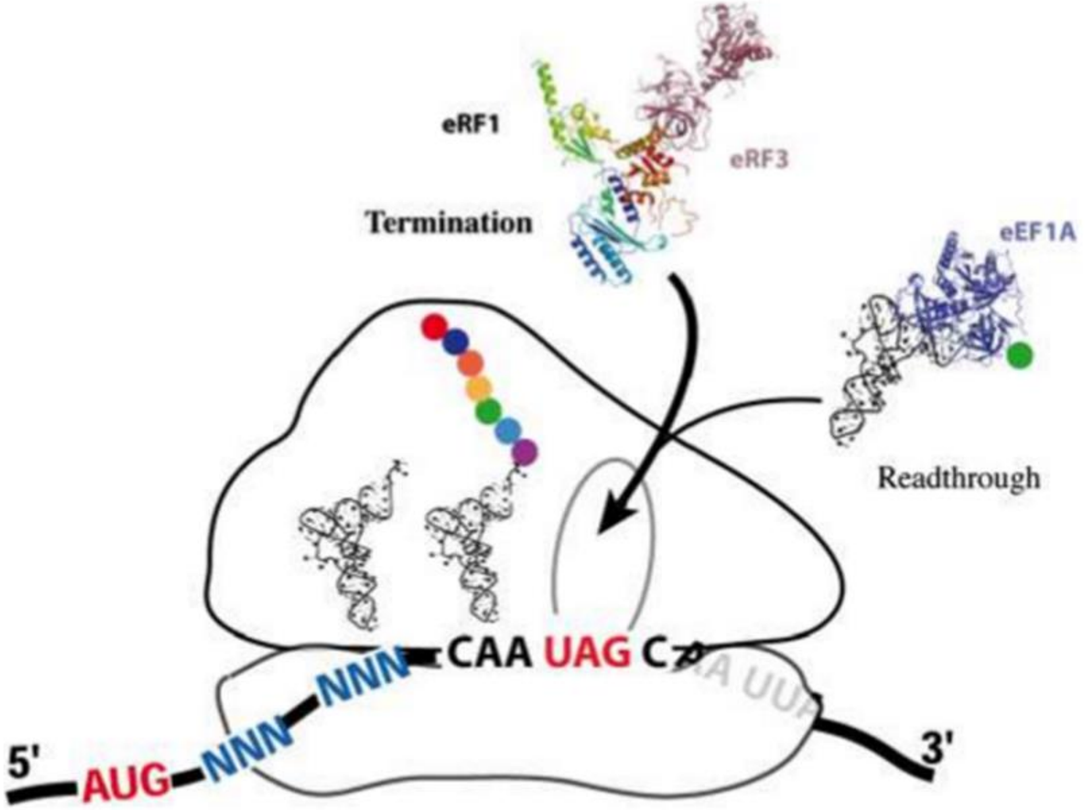
Ribosome readthrough



Starting from the base…PROTEIN SYNTHESIS

Eukaryotic translation can be divided into four stages: Initiation, Elongation, Termination and Recycling

During translation, the ribosome catalyzes the sequential addition of amino acids to a growing polypeptide chain, using an mRNA as template and aminoacyl-tRNAs as substrates

Correct base pairing between the three bases of the codon on mRNA and those of the anticodon of the aa-tRNA dictates the sequence of the polypeptide chain

Translation termination

When the ribosome arrives at a **stop codon**, there is **no corresponding tRNA**. Instead, a **release factor** enters the assembly site and **synthesis is terminated**, releasing the completed polypeptide from the ribosome.

Translation termination

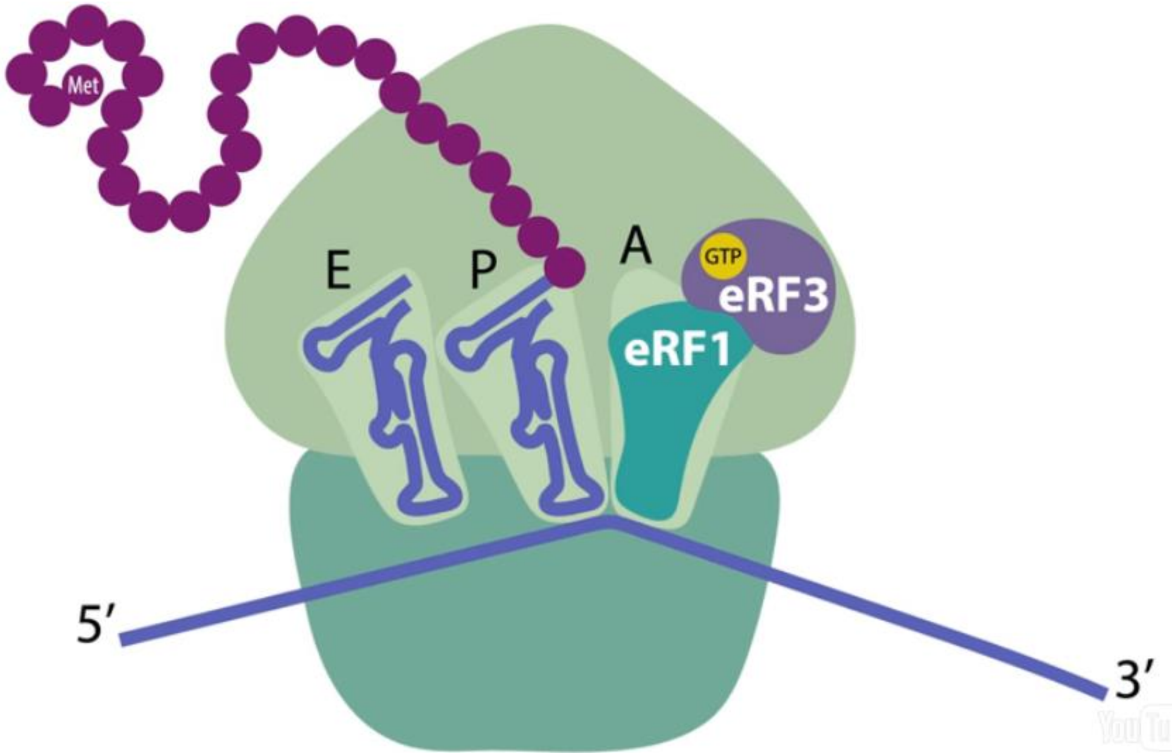
When the ribosome arrives at a **stop codon**, there is **no corresponding tRNA**. Instead, a **release factor** enters the assembly site and **synthesis is terminated**, releasing the completed polypeptide from the ribosome.

Translation termination in eukaryotes is mediated by two release factors:

- **eRF1** recognizes each of the three stop codons (UAG, UAA, and UGA) and facilitates release of the nascent polypeptide chain
- **eRF3** is a GTP binding protein that facilitate the termination process

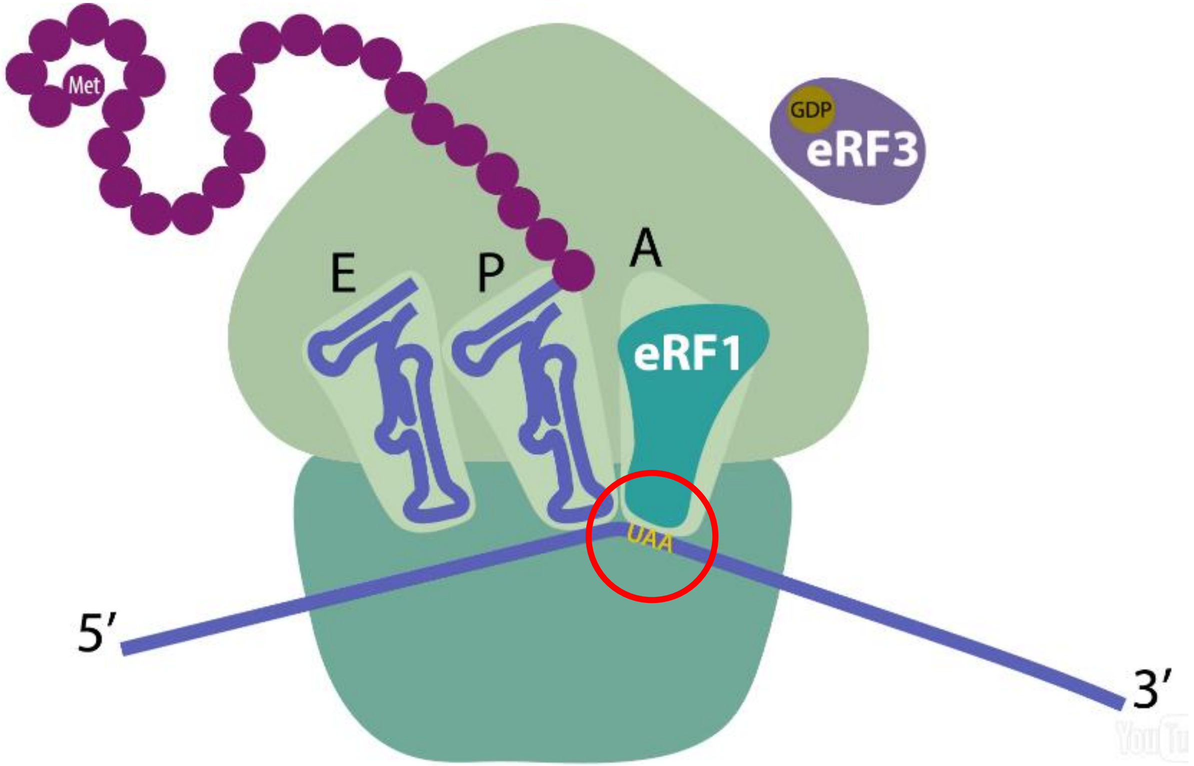
Translation termination

1. A complex formed by **eRF1** and **eRF3-GTP** enters the ribosome



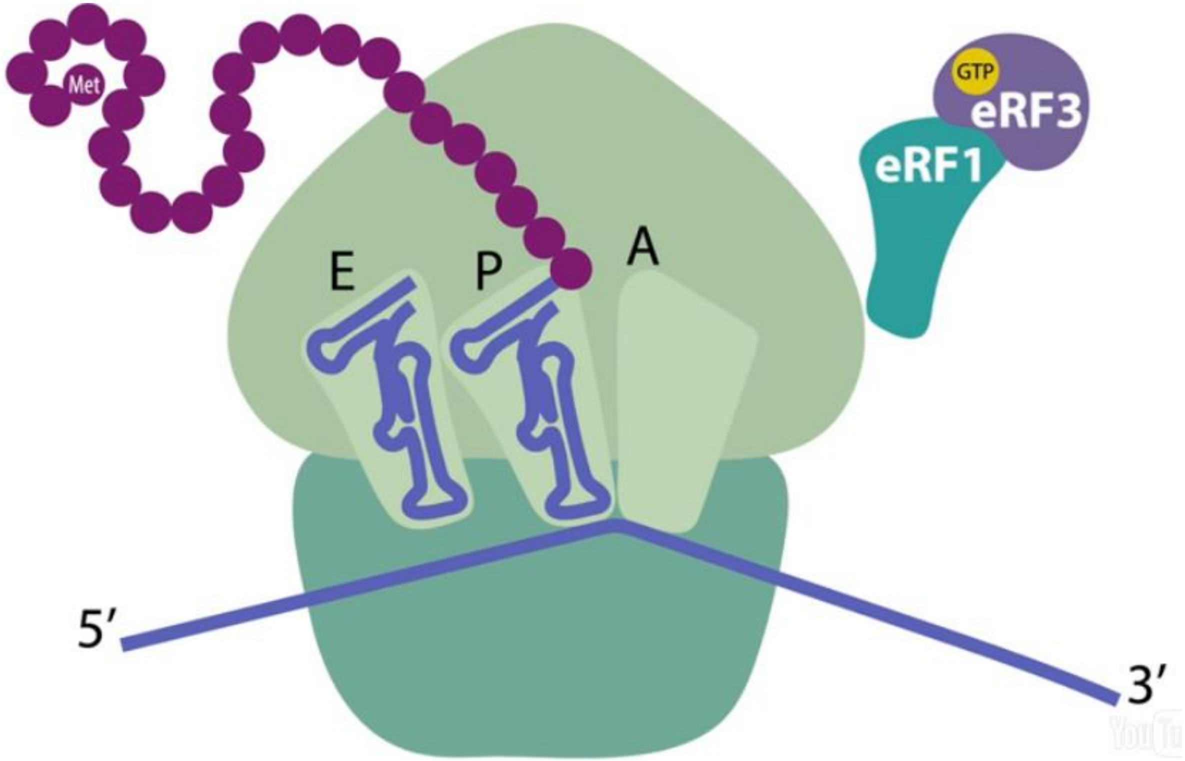
Translation termination

1. A complex of eRF1 and eRF3-GTP enters the ribosome
2. The **stable interaction** between eRF1 and a stop codon in the ribosomal A site stimulates **GTP hydrolysis** by eRF3



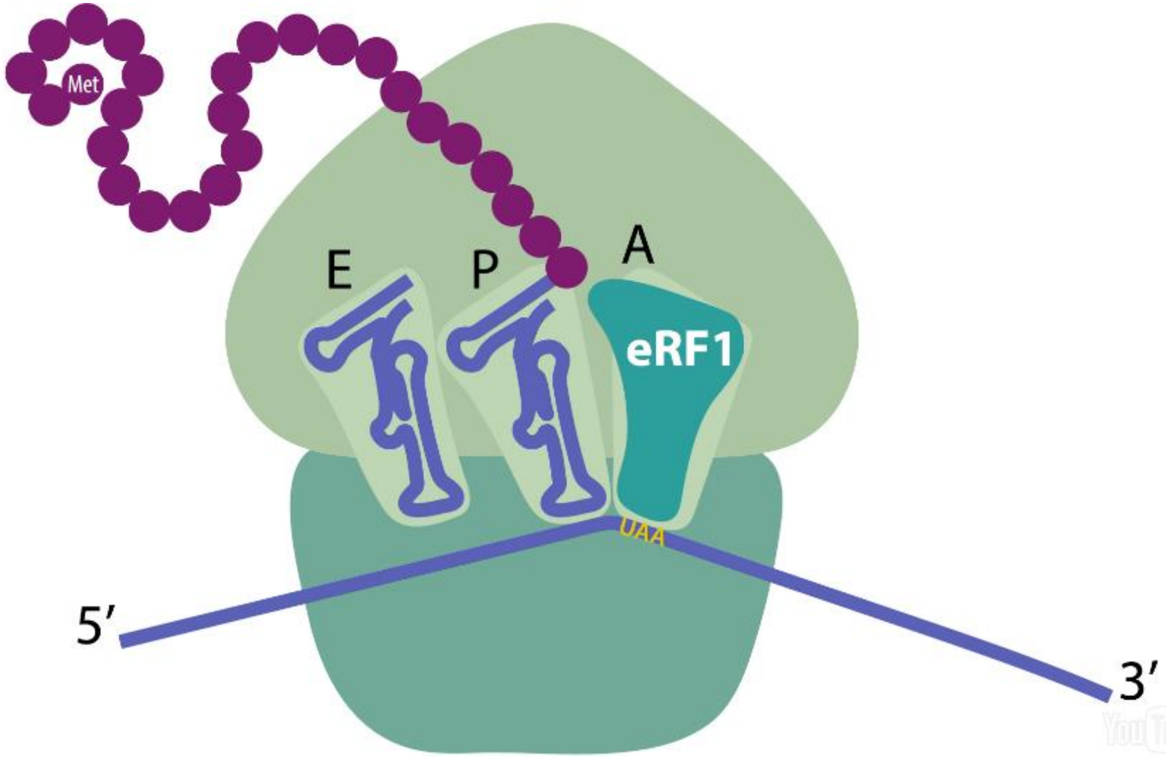
Translation termination

1. A complex of eRF1 and eRF3-GTP enters the ribosome
2. The stable interaction between eRF1 and a stop codon in the ribosomal A site stimulates GTP hydrolysis by eRF3 (a **not perfect** interaction causes the **dissociation** of the release complex)



Translation termination

1. A complex of eRF1 and eRF3-GTP enters the ribosome
2. The stable interaction between eRF1 and a stop codon in the ribosomal A site stimulates GTP hydrolysis by eRF3 (a not perfect interaction cause the dissociation of the release complex)
3. GTP hydrolysis **activates eRF1** so that it can efficiently stimulate nascent chain release

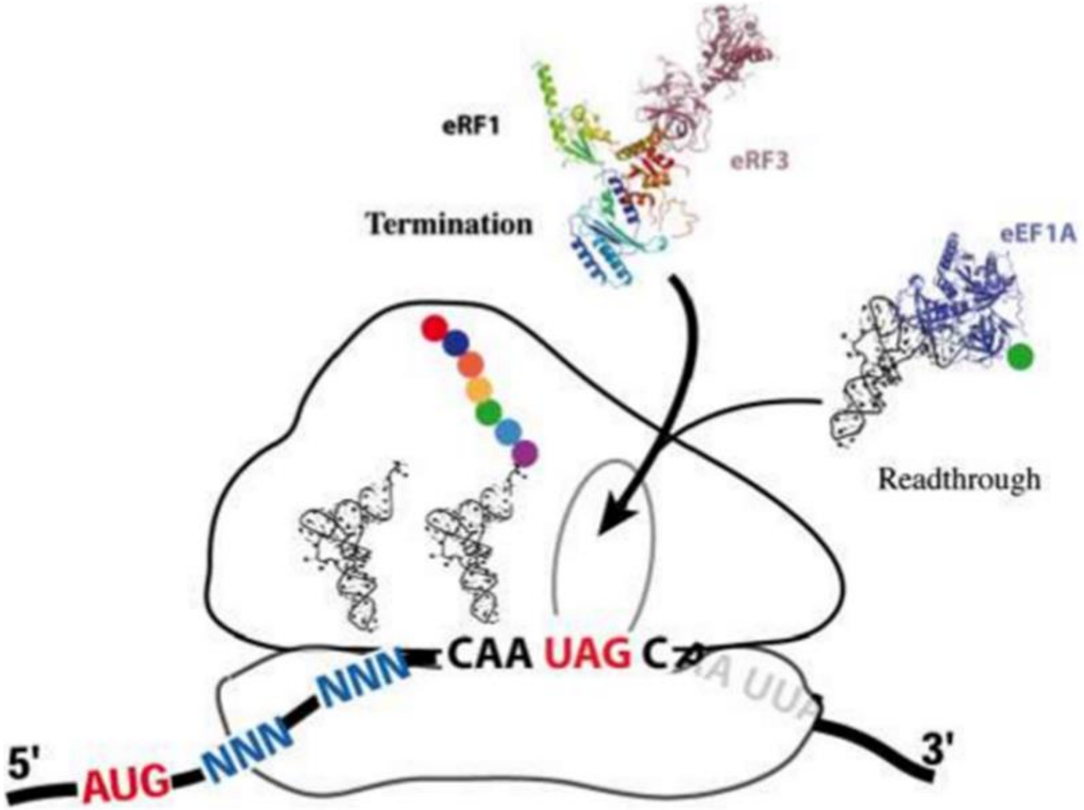


Translation termination is normally a highly efficient process

BUT occasionally stop codon recognition by eRF1 can be superseded by selected aminoacyl-tRNAs, resulting in **stop codon suppression**

Translation termination is normally a highly efficient process

BUT occasionally stop codon recognition by eRF1 can be superseded by selected aminoacyl-tRNAs, resulting in **stop codon suppression**



This event is called **READTHROUGH** and corresponds to the **incorporation of a tRNA**, or natural suppressor**, at the stop codon**, allowing translation to continue in the same frame until the ribosome reaches the next stop

The more efficient is translation termination, the less frequent is readthrough (and viceversa)

