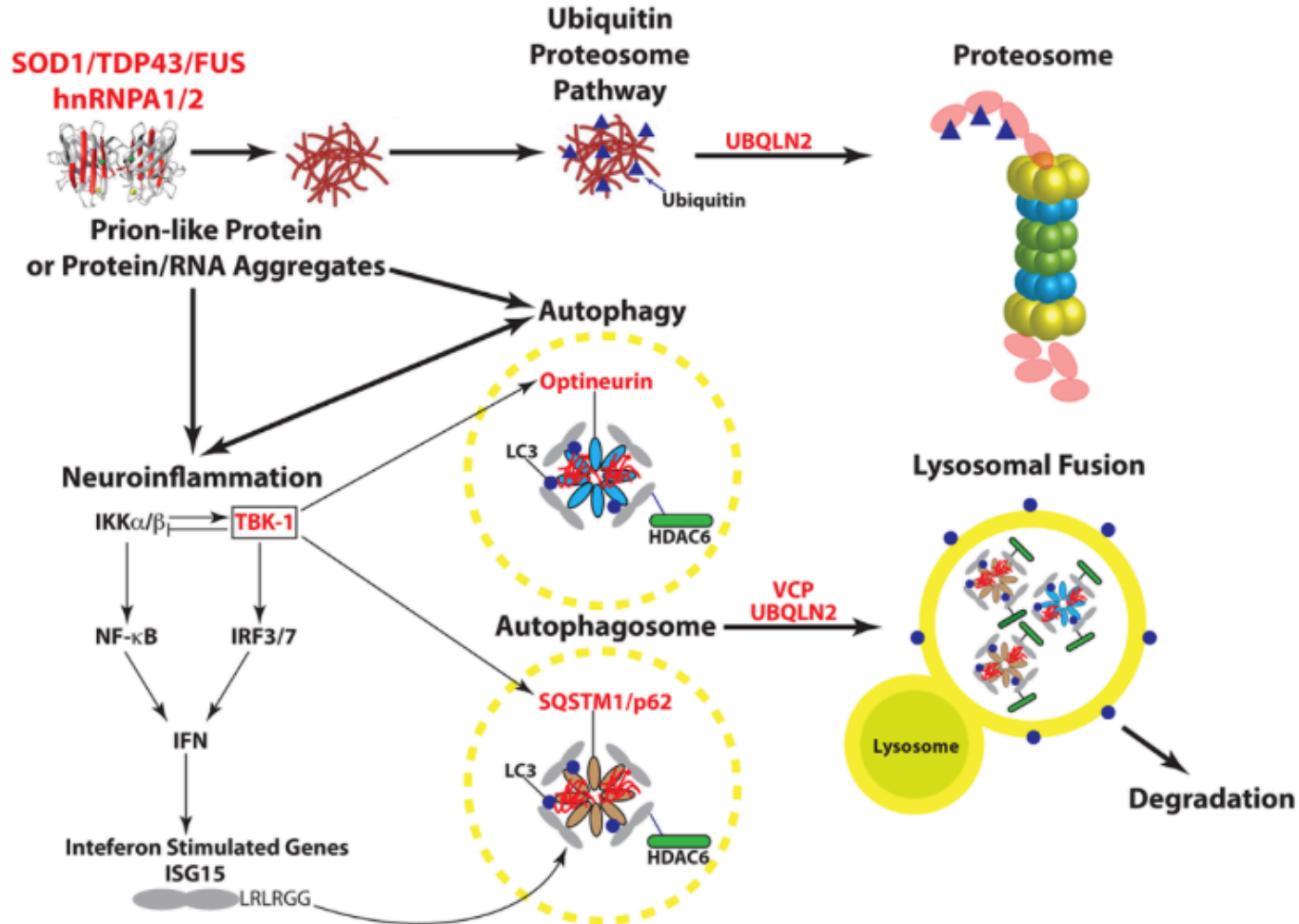
↓ Sporadic Cell Death



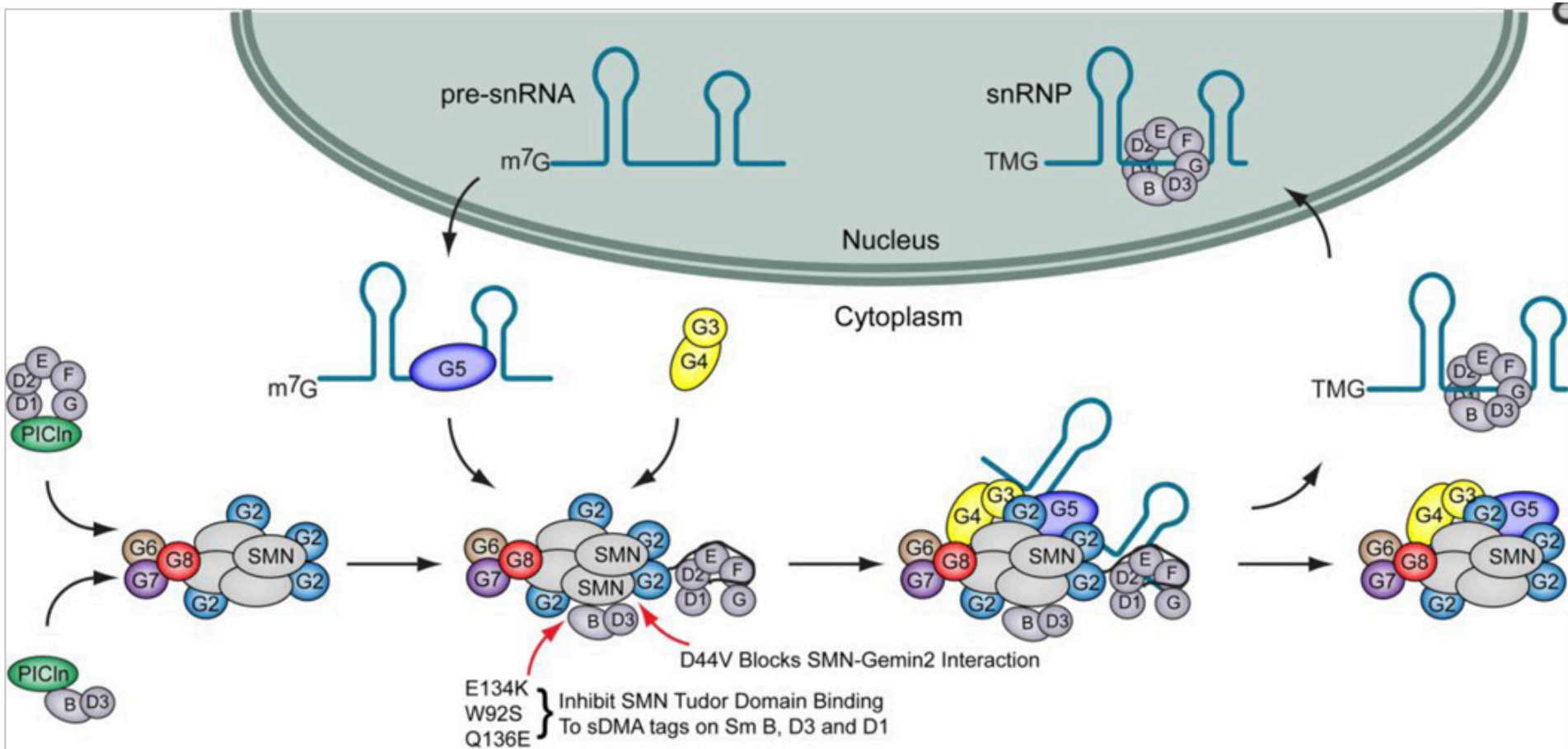