Readthrough

Termination efficiency

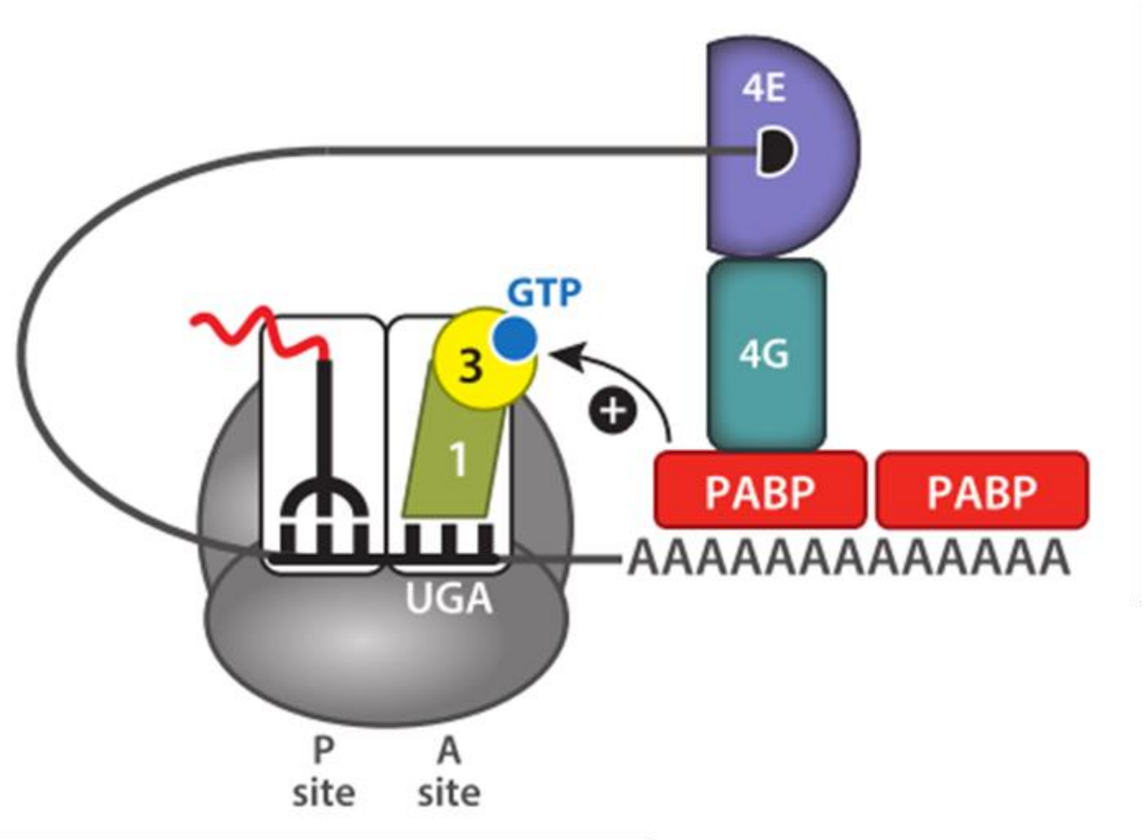
The efficiency of translation termination (and the occurrence of readthrough) can vary depending on many factors

The efficiency of translation termination (and the occurrence of readthrough) can vary depending on:

1) The efficiency of termination differs between normal stop codons and premature termination codons (PTC)

Normal STOP codon

PABP interacts with eRF3, promoting translation termination



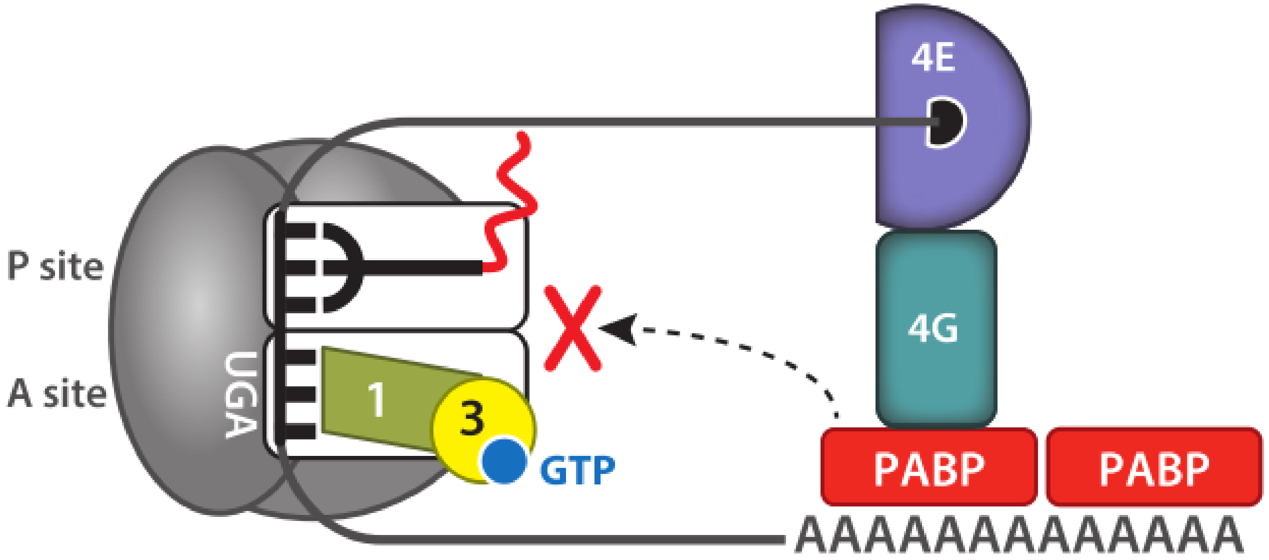
Keeling et al. 2014

The efficiency of translation termination (and the occurrence of readthrough) can vary depending on:

1) The efficiency of termination differs between normal stop codons and premature termination codons (PTC)

Premature STOP codon

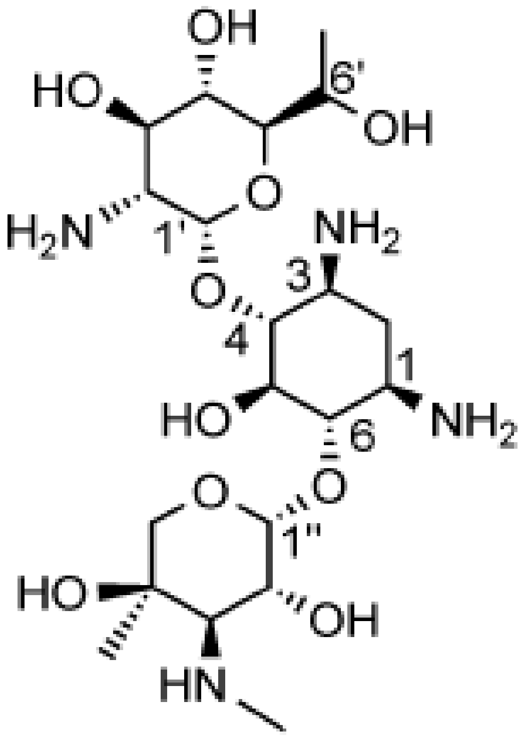
PABP can not interact with eRF3, leading to prolonged ribosomal pausing at PTC and increasing aa-tRNA sampling



Keeling et al. 2014

2) Aminoglycosides can decrease the fidelity of translation, causing higher frequencies of readthrough

Aminoglycosides are a class of antibiotics that interfere with bacterial-protein synthesis. They all have a common 2-deoxystreptamine ring structure, which binds to the ribosome decoding center.



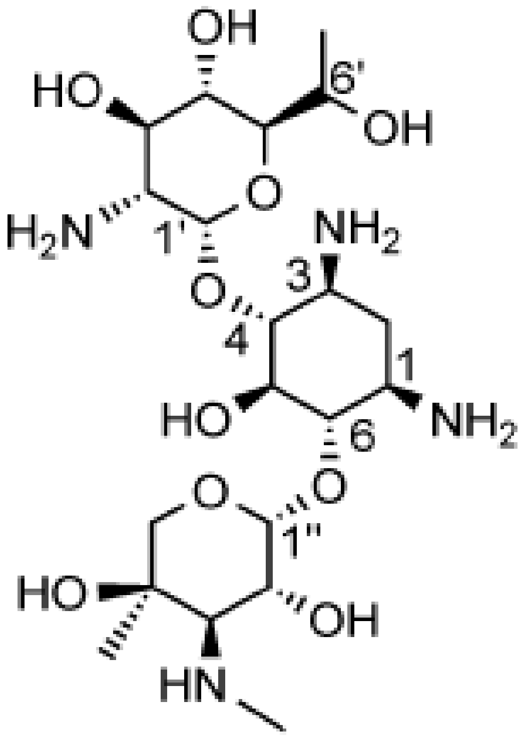
Geneticin (G418)

2) Aminoglycosides can decrease the fidelity of translation, causing higher frequencies of readthrough

Aminoglycosides are a class of antibiotics that interfere with bacterial-protein synthesis. They all have a common 2-deoxystreptamine ring structure, which binds to the ribosome decoding center.

Ribosome is composed by **two subunits**:

- The large subunit contains the peptidyl transferase center, in which peptide bonds are formed
- The **small subunit** contains the **decoding center**, a region in which the correct codon-anticodon pairing between mRNA and tRNAs is monitored

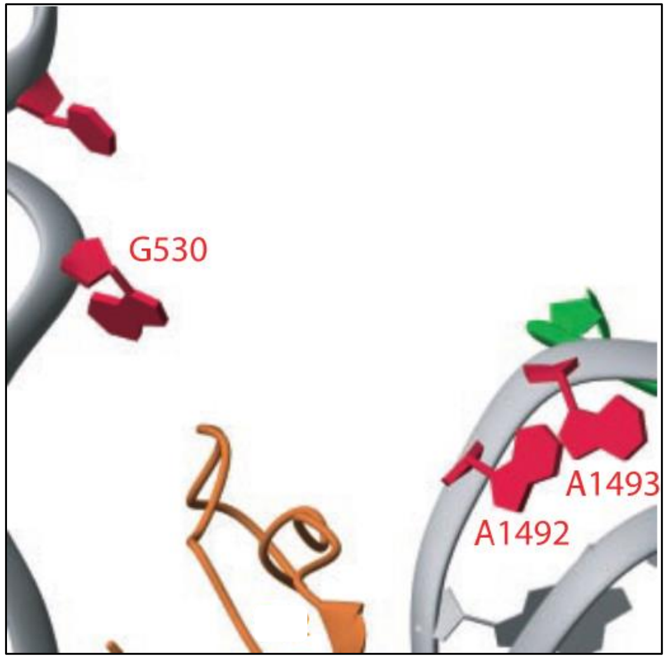


Geneticin (G418)

2) Aminoglycosides can decrease the fidelity of translation, causing higher frequencies of readthrough

Mechanism of action: aminoglycosides binding to ribosome decoding site induces a conformational change similar to the transition caused by a tRNA binding

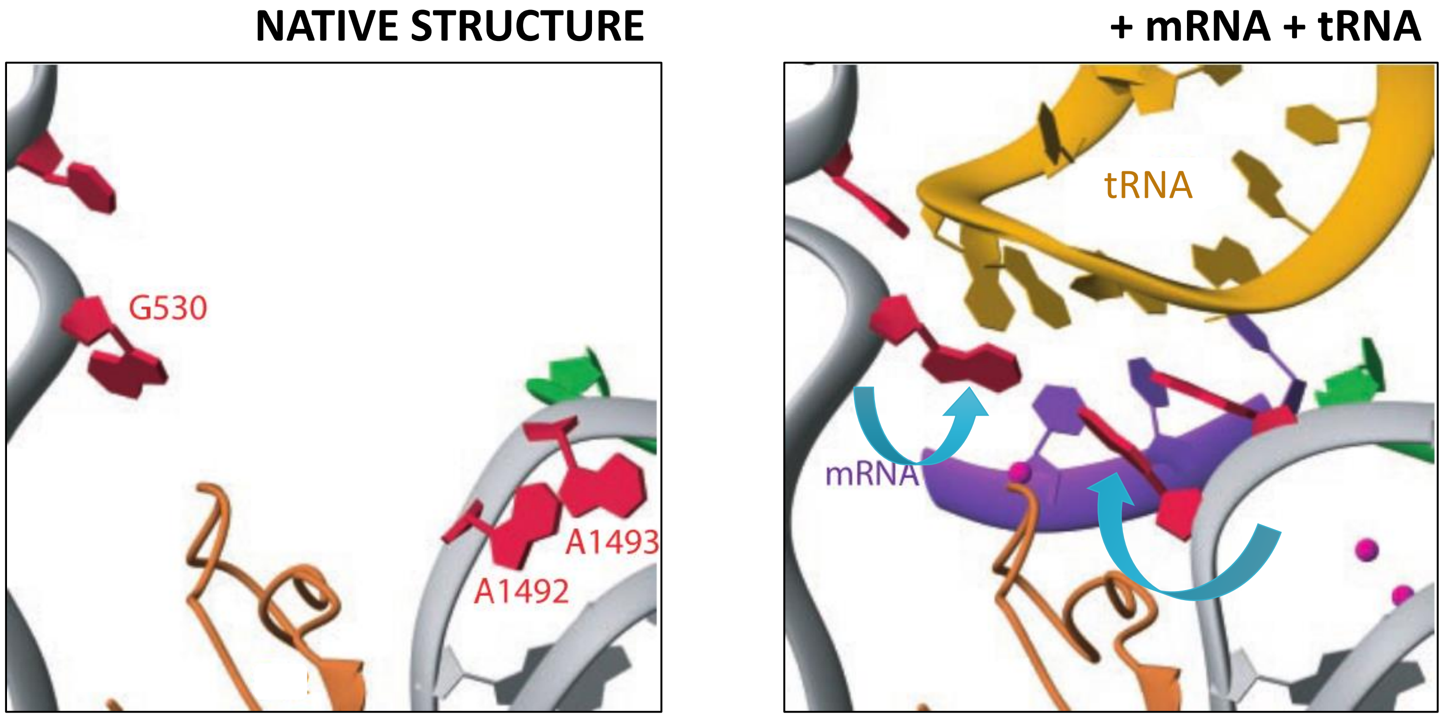
NATIVE STRUCTURE



Ogle et al. 2001

2) Aminoglycosides can decrease the fidelity of translation, causing higher frequencies of readthrough

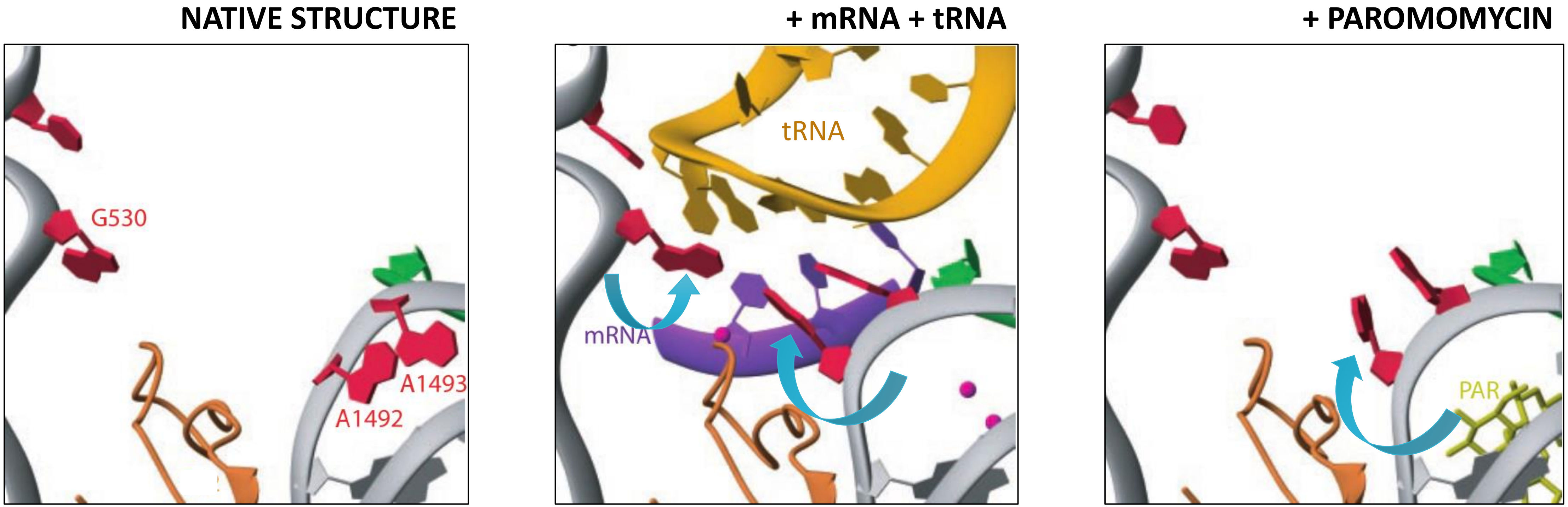
Mechanism of action: aminoglycosides binding to ribosome decoding site induces a conformational change similar to the transition caused by a tRNA binding



Ogle et al. 2001

2) Aminoglycosides can decrease the fidelity of translation, causing higher frequencies of readthrough

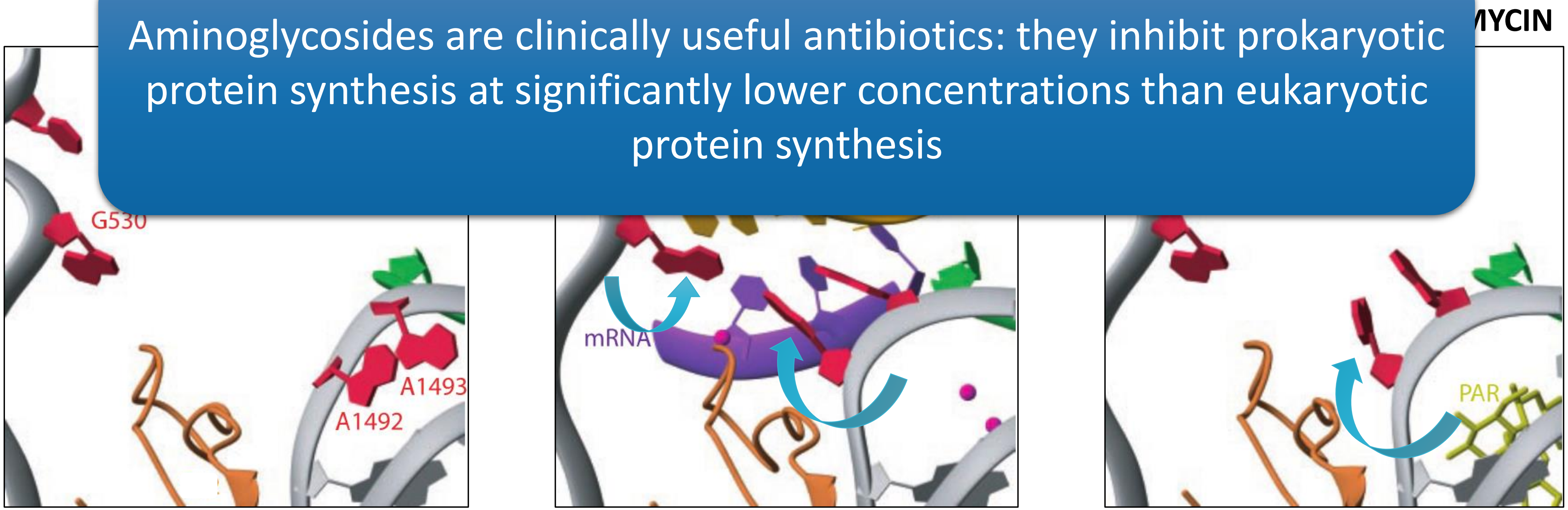
Mechanism of action: aminoglycosides binding to ribosome decoding site induces a conformational change similar to the transition caused by a tRNA binding



Ogle et al. 2001

2) Aminoglycosides can decrease the fidelity of translation, causing higher frequencies of readthrough

Mechanism of action: aminoglycosides binding to ribosome decoding site induces a conformational change similar to the transition caused by a tRNA binding



Aminoglycosides are clinically useful antibiotics: they inhibit prokaryotic protein synthesis at significantly lower concentrations than eukaryotic protein synthesis

Ogle et al. 2001

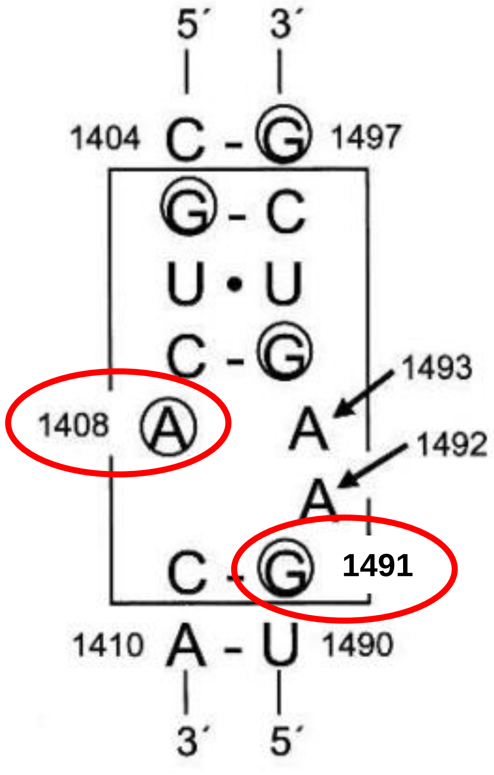
2) Aminoglycosides can decrease the fidelity of translation, causing higher frequencies of readthrough

The major determinants of the **differential** aminoglycoside **sensitivity** between prokaryotes and eukaryotes are **two non conserved residues** of the **decoding center**

2) Aminoglycosides can decrease the fidelity of translation, causing higher frequencies of readthrough

The major determinants of the **differential** aminoglycoside **sensitivity** between prokaryotes and eukaryotes are **two non conserved residues** of the **decoding center**

A1408 and **G1491**



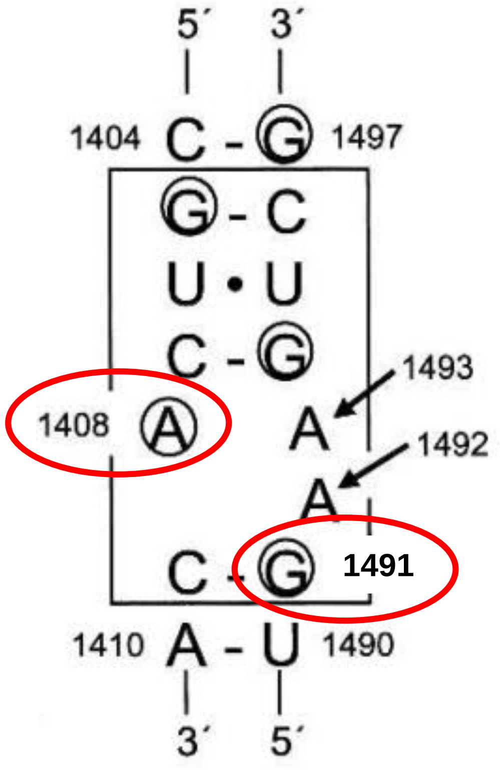
Helix 44
(*E. coli*)

Fan-Minogue et al. 2008

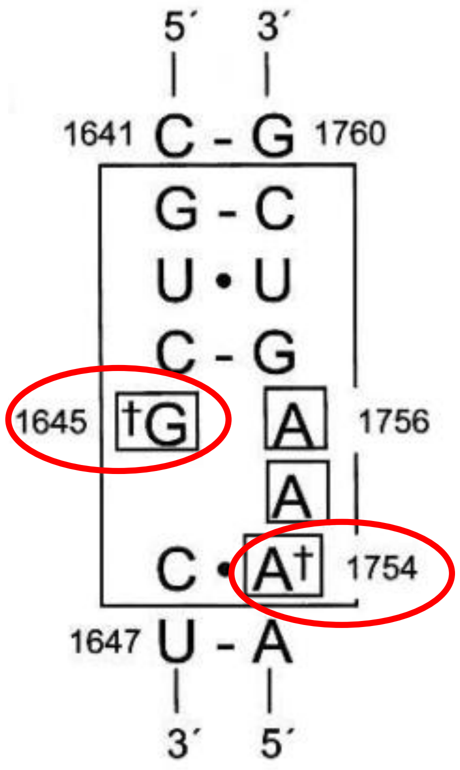
2) Aminoglycosides can decrease the fidelity of translation, causing higher frequencies of readthrough

The major determinants of the **differential** aminoglycoside **sensitivity** between prokaryotes and eukaryotes are **two non conserved residues** of the **decoding center**

A1408 and **G1491** **VS** **G1645** and **A1754**



Helix 44
(*E. coli*)



Helix 44
(*S. cerevisiae*)

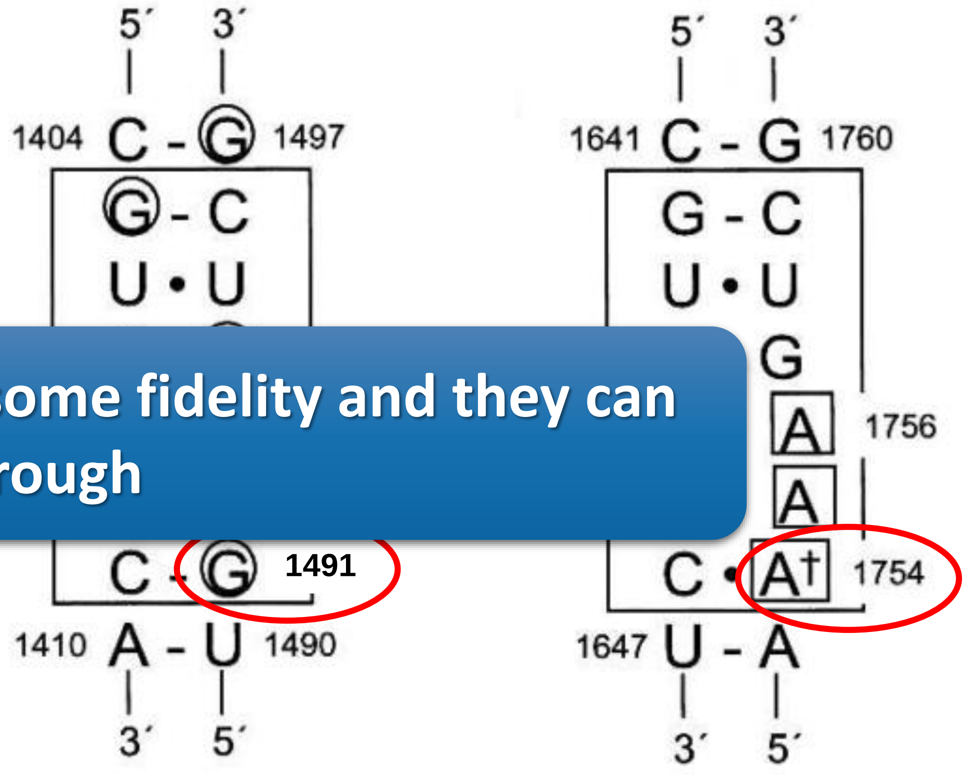
Fan-Minogue et al. 2008

2) Aminoglycosides can decrease the fidelity of translation, causing higher frequencies of readthrough

The major determinants of the **differential** aminoglycoside **sensitivity** between prokaryotes and eukaryotes are **two non** **con**

In eukaryotes aminoglycosides decrease ribosome fidelity and they can be used to induce readthrough

A1408 and **G1491** **VS** **G1645** and **A1754**



Helix 44
(*E. coli*)

Helix 44
(*S. cerevisiae*)

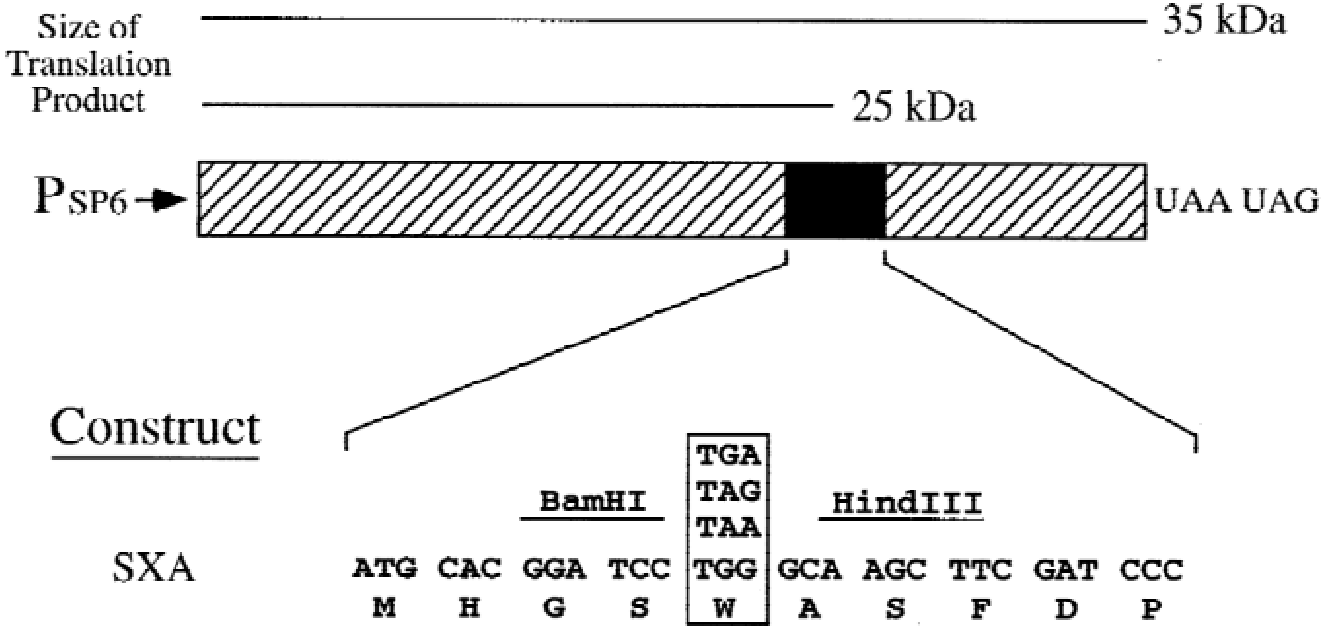
Fan-Minogue et al. 2008

3) The **nucleotide context** strongly influences efficiency of translation termination and, as a consequence, occurrence of readthrough

3) The **nucleotide context** strongly influences efficiency of translation termination and, as a consequence, occurrence of readthrough

Different stop codons promote translation termination with different efficiencies

Readthrough reporter system:

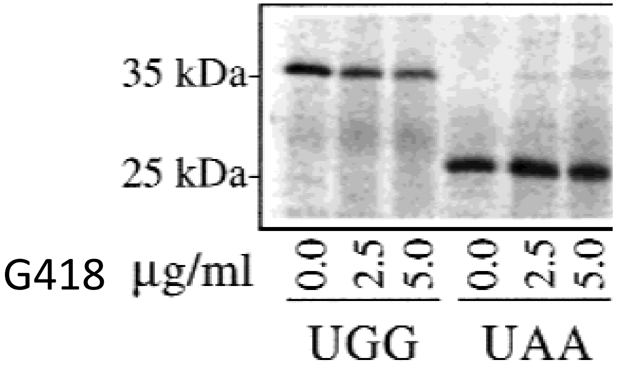


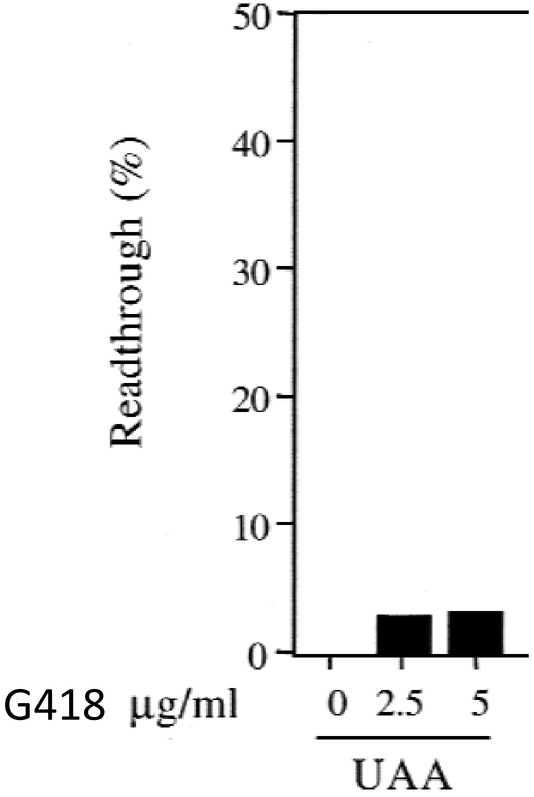
Manuvakhova et al. 2000

3) The nucleotide context strongly influences efficiency of translation termination and, as a consequence, occurrence of readthrough

Different stop codons promote translation termination with different efficiencies

UAA



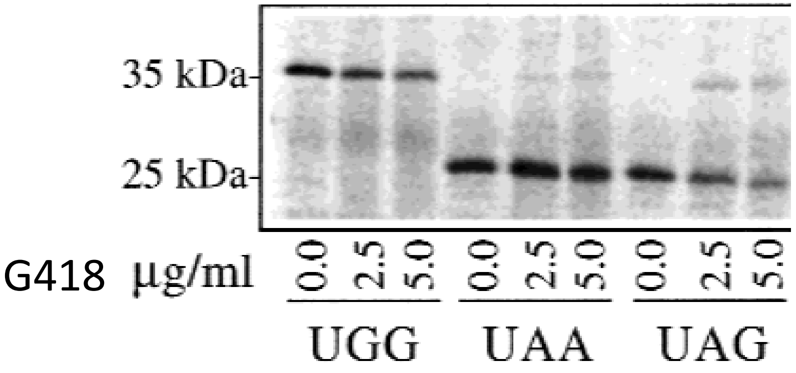


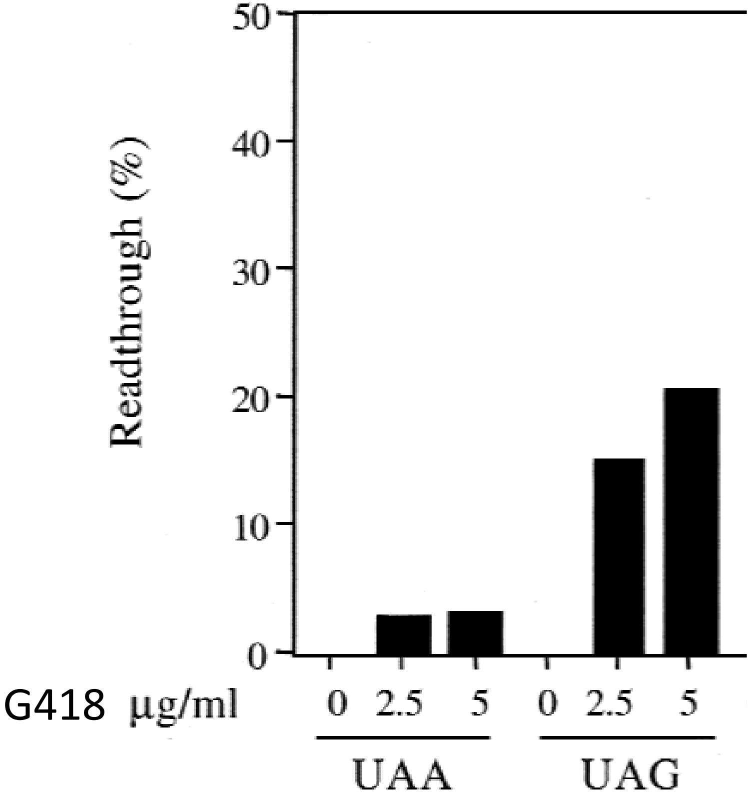
Manuvakhova et al. 2000

3) The nucleotide context strongly influences efficiency of translation termination and, as a consequence, occurrence of readthrough

Different stop codons promote translation termination with different efficiencies

UAA > UAG



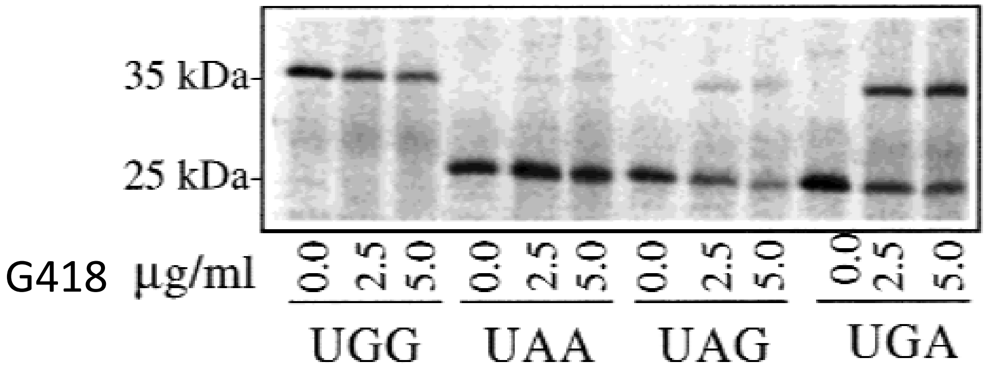


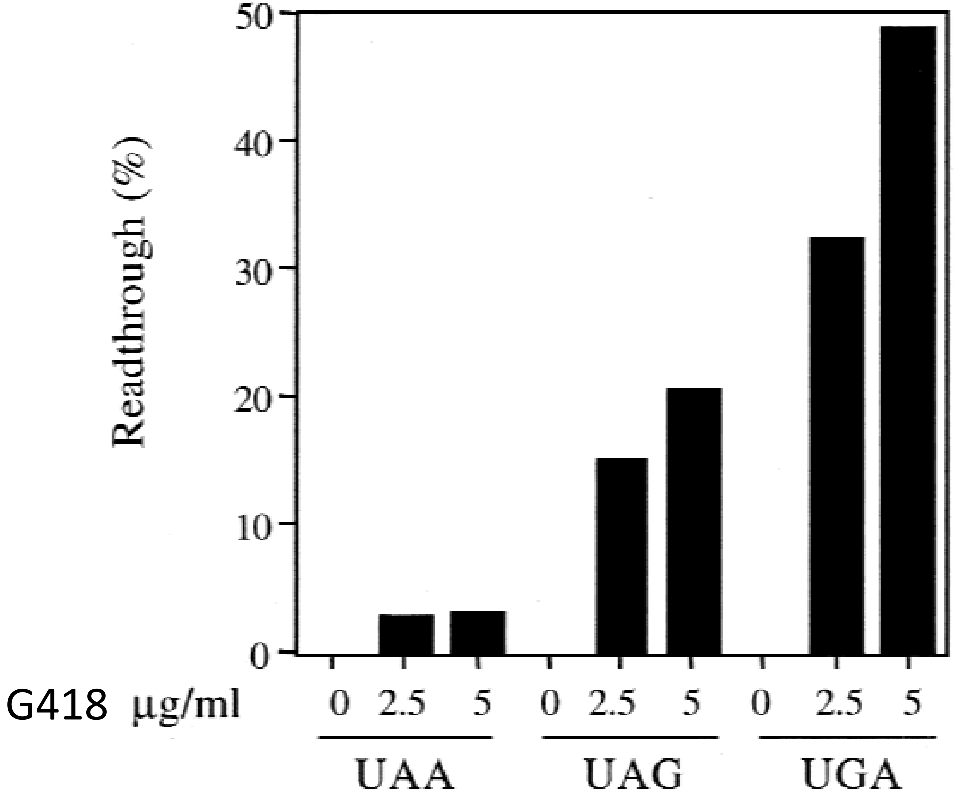
Manuvakhova et al. 2000

3) The nucleotide context strongly influences efficiency of translation termination and, as a consequence, occurrence of readthrough

Different stop codons promote translation termination with different efficiencies

UAA > UAG ≥ UGA



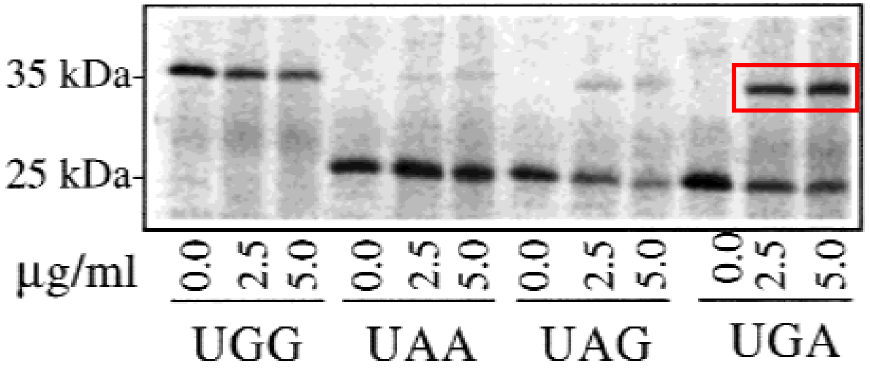


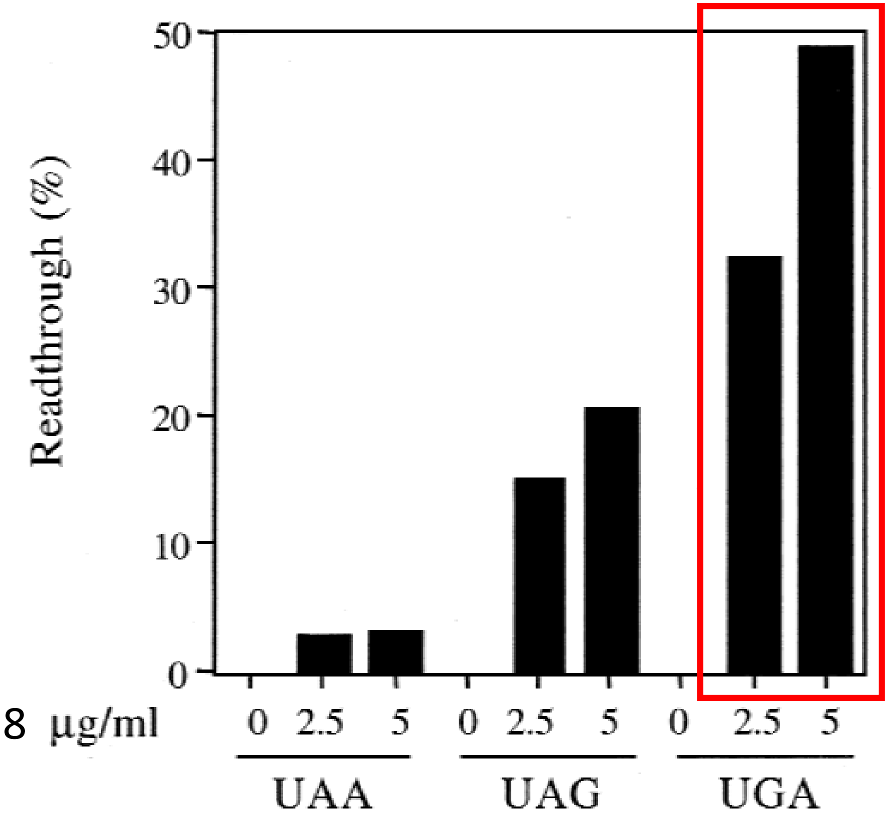
Manuvakhova et al. 2000

3) The nucleotide context strongly influences efficiency of translation termination and, as a consequence, occurrence of readthrough