↓ Maintenance of Functional Organ

Connectivity of neurons causes systemic spread and functional failure

# Putative downstream consequences of aberrant RNP formation

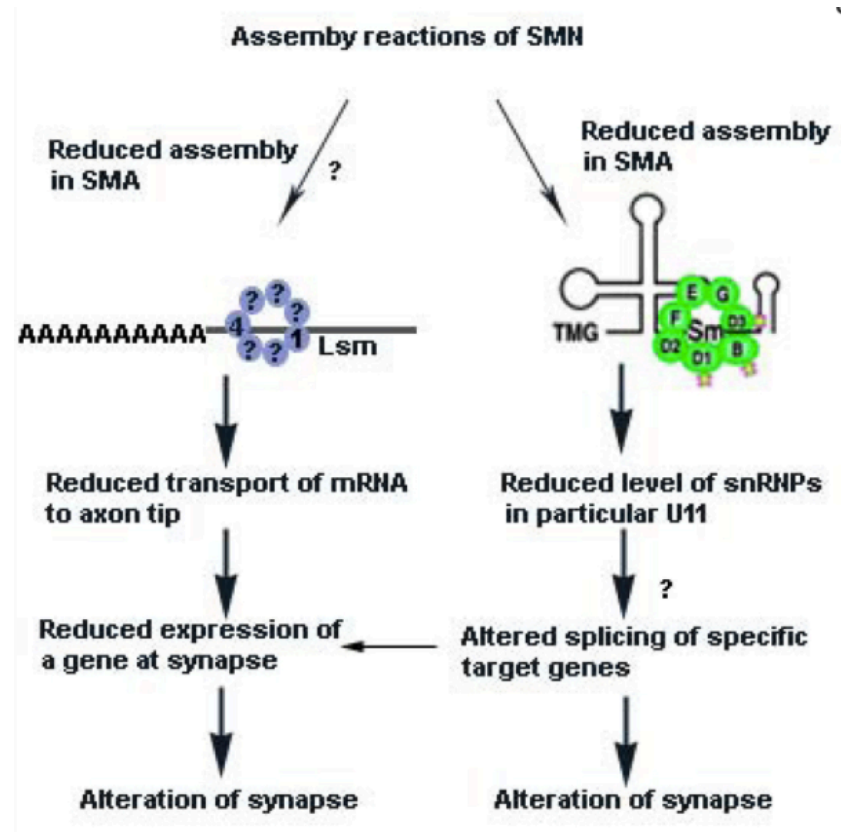
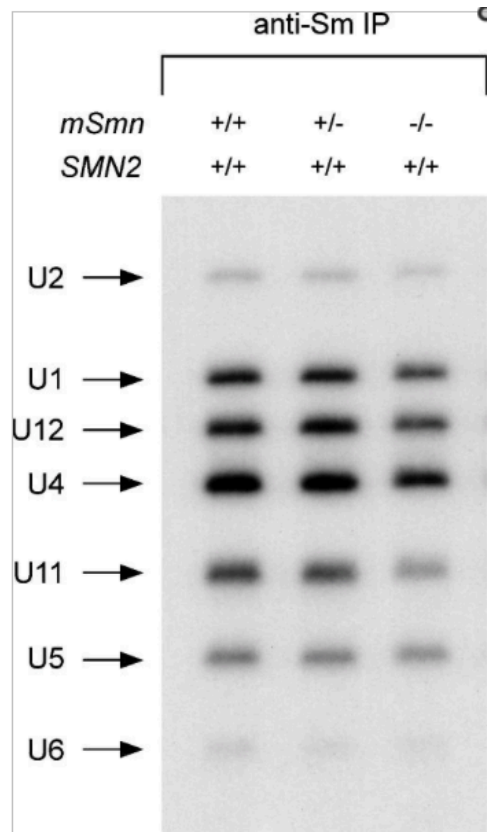