Different stop codons promote translation termination with different efficiencies

UAA > UAG ≥ UGA


G418


G418

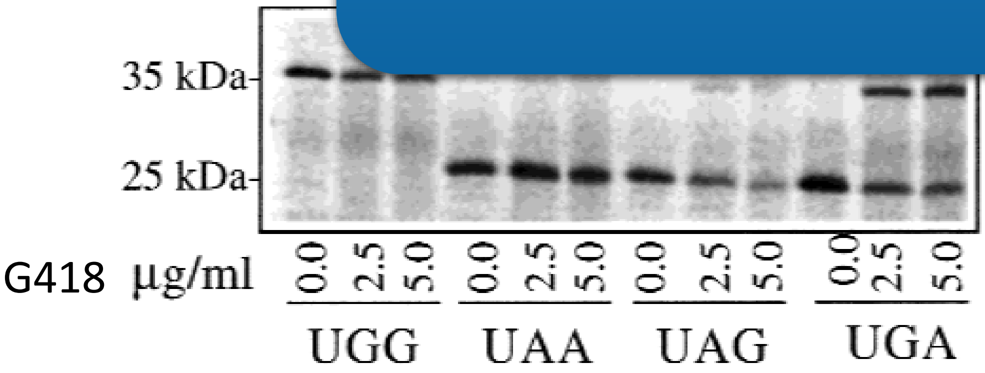
Manuvakhova et al. 2000

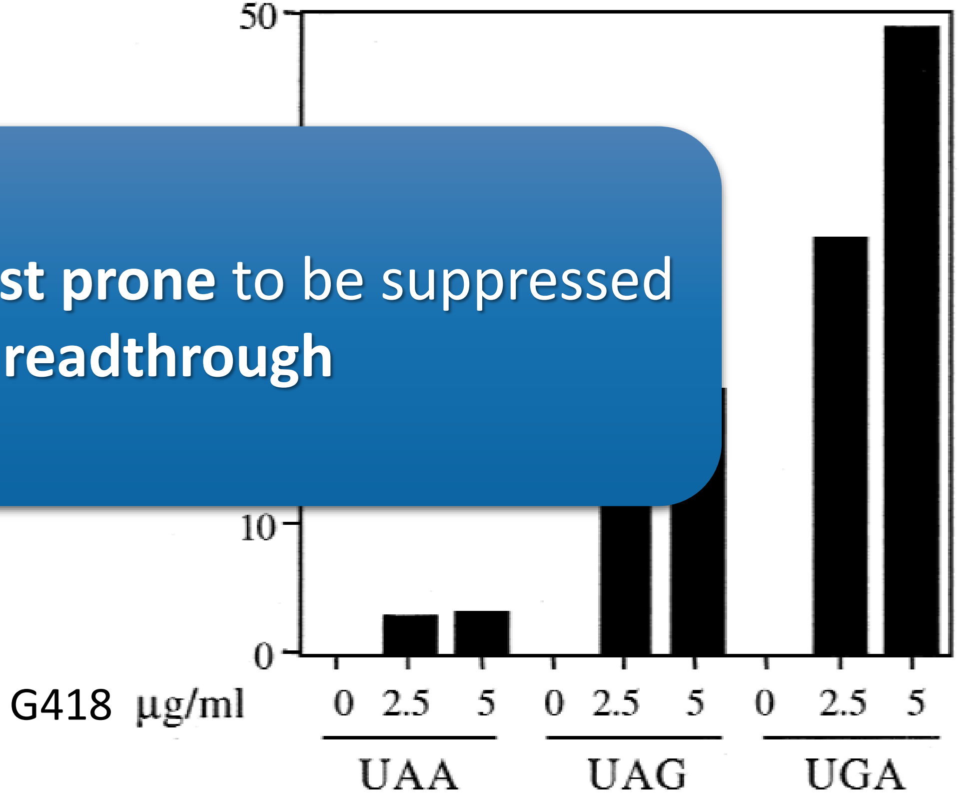
3) The nucleotide context strongly influences efficiency of translation termination and, as a consequence, occurrence of readthrough

Different stop codons promote translation termination with different efficiencies

UAA

UGA stop codon is the **most prone** to be suppressed by **ribosome readthrough**



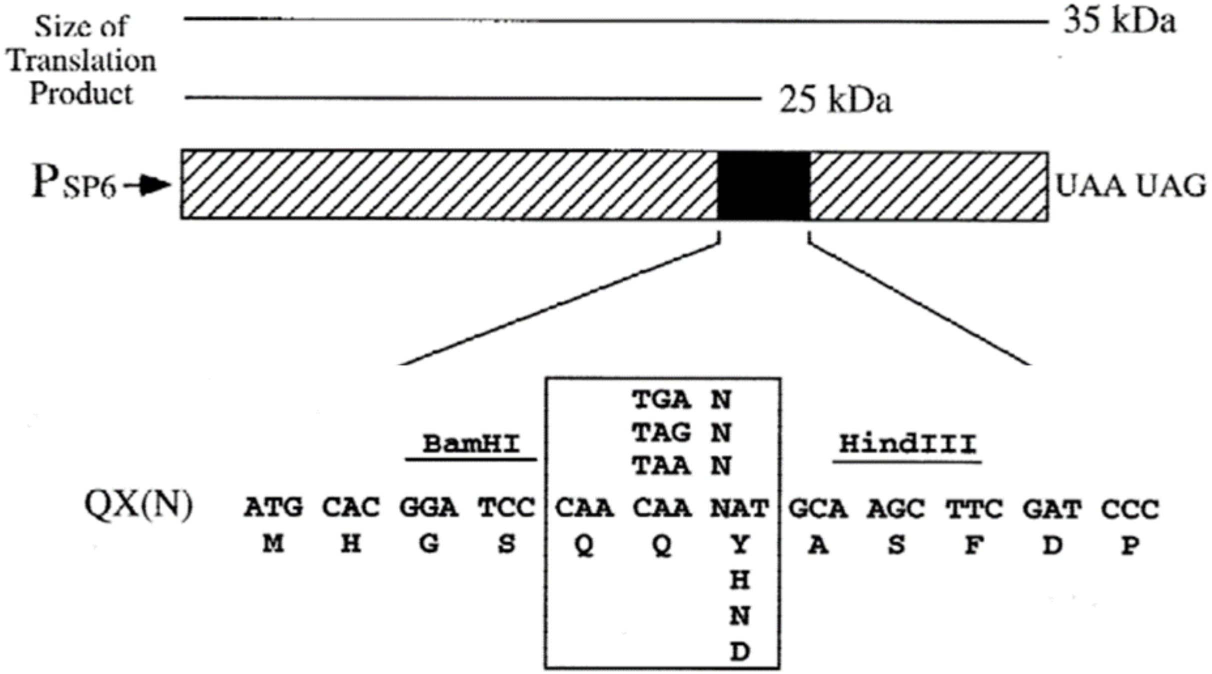


Manuvakhova et al. 2000

Also the 4th nucleotide strongly influences the occurrence of readthrough

Also the 4th nucleotide strongly influences the occurrence of readthrough

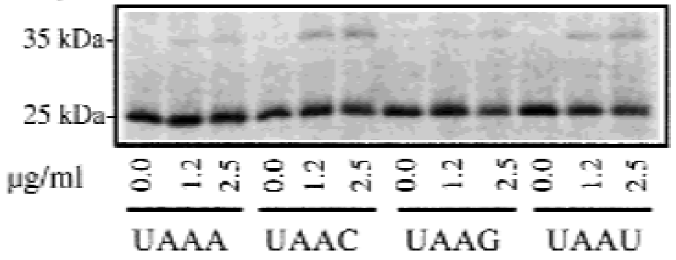
Readthrough reporter system:



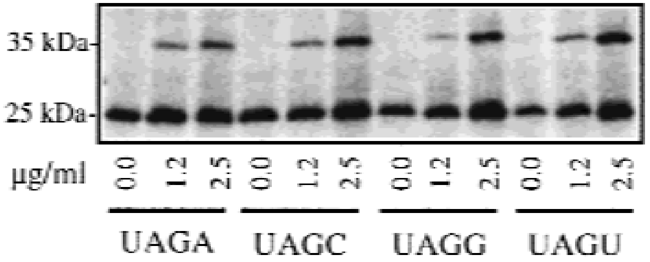
All possible combinations of stop codon and 4th nucleotide

Manuvakhova et al. 2000

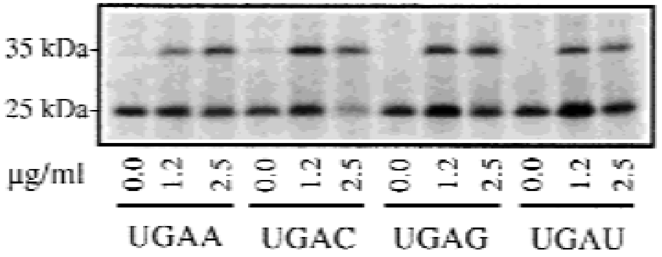
Also the 4th nucleotide strongly influences the occurrence of readthrough



UAA



UAG

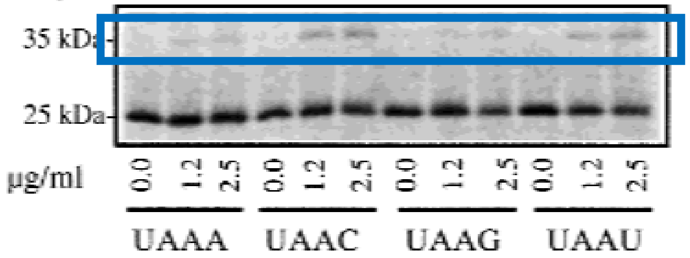


UGA

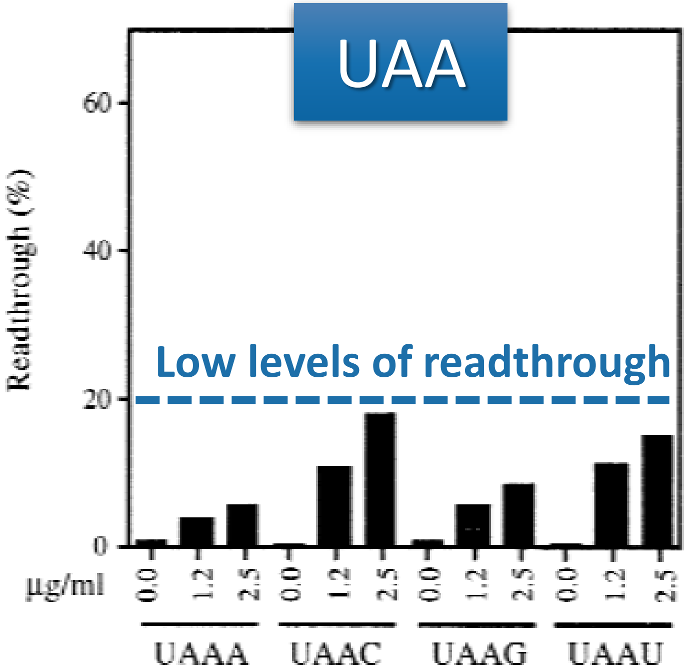
Manuvakhova et al. 2000

Also the 4th nucleotide strongly influences the occurrence of readthrough

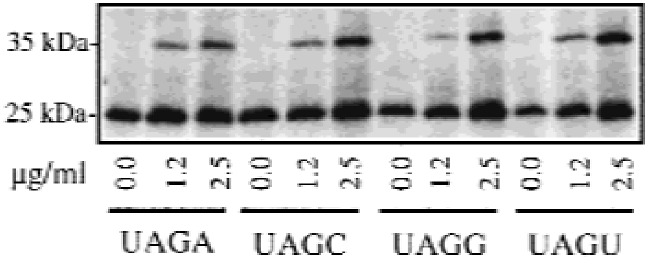
Efficient translation termination



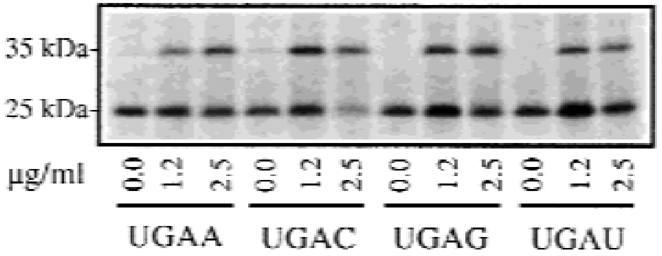
UAA



Low levels of readthrough



UAG

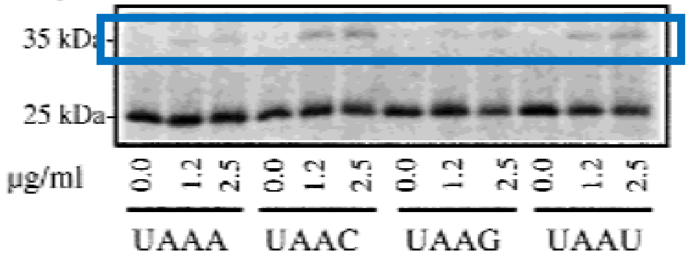


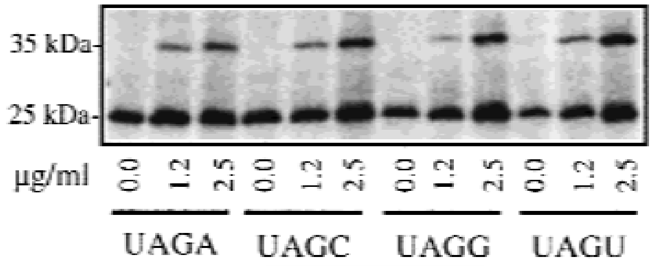
UGA

Manuvakhova et al. 2000

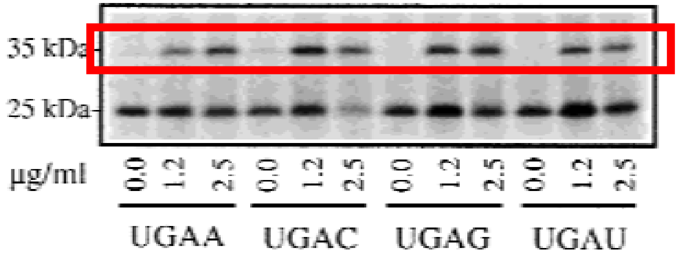
Also the 4th nucleotide strongly influences the occurrence of readthrough

Efficient translation termination

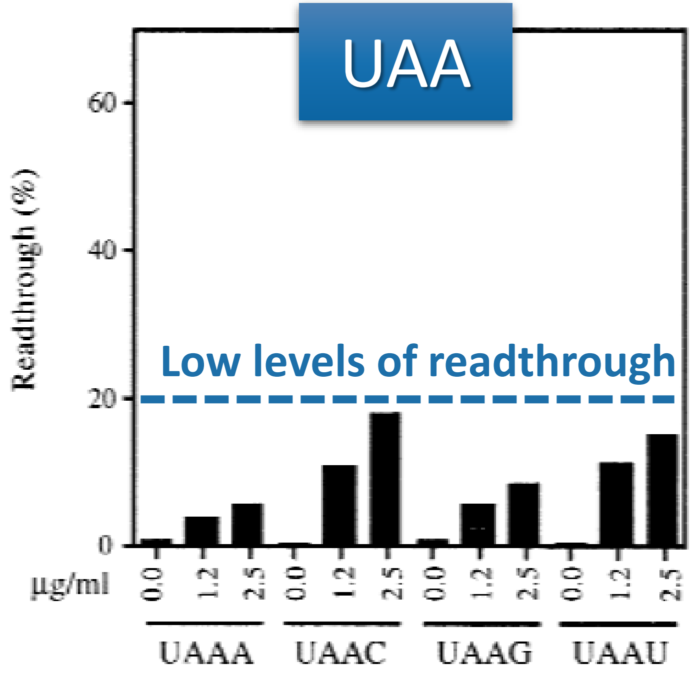




Less efficient translation termination



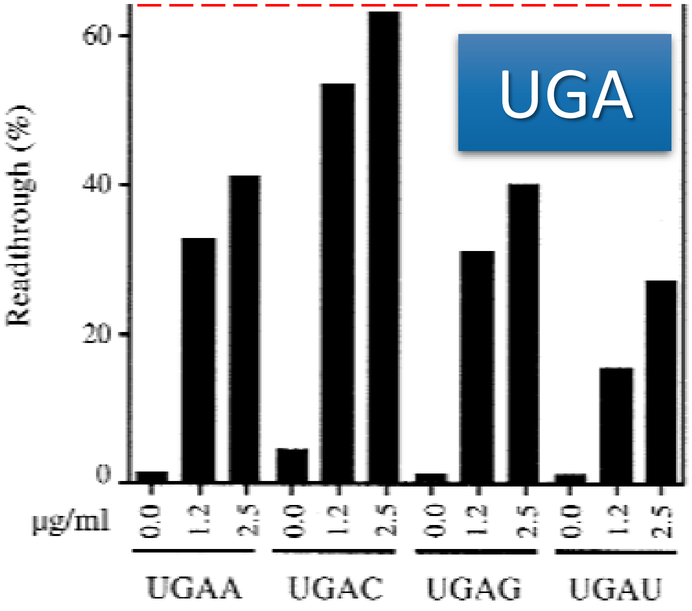
UAA



Low levels of readthrough

UAG

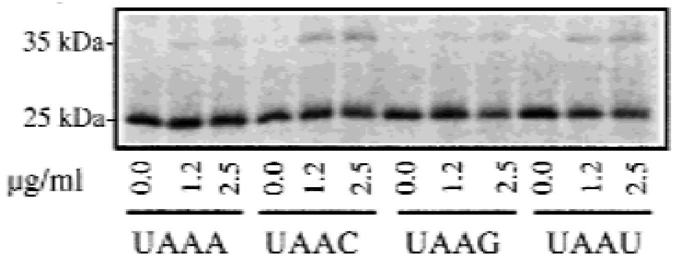
High levels of readthrough

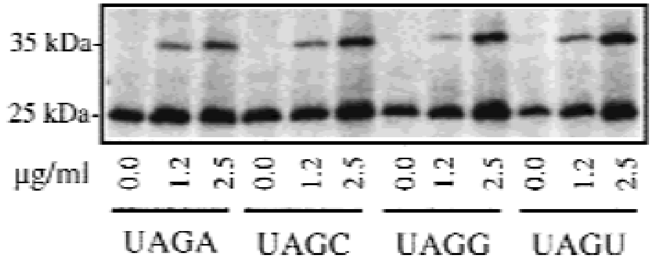


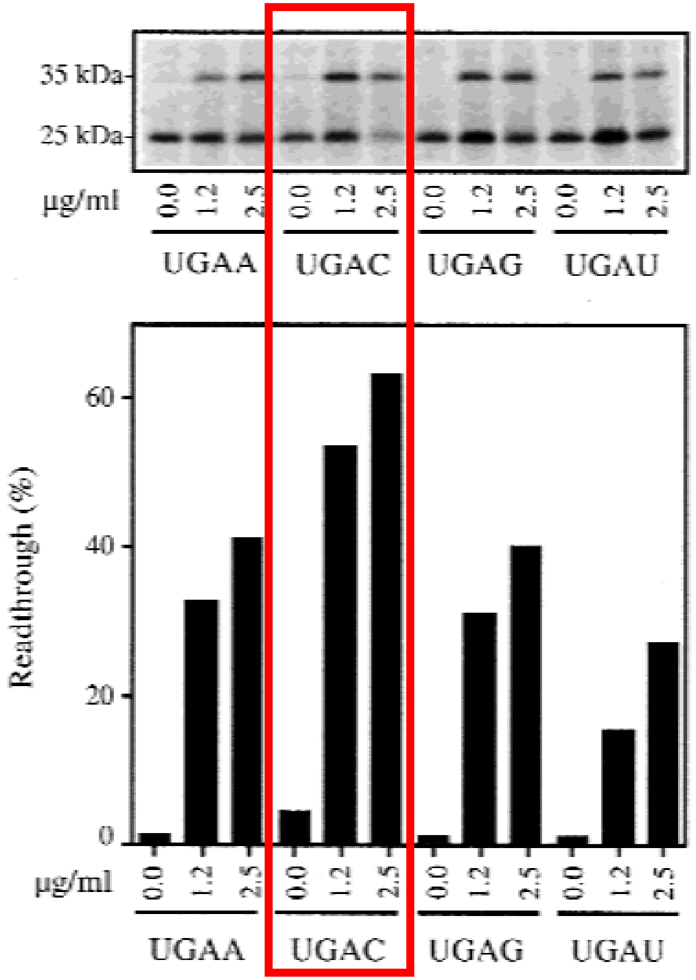
UGA

Manuvakhova et al. 2000

Also the 4th nucleotide strongly influences the occurrence of readthrough







The tetranucleotide **UGAC** shows the most frequent stop codon suppression, with readthrough occurring at a frequency of 3–4% (spontaneous) and 63% (G418-induced)

Manuvakhova et al. 2000

The efficiency of translation termination (and the occurrence of readthrough) can vary depending on many factors

1) The efficiency of termination differs between normal stop codons and premature termination codons
2) Aminoglycosides can decrease the fidelity of translation, causing higher frequencies of readthrough
3) The stop codon type and the 4th nucleotide strongly influence efficiency of translation termination and, as a consequence, occurrence of readthrough

The restoration of protein activity depends strongly on the identity of the amino acid inserted during PTC readthrough

The restoration of protein activity depends strongly on the identity of the amino acid inserted during PTC readthrough

Published online 23 July 2014 *Nucleic Acids Research, 2014, Vol. 42, No. 15* ***10061–10072***
doi: 10.1093/nar/gku663

New insights into the incorporation of natural suppressor tRNAs at stop codons in *Saccharomyces cerevisiae*

Sandra Blanchet[1], David Cornu[2], Manuela Argentini[2] and Olivier Namy[1,3,*]

Development of an *in vivo* reporter system to study amino acid insertion at all stop codons

The restoration of protein activity depends strongly on the identity of the amino acid inserted during PTC readthrough

Results

- The main determinant of amino acid incorporation is the sequence of the stop codon

The restoration of protein activity depends strongly on the identity of the amino acid inserted during PTC readthrough

Results

- The main determinant of amino acid incorporation is the sequence of the stop codon
- Only a subset of predictable suppressor tRNAs are actually incorporated at the various stop codons

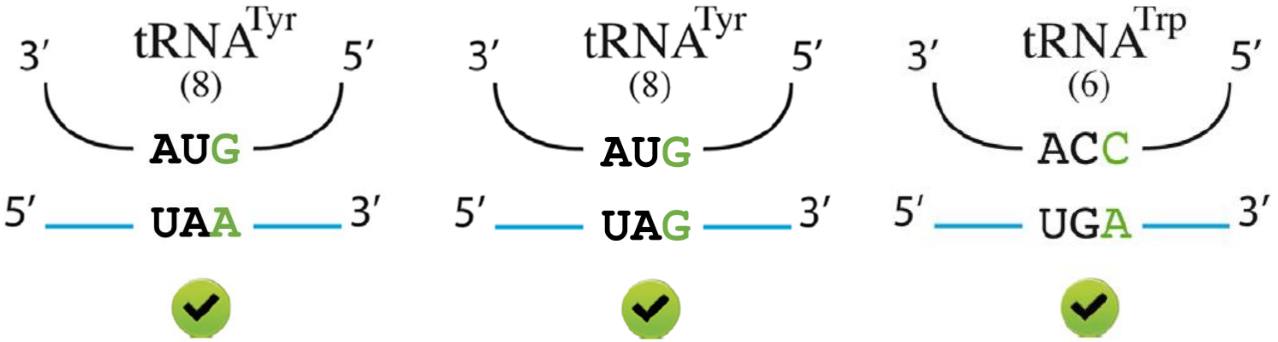
The restoration of protein activity depends strongly on the identity of the amino acid inserted during PTC readthrough

Results

- The main determinant of amino acid incorporation is the sequence of the stop codon
- Only a subset of predictable suppressor tRNAs are actually incorporated at the various stop codons

Tyrosine, **glutamine** and **lysine** can be inserted at **UAA** and **UAG** codons

Tryptophan, **cysteine** and **arginine** can be inserted at **UGA** codons



Near-cognate tRNAs: different in only one position of the codon-anticodon pairing

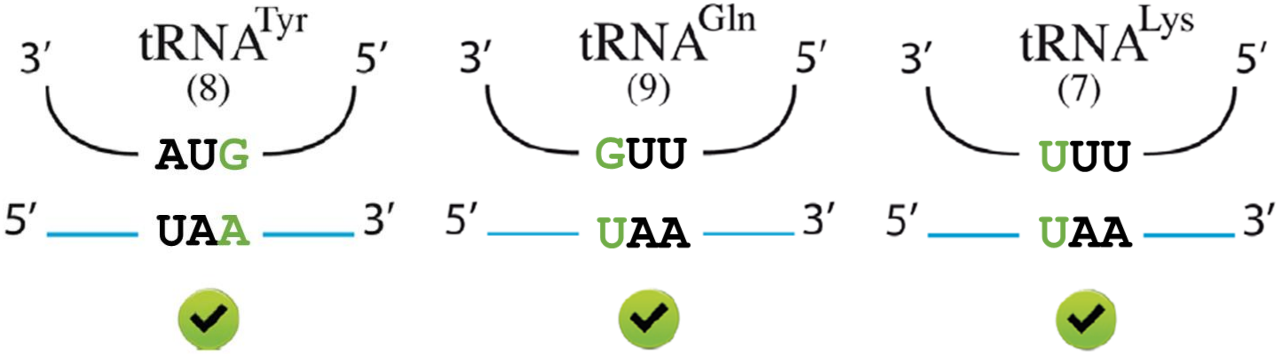
The restoration of protein activity depends strongly on the identity of the amino acid inserted during PTC readthrough

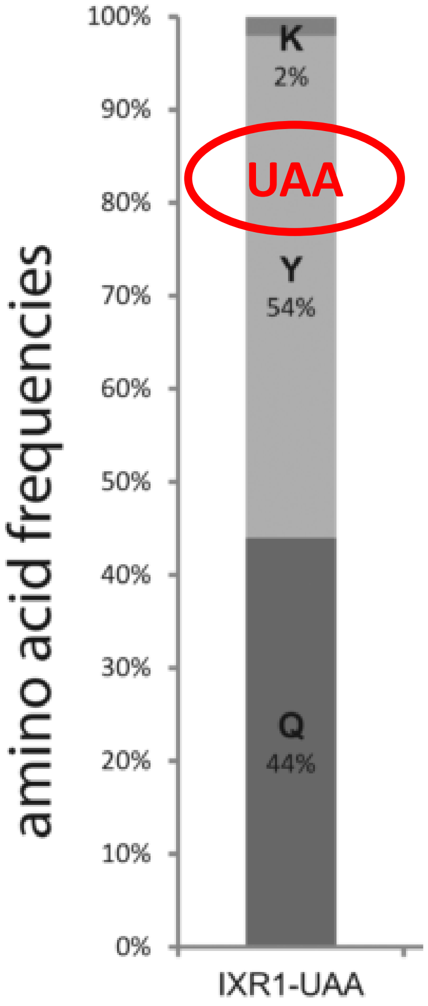
Results

- The main determinant of amino acid incorporation is the sequence of the stop codon
- Only a subset of predictable suppressor tRNAs are actually incorporated at the various stop codons
- Suppressor tRNAs are not incorporated at the same frequency at each stop codon

The restoration of protein activity depends strongly on the identity of the amino acid inserted during PTC readthrough

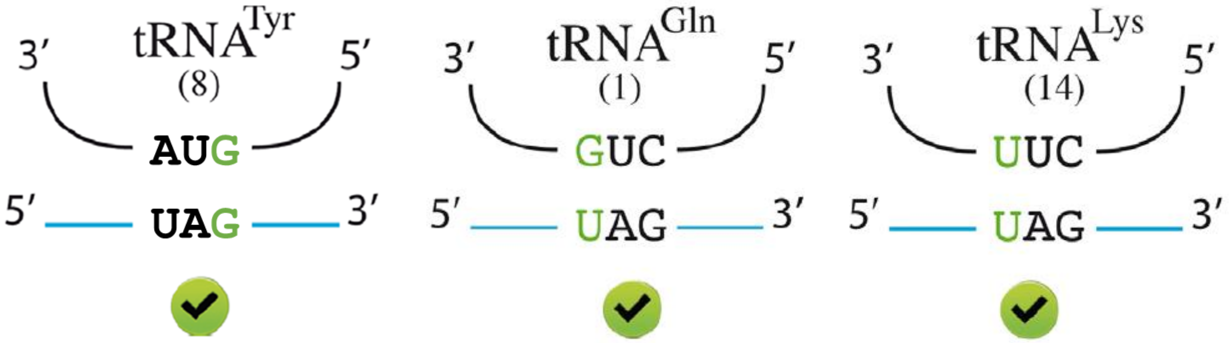
- Suppressor tRNAs are not incorporated at the same frequency at each stop codon

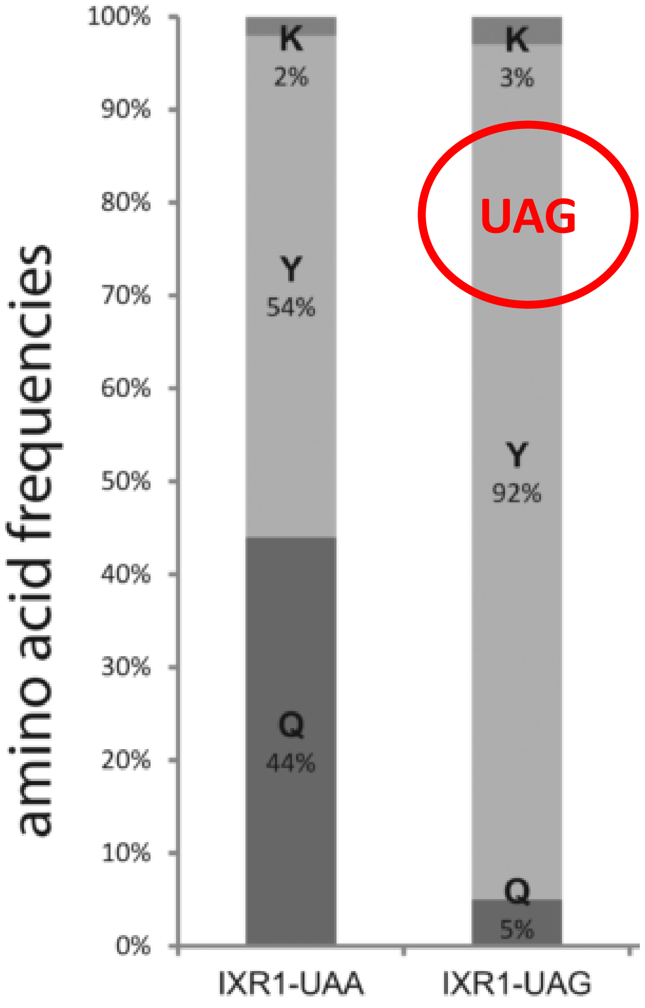




The restoration of protein activity depends strongly on the identity of the amino acid inserted during PTC readthrough

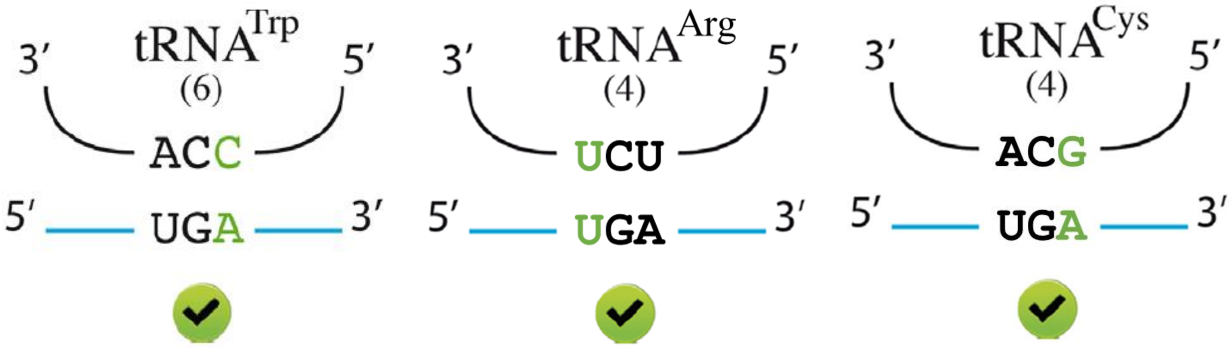
- Suppressor tRNAs are not incorporated at the same frequency at each stop codon

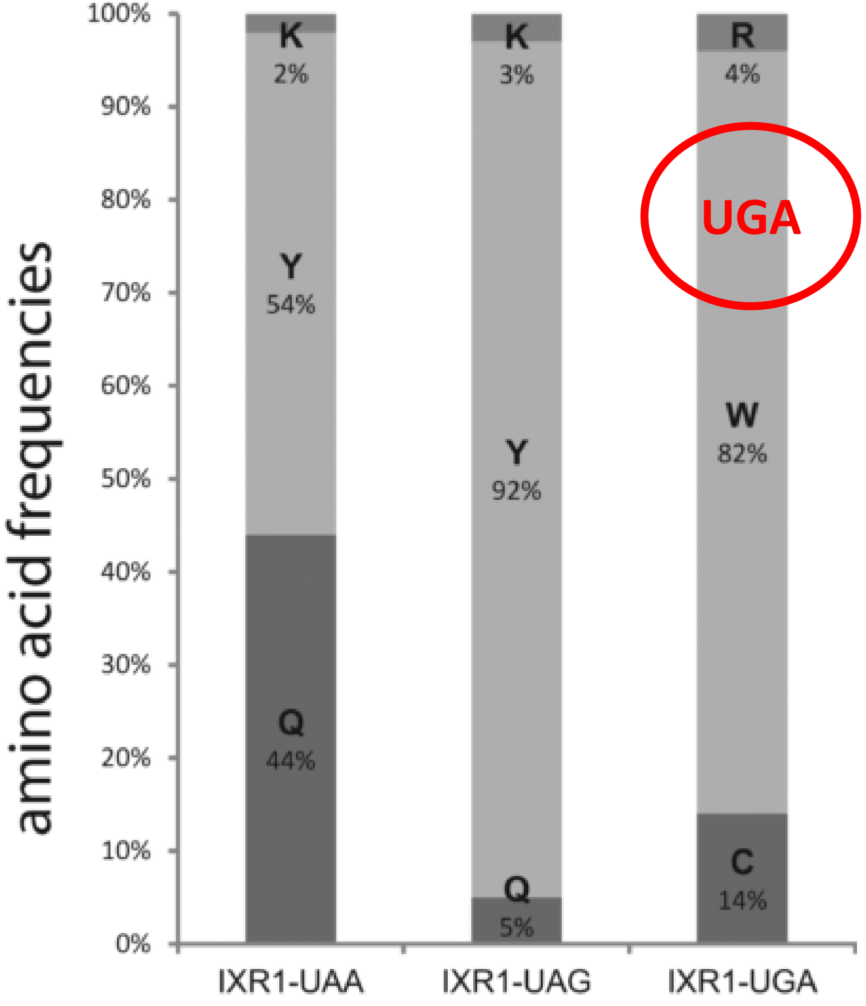




The restoration of protein activity depends strongly on the identity of the amino acid inserted during PTC readthrough

- Suppressor tRNAs are not incorporated at the same frequency at each stop codon

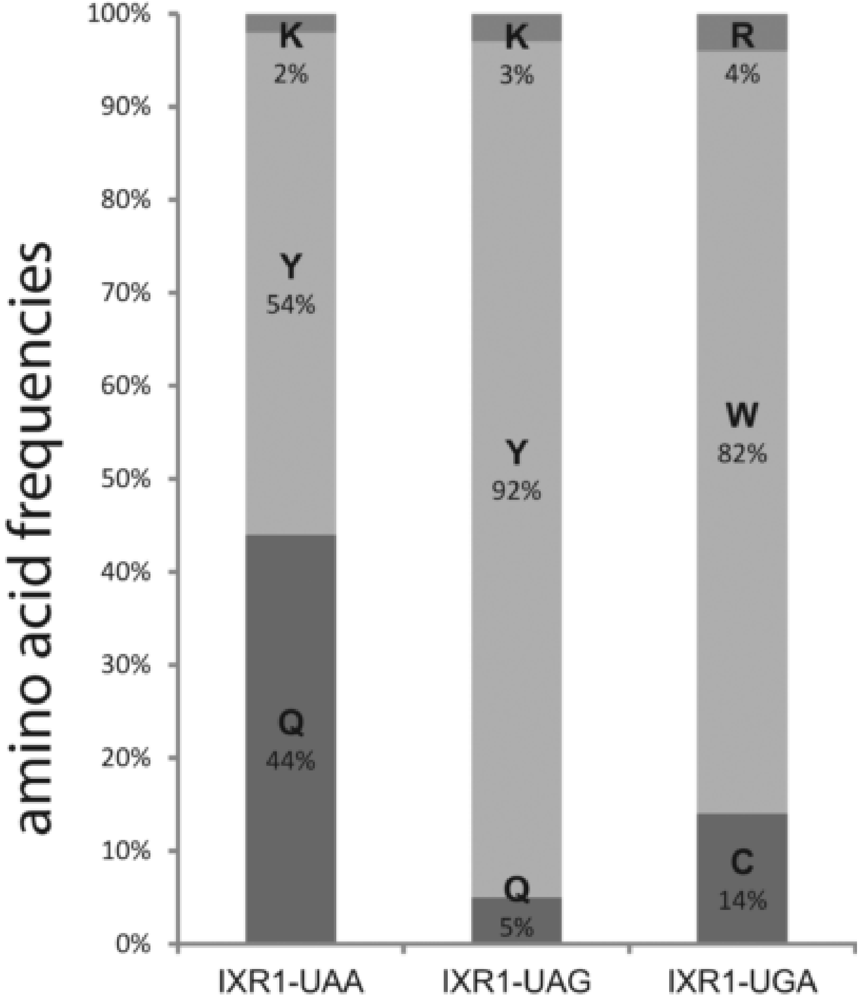




The restoration of protein activity depends strongly on the identity of the amino acid inserted during PTC readthrough

- Suppressor tRNAs are not incorporated at the same frequency at each stop codon

It is possible to predict the probable protein sequences arising from a readthrough event on the basis of the stop codon present



Brief overview…

1) The efficiency of translation termination differs between normal stop codons and premature termination codons

Brief overview…

1) The efficiency of translation termination differs between normal stop codons and premature termination codons
2) Aminoglycosides can decrease the fidelity of translation, causing higher frequencies of readthrough

Brief overview…

1) The efficiency of translation termination differs between normal stop codons and premature termination codons
2) Aminoglycosides can decrease the fidelity of translation, causing higher frequencies of readthrough
3) The stop codon type and the 4th nucleotide strongly influence efficiency of translation termination and, as a consequence, occurrence of readthrough

Brief overview…

1) The efficiency of translation termination differs between normal stop codons and premature termination codons
2) Aminoglycosides can decrease the fidelity of translation, causing higher frequencies of readthrough
3) The stop codon type and the 4th nucleotide strongly influence efficiency of translation termination and, as a consequence, occurrence of readthrough
4) It is possible to predict the probable protein sequences arising from a readthrough event on the basis of the stop codon present

Journal of Thrombosis and Haemostasis, **14**: 1994–2000 DOI: 10.1111/jth.13443

BRIEF REPORT

Differential functional readthrough over homozygous nonsense mutations contributes to the bleeding phenotype in coagulation factor VII deficiency

A. BRANCHINI,*† M. FERRARESE,* S. LOMBARDI,* R. MARI,‡ F. BERNARDI*† and M. PINOTTI*†

Journal of Thrombosis and Haemostasis, **14**: 1994–2000 DOI: 10.1111/jth.13443

BRIEF REPORT

Differential functional readthrough over homozygous nonsense mutations contributes to the bleeding phenotype in coagulation factor VII deficiency