# The example of Spinal Muscular Atrophy



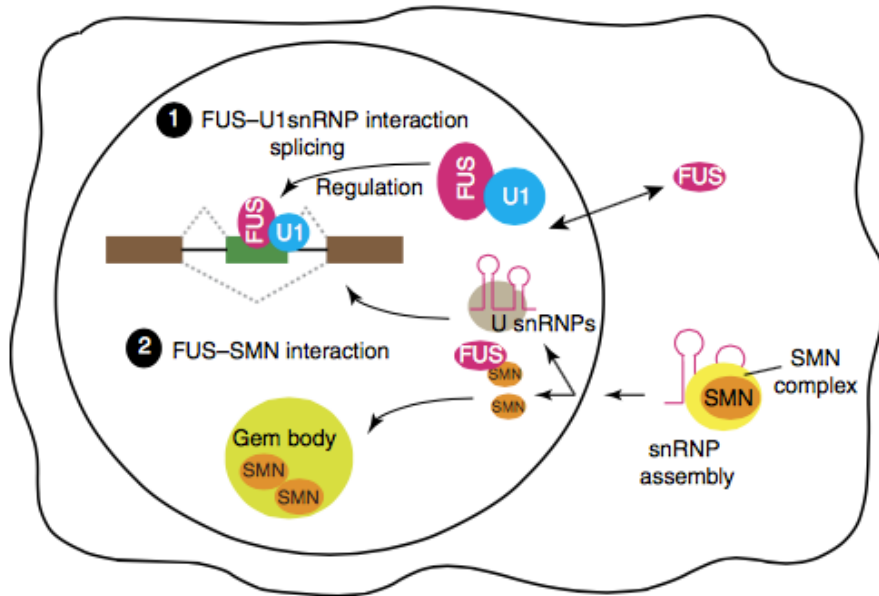
# The example of Spinal Muscular Atrophy

## Reduced snRNP Assembly

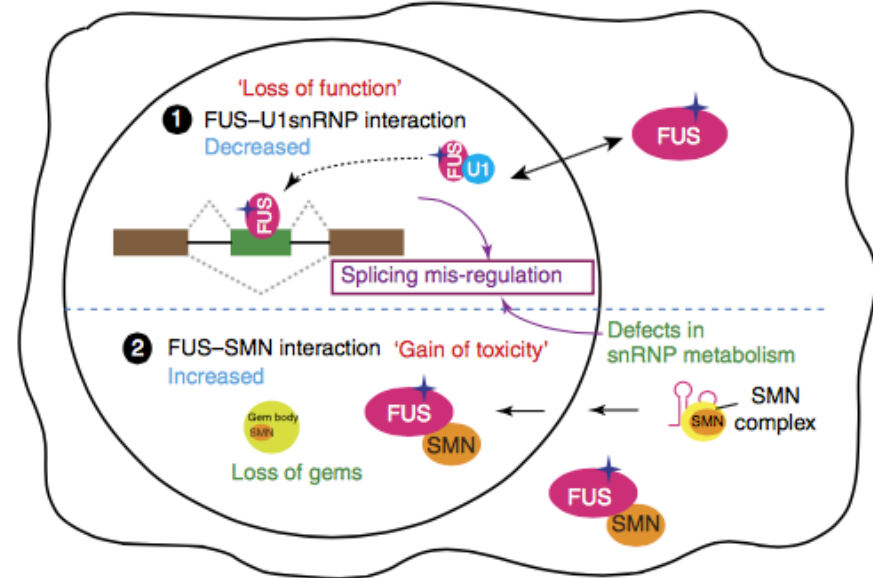


# Another example of Molecular Convergence

Wild-type FUS/TLS



ALS-causative mutant FUS/TLS  
(with or without obvious cytosol mis-localization)



# “Final Common Pathway?”

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- How best to study RNA processing events in neurons and relevant non-neuronal cells?
- What is the molecular “tipping point” for neuronal death?
- Why is there a precipitous “spread” of neuronal death once the “tipping point” is realized?
  - Multiple types of therapy?
- What type of biomarkers can we develop that are based upon RNA processing defects?
- What are the therapeutic targets?



Charles Scott Sherrington 1857-1952

**What is the molecular basis of motor neuron vulnerability?**



“Let us keep looking, in spite of everything. Let us keep searching. It is indeed the best method of finding, and perhaps thanks to our efforts, the verdict we will give such a patient tomorrow will not be the same we must give this man today.”

*Charcot (1889)*

# PILE 'EM HIGH

KipperWilliams