A. BRANCHINI,*† M. FERRARESE,* S. LOMBARDI,* R. MARI,‡ F. BERNARDI*† and M. PINOTTI*†

Objective

Evaluate the spontaneous and drug-induced readthrough levels of two nonsense mutations in coagulation factor VII (FVII) : **p.Ser112X** and **p.Cys132X**

Expected to be lethal


Journal of Thrombosis and Haemostasis, **14**: 1994–2000 DOI: 10.1111/jth.13443

BRIEF REPORT

Differential functional readthrough over homozygous nonsense mutations contributes to the bleeding phenotype in coagulation factor VII deficiency

A. BRANCHINI,*† M. FERRARESE,* S. LOMBARDI,* R. MARI,‡ F. BERNARDI*† and M. PINOTTI*†

Objective

Evaluate the spontaneous and drug-induced readthrough levels of two nonsense mutations in coagulation factor VII (FVII) : **p.Ser112X** and **p.Cys132X**

Life-threatening bleeding symptoms

Moderate bleeding symptoms

Journal of Thrombosis and Haemostasis, **14**: 1994–2000
DOI: 10.1111/jth.13443

BRIEF REPORT

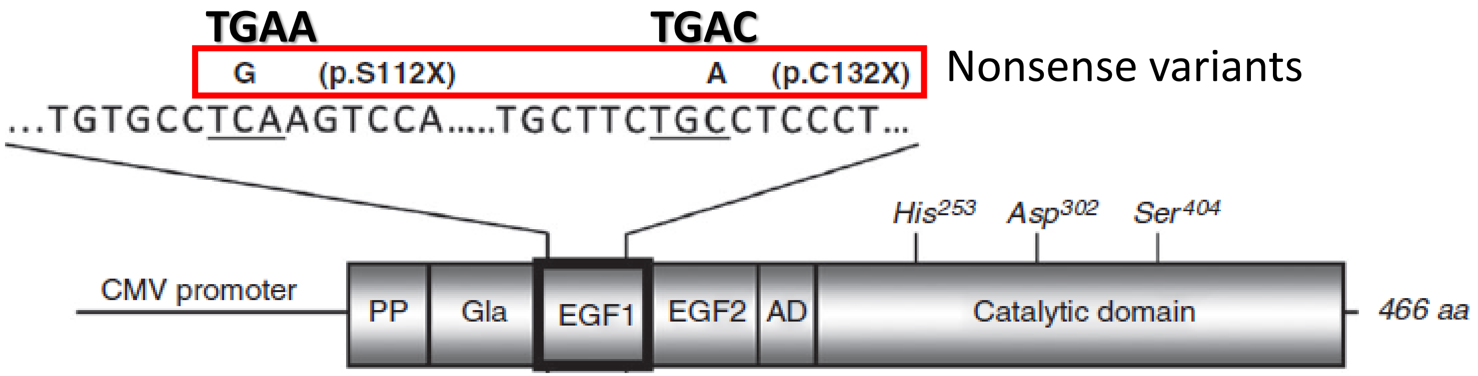
Differential functional readthrough over homozygous nonsense mutations contributes to the bleeding phenotype in coagulation factor VII deficiency

A. BRANCHINI,*† M. FERRARESE,* S. LOMBARDI,* R. MARI,‡ F. BERNARDI*† and M. PINOTTI*†

Methods

1. Creation of a cellular model through the transient expression of recombinant FVII **nonsense** variants

2. Evaluation of secreted levels of rFVII by ELISA



Journal of Thrombosis and Haemostasis, **14**: 1994–2000 DOI: 10.1111/jth.13443

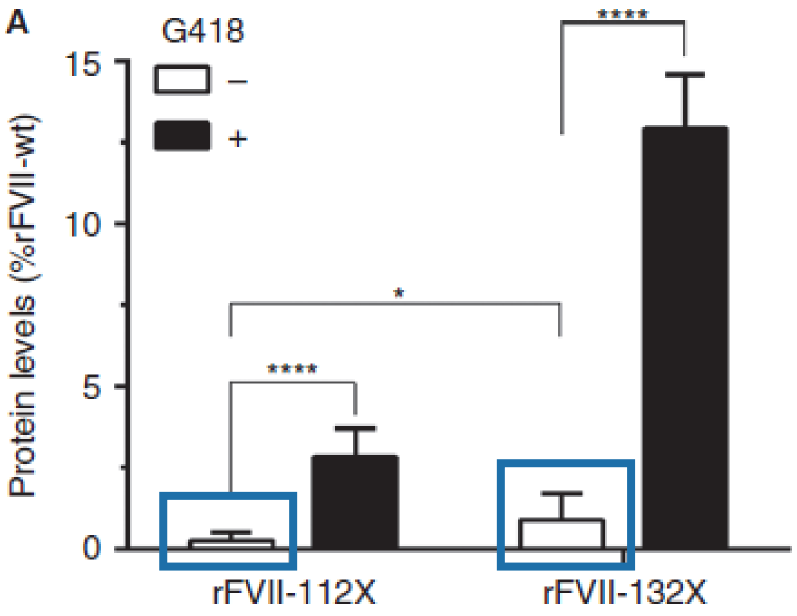
BRIEF REPORT

Differential functional readthrough over homozygous nonsense mutations contributes to the bleeding phenotype in coagulation factor VII deficiency

A. BRANCHINI,*† M. FERRARESE,* S. LOMBARDI,* R. MARI,‡ F. BERNARDI*† and M. PINOTTI*†

Results

Secretion levels of rFVII nonsense variants



SPONTANEOUS

Journal of Thrombosis and Haemostasis, **14**: 1994–2000 DOI: 10.1111/jth.13443

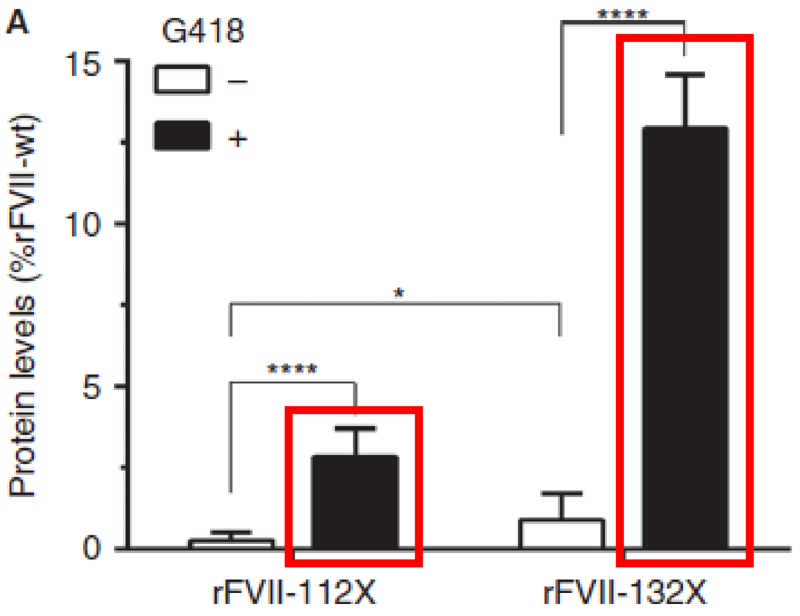
BRIEF REPORT

Differential functional readthrough over homozygous nonsense mutations contributes to the bleeding phenotype in coagulation factor VII deficiency

A. BRANCHINI,*† M. FERRARESE,* S. LOMBARDI,* R. MARI,‡ F. BERNARDI*† and M. PINOTTI*†

Results

Secretion levels of rFVII nonsense variants



G418-induced

Journal of Thrombosis and Haemostasis, **14**: 1994–2000

DOI: 10.1111/jth.13443

BRIEF REPORT

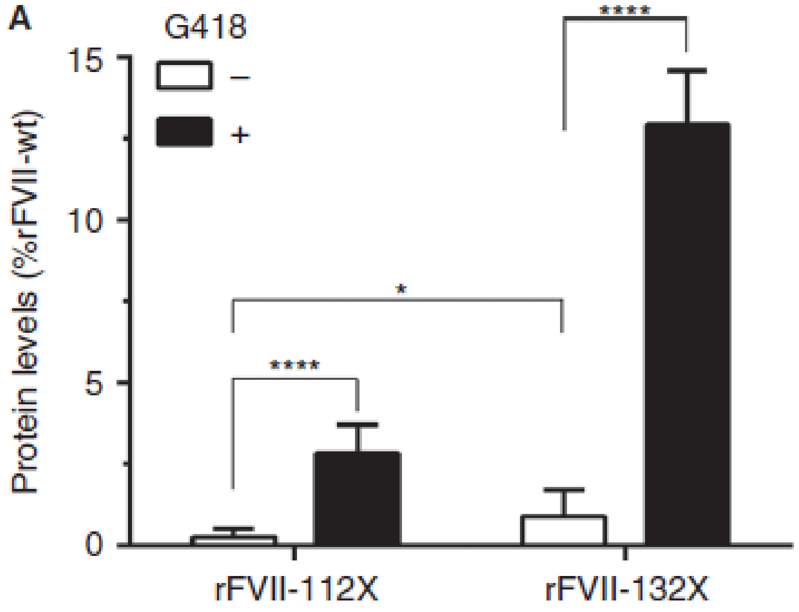
Differential functional readthrough over homozygous nonsense mutations contributes to the bleeding phenotype in coagulation factor VII deficiency

A. BRANCHINI,*† M. FERRARESE,* S. LOMBARDI,* R. MARI,‡ F. BERNARDI*† and M. PINOTTI*†

Results

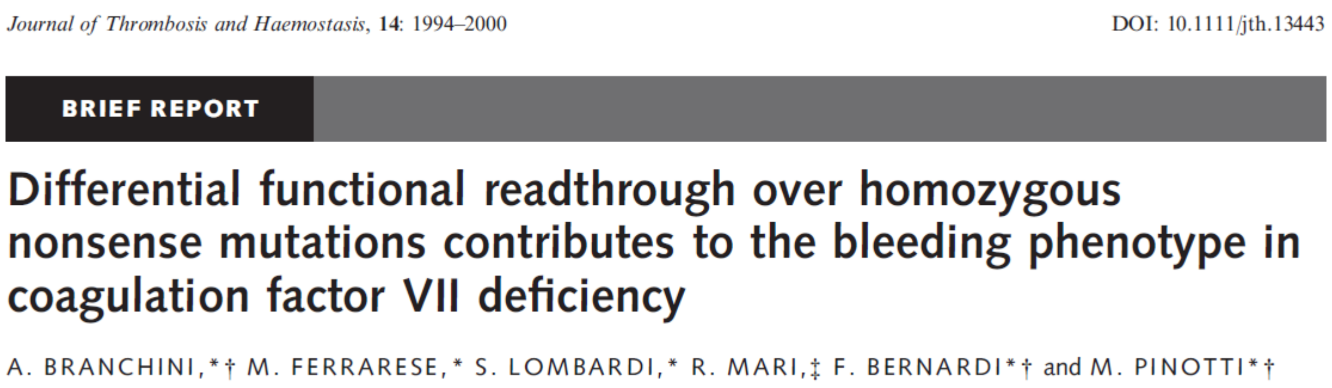
Secretion and activity levels of rFVII nonsense variants

rFVII C132X shows the higher degree of suppression, probably due to the more readthrough-favourable sequence context



TGA A

TGA C



Journal of Thrombosis and Haemostasis, **14**: 1994–2000 DOI: 10.1111/jth.13443

BRIEF REPORT

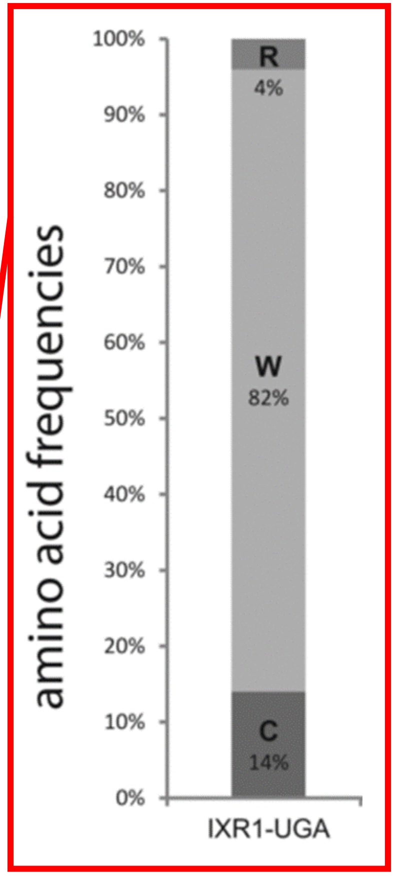
Differential functional readthrough over homozygous nonsense mutations contributes to the bleeding phenotype in coagulation factor VII deficiency

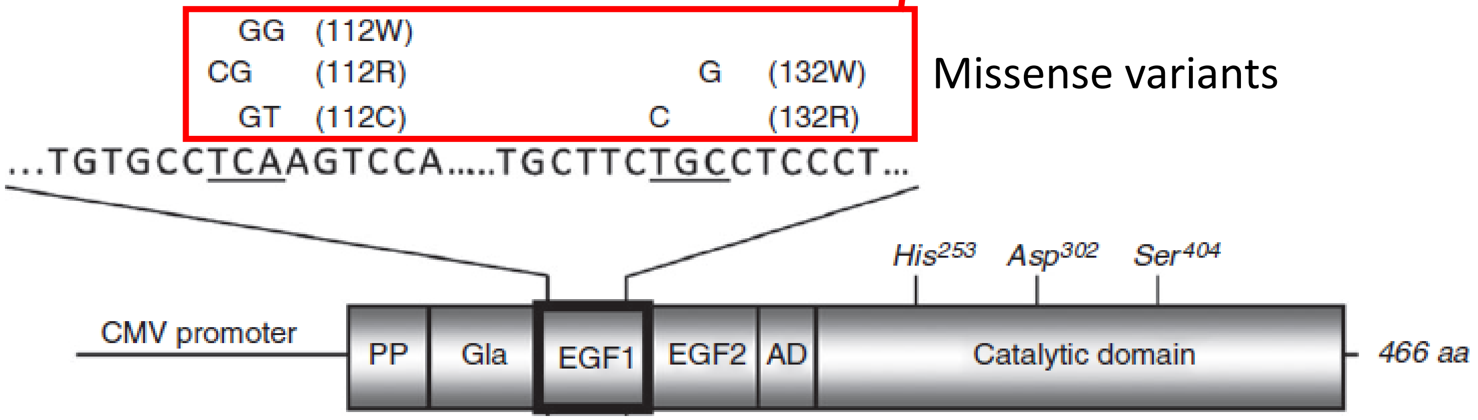
A. BRANCHINI,*† M. FERRARESE,* S. LOMBARDI,* R. MARI,‡ F. BERNARDI*† and M. PINOTTI*†

Methods

1. Creation of a cellular model through the transient expression of recombinant FVII **missense** variants

2. Evaluation of rFVII protein and **functional** levels by ELISA and activity assays





Journal of Thrombosis and Haemostasis, **14**: 1994–2000

DOI: 10.1111/jth.13443

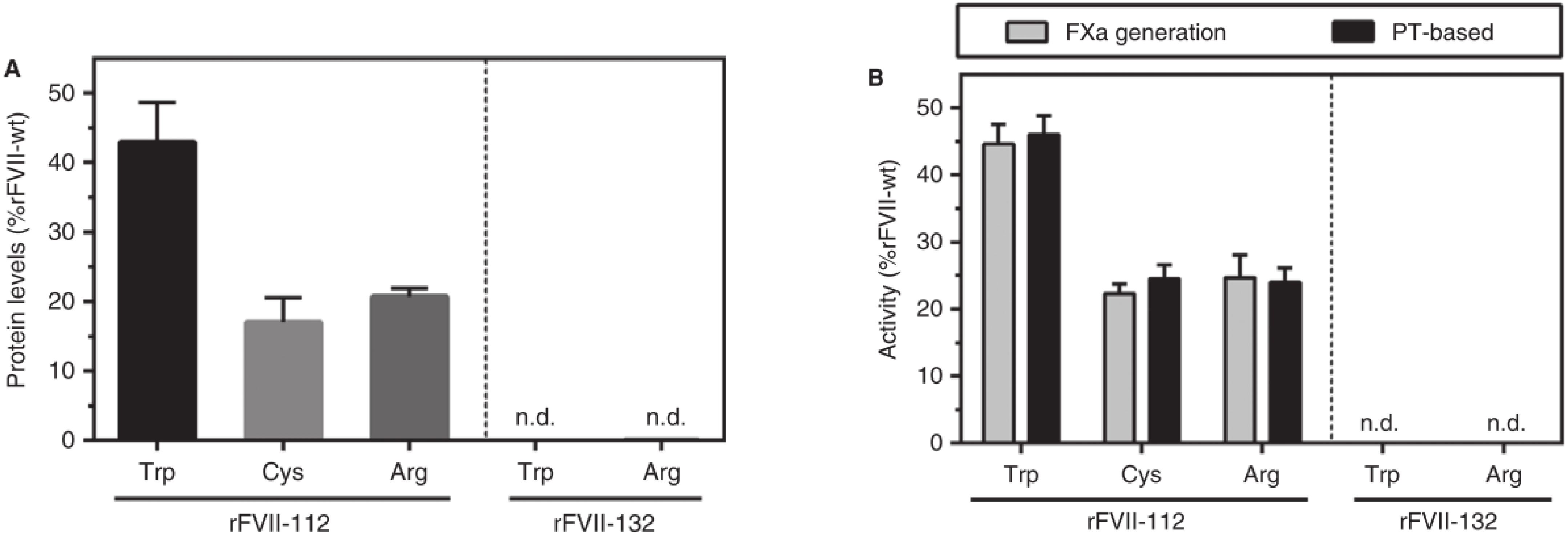
BRIEF REPORT

Differential functional readthrough over homozygous nonsense mutations contributes to the bleeding phenotype in coagulation factor VII deficiency

A. BRANCHINI,*† M. FERRARESE,* S. LOMBARDI,* R. MARI,‡ F. BERNARDI*† and M. PINOTTI*†

Results

Secretion and activity levels of rFVII missense variants



Journal of Thrombosis and Haemostasis, **14**: 1994–2000 DOI: 10.1111/jth.13443

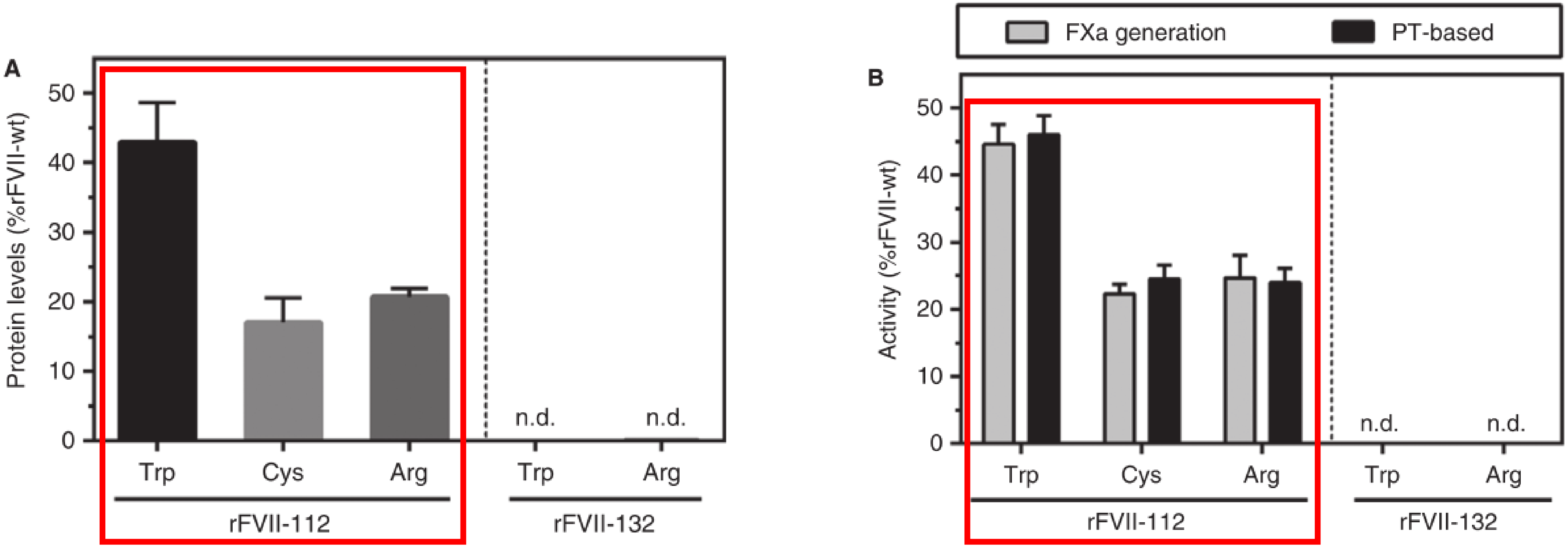
BRIEF REPORT

Differential functional readthrough over homozygous nonsense mutations contributes to the bleeding phenotype in coagulation factor VII deficiency

A. BRANCHINI,*† M. FERRARESE,* S. LOMBARDI,* R. MARI,‡ F. BERNARDI*† and M. PINOTTI*†

Results

Secretion and activity levels of rFVII missense variants



Journal of Thrombosis and Haemostasis, **14**: 1994–2000 DOI: 10.1111/jth.13443

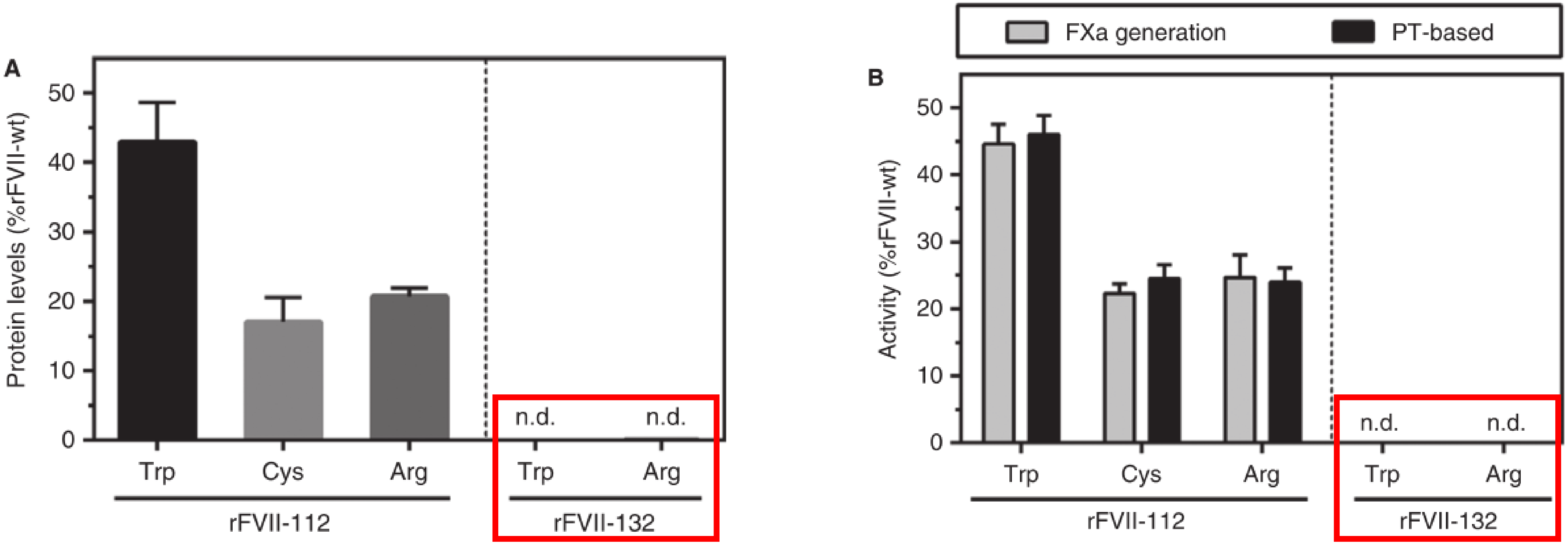
BRIEF REPORT

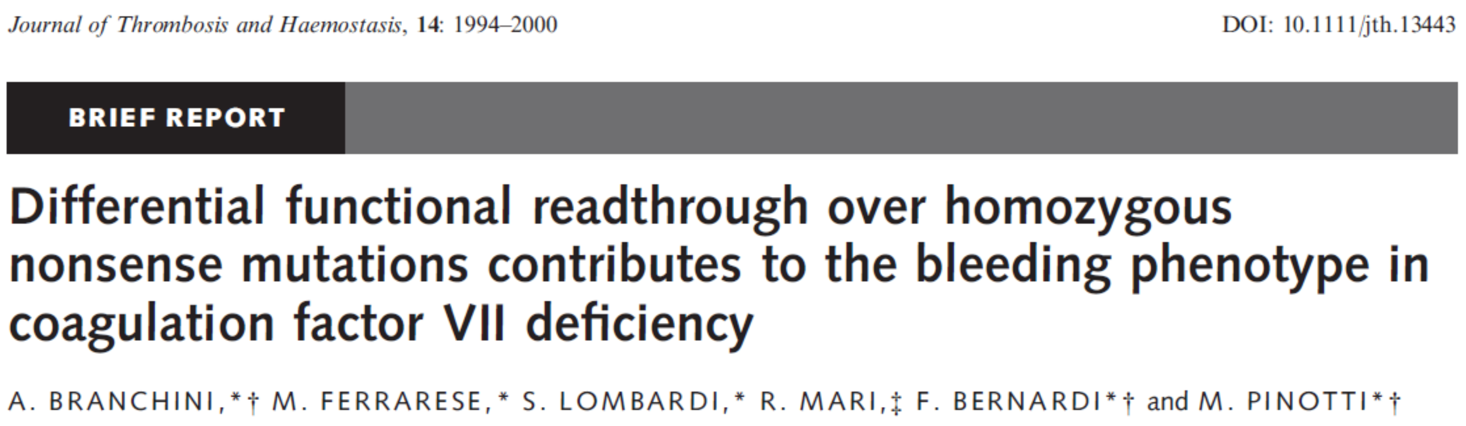
Differential functional readthrough over homozygous nonsense mutations contributes to the bleeding phenotype in coagulation factor VII deficiency

A. BRANCHINI,*† M. FERRARESE,* S. LOMBARDI,* R. MARI,‡ F. BERNARDI*† and M. PINOTTI*†

Results

Secretion and activity levels of rFVII missense variants





Journal of Thrombosis and Haemostasis, **14**: 1994–2000 DOI: 10.1111/jth.13443

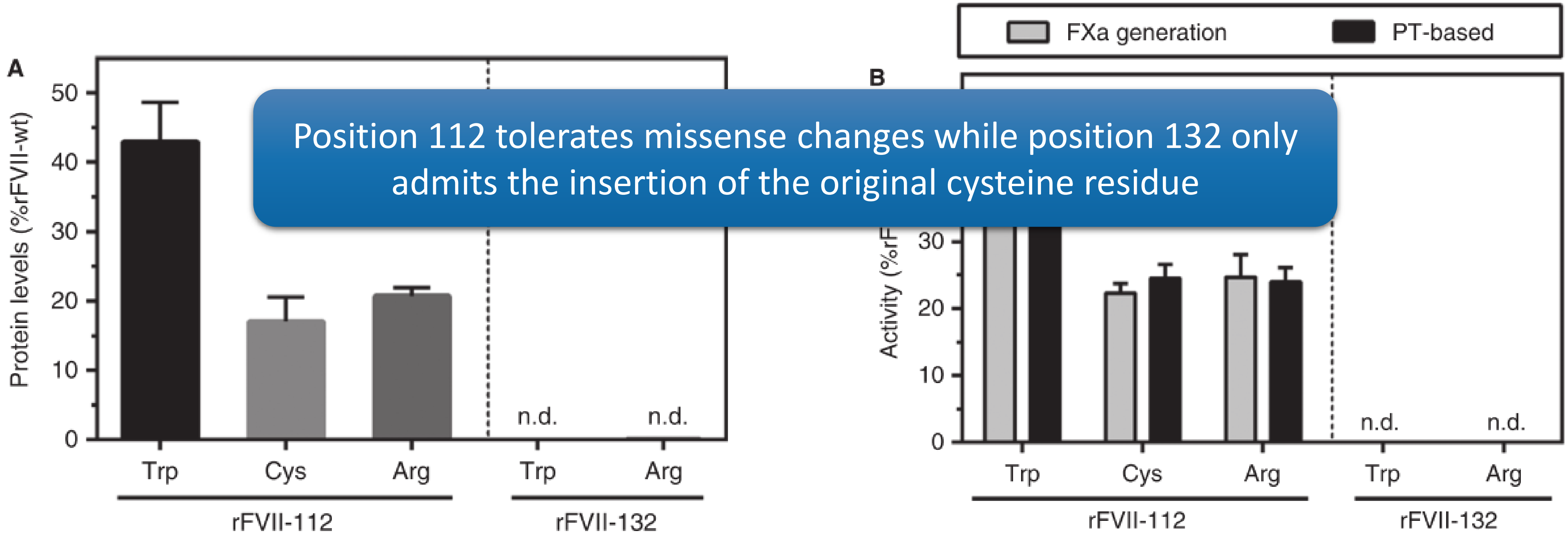
BRIEF REPORT

Differential functional readthrough over homozygous nonsense mutations contributes to the bleeding phenotype in coagulation factor VII deficiency

A. BRANCHINI,*† M. FERRARESE,* S. LOMBARDI,* R. MARI,‡ F. BERNARDI*† and M. PINOTTI*†

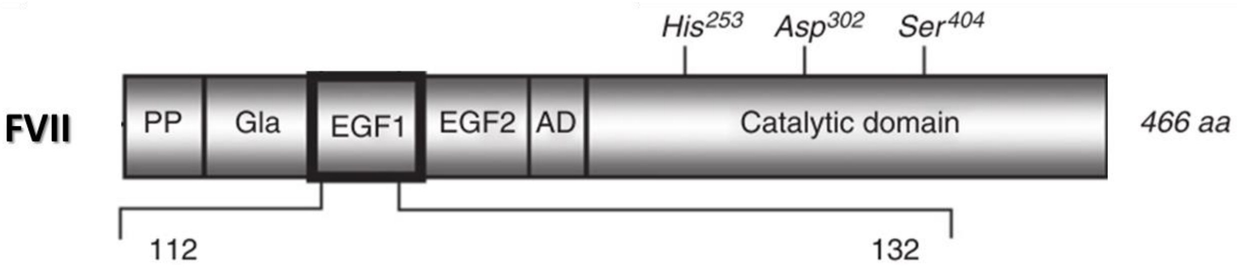
Results

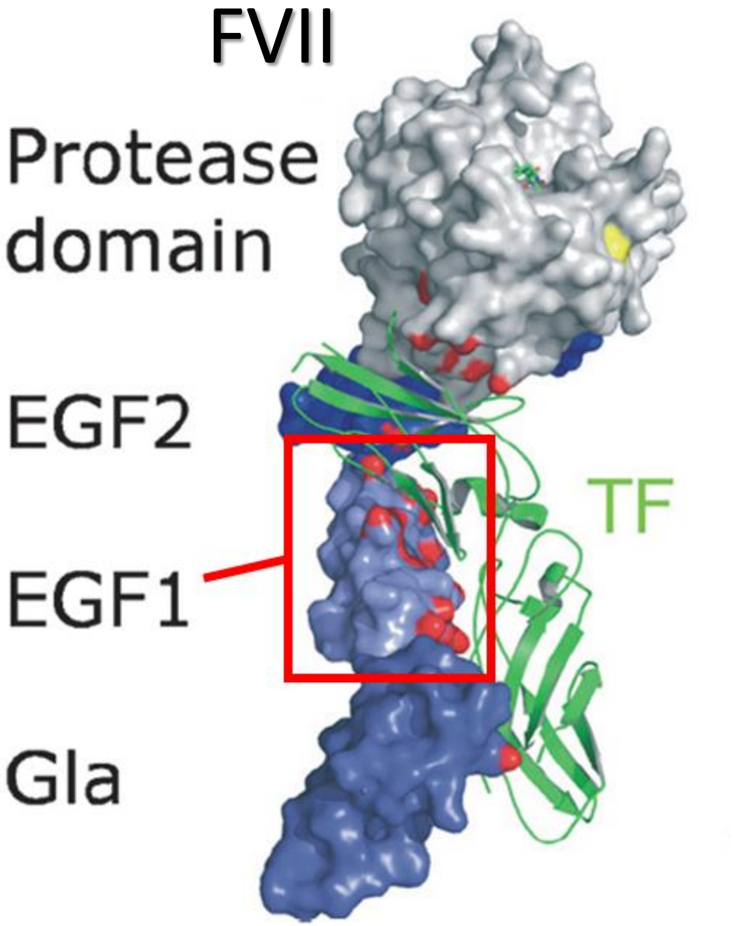
Secretion and activity levels of rFVII missense variants



Position 112 tolerates missense changes while position 132 only admits the insertion of the original cysteine residue

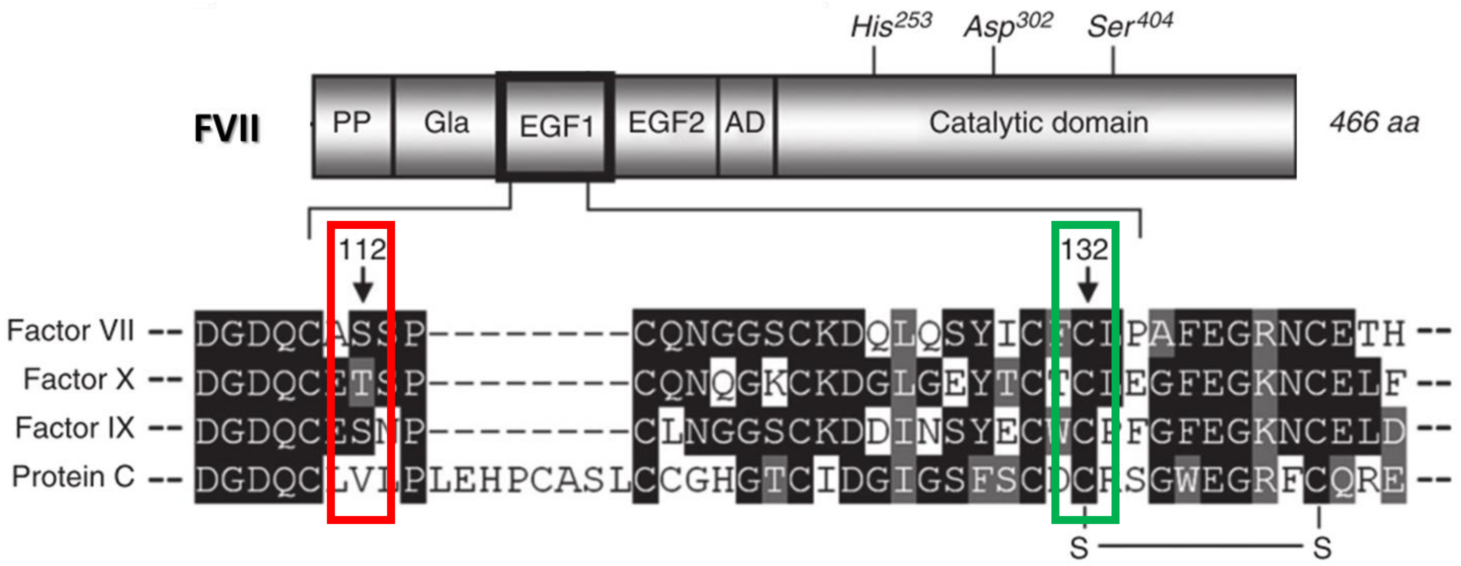
Position 112 tolerates missense changes while position 132 only admits the insertion of the original cysteine residue

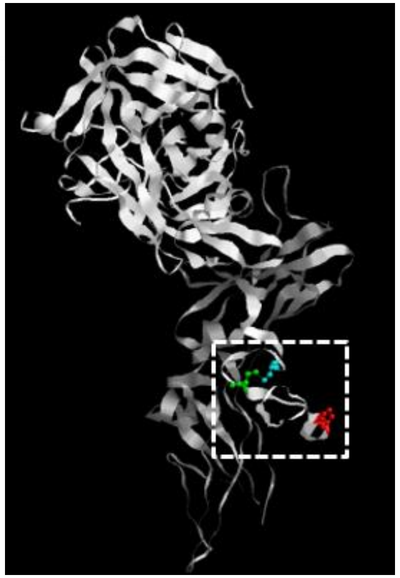


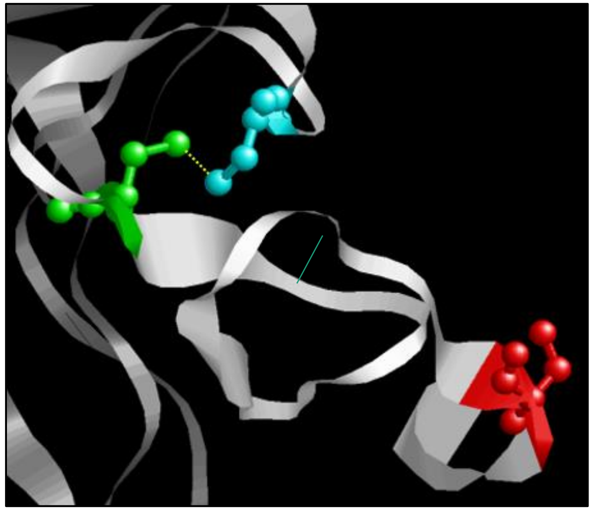


Both residues are part of the first EGF domain of FVII, which is involved in the interaction with tissue factor (TF, the FVII cofactor)

Position 112 tolerates missense changes while position 132 only admits the insertion of the original cysteine residue



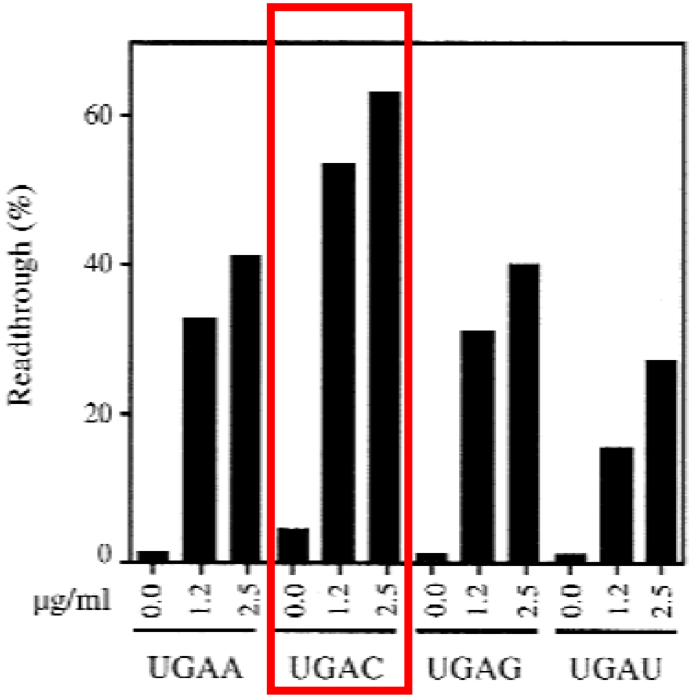


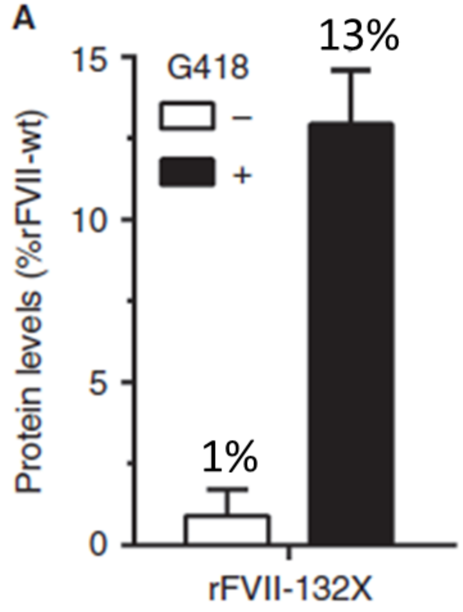


But whereas **Ser112** is surface-exposed and only partially conserved among others coagulation factors, **Cys132** forms a disulfide bridge with **Cys141** within EGF1 and is fully conserved.

In conclusion:

- **p.C132X** variant shows the **most readthrough favourable sequence context**

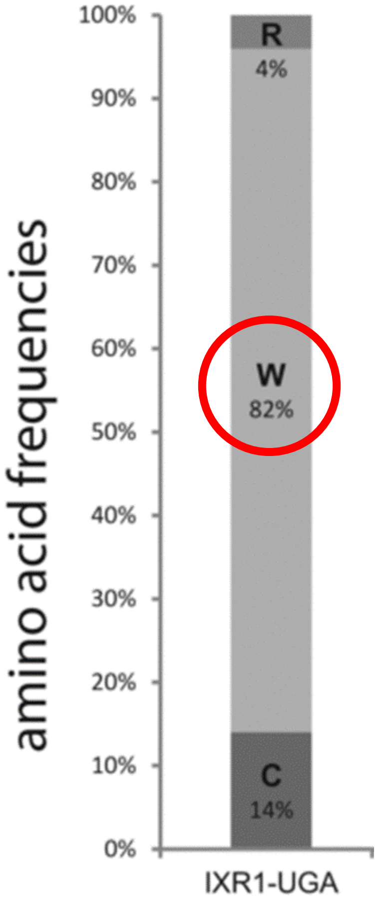


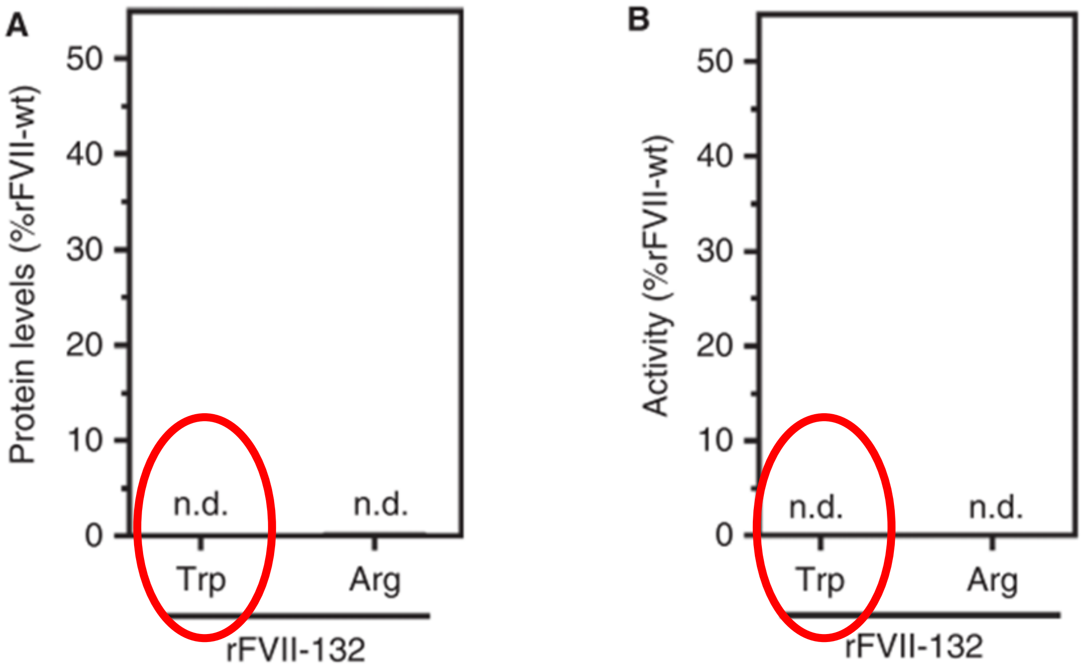


Moderate bleeding phenotype

In conclusion:

- **p.C132X** variant shows the most readthrough favourable sequence context
- PTC suppression can reinsert the original amino acid, thus leading to the production of wild-type FVII, whereas **other amino acids in this position are not tolerated** for protein secretion and function

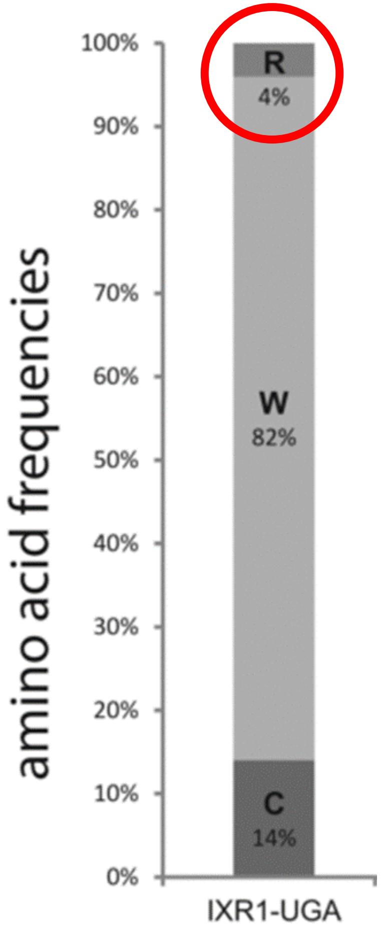


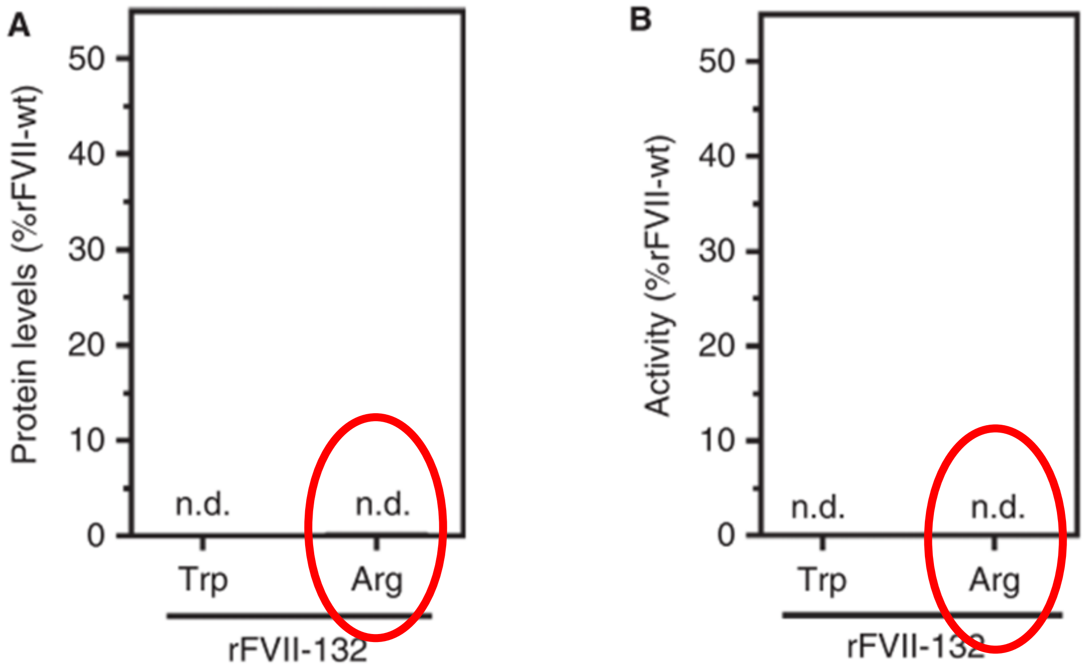


Moderate bleeding phenotype

In conclusion:

- **p.C132X** variant shows the most readthrough favourable sequence context
- PTC suppression can reinsert the original amino acid, thus leading to the production of wild-type FVII, whereas **other amino acids in this position are not tolerated** for protein secretion and function

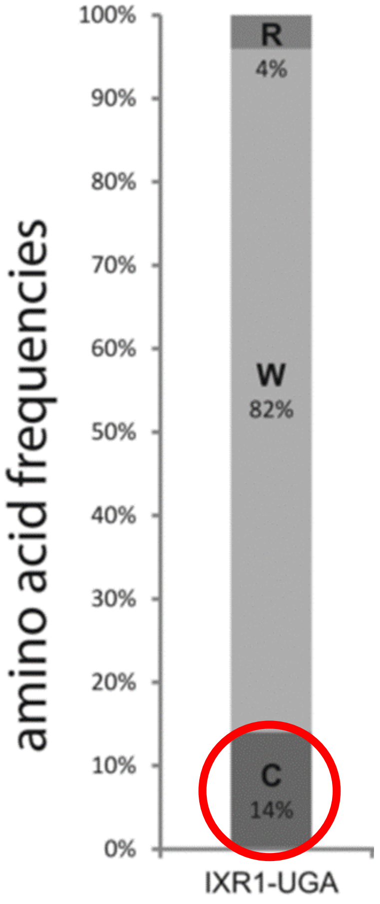


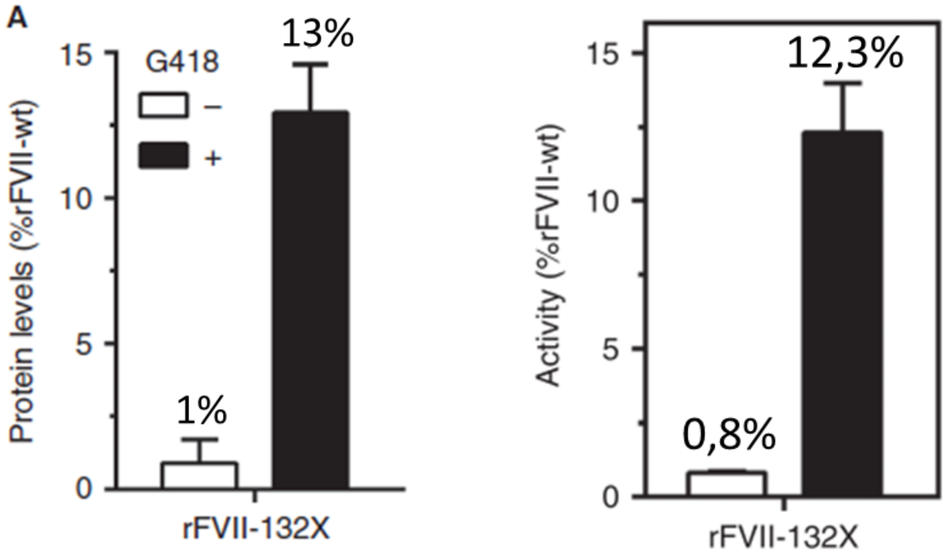


Moderate bleeding phenotype

In conclusion:

- **p.C132X** variant shows the most readthrough favourable sequence context
- PTC suppression can reinsert the original amino acid, thus leading to the production of wild-type FVII, whereas **other amino acids in this position are not tolerated** for protein secretion and function



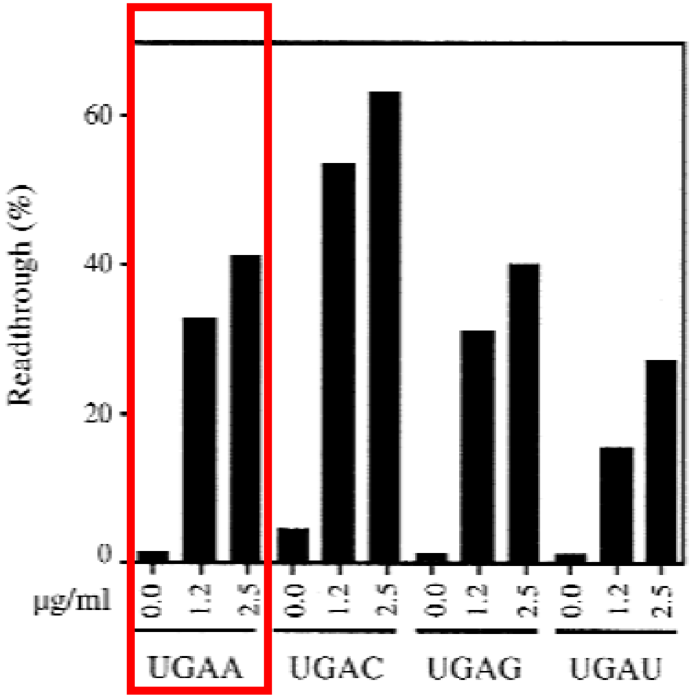


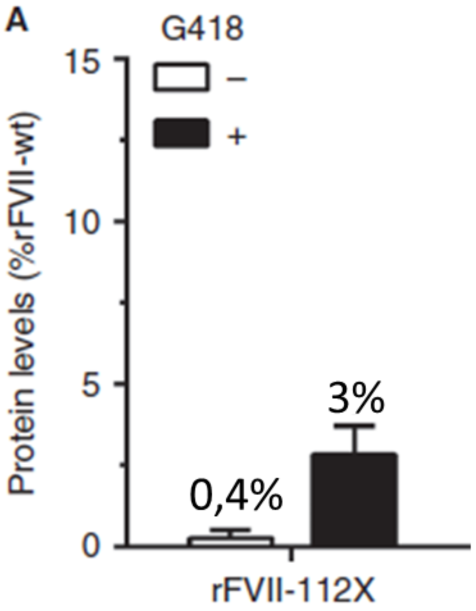
Moderate bleeding phenotype

Insertion of original amino acid and production of full-lenght wild-type protein

In conclusion:

- In the context of **p.S112X** the readthrough is predicted to occur with **lower efficiency**

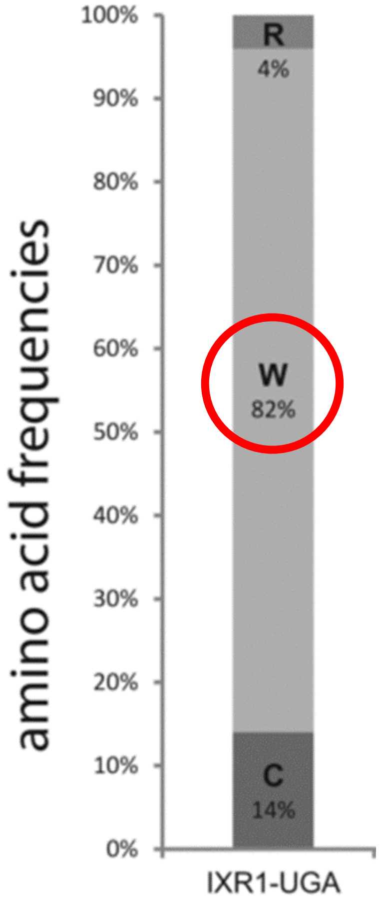


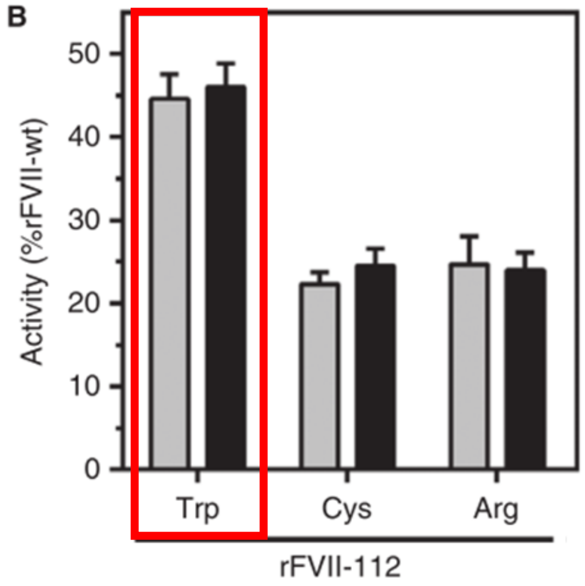


Life-threatening bleeding phenotype

In conclusion:

- In the context of **p.S112X** the readthrough is predicted to occur with **lower efficiency**
- The original amino acid (serine) can not be re-inserted by readthrough but this position significantly **tolerates** the most probable amino acid **substitutions**

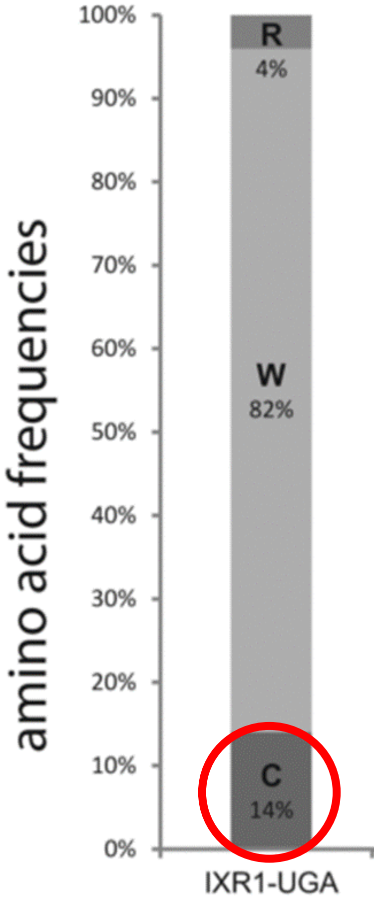


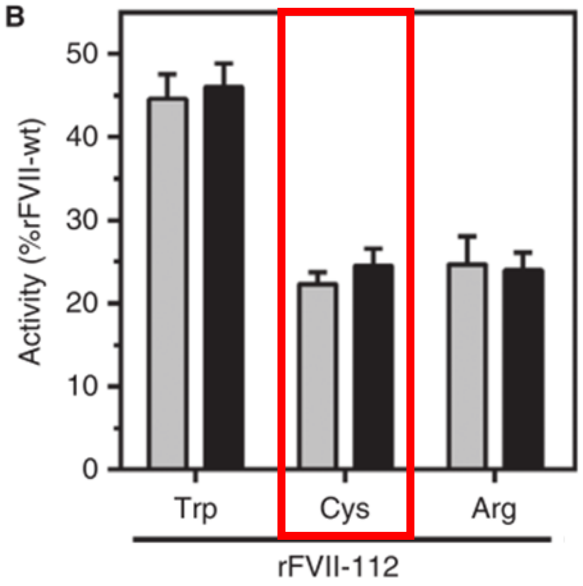


Life-threatening bleeding phenotype

In conclusion:

- In the context of **p.S112X** the readthrough is predicted to occur with **lower efficiency**
- The original amino acid (serine) can not be re-inserted by readthrough but this position significantly **tolerates** the most probable amino acid **substitutions**

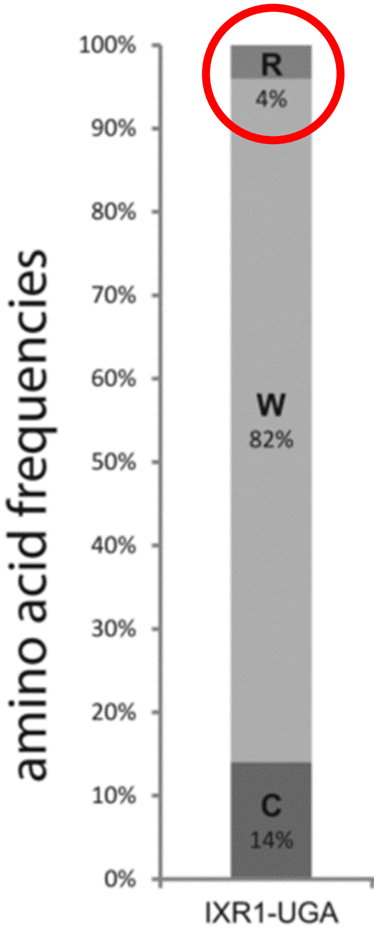


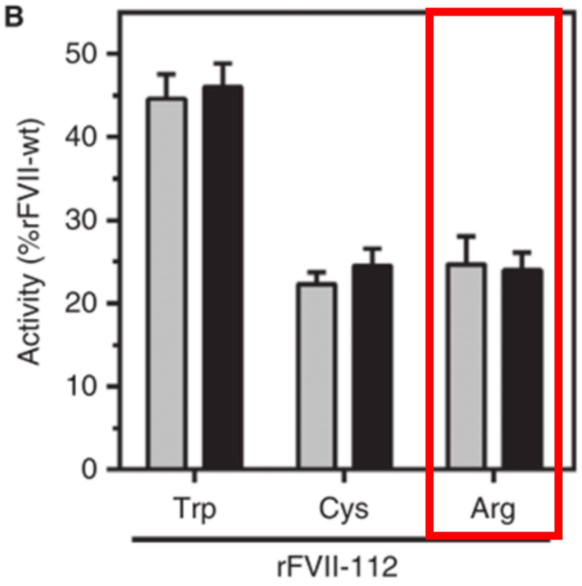


Life-threatening bleeding phenotype

In conclusion:

- In the context of **p.S112X** the readthrough is predicted to occur with **lower efficiency**
- The original amino acid (serine) can not be re-inserted by readthrough but this position significantly **tolerates** the most probable amino acid **substitutions**





Life-threatening bleeding phenotype

Experimental findings are consistent with the complex and integrated scenario depicted above and support the notion that many elements account for readthrough efficiency and protein function restoration

Stop codon readthrough is a process that increases the diversity of genomic information.

This mechanism is well documented with respect to viruses, yeast and *Drosophila,* but is believed to occur also in higher animals.

Stop codon readthrough is a process that increases the diversity of genomic information.

This mechanism is well documented with respect to viruses, yeast and *Drosophila,* but is believed to occur also in higher animals.

L-MPZ, a Novel Isoform of Myelin P0, Is Produced by Stop Codon Readthrough*

Received for publication, October 28, 2011, and in revised form, March 22, 2012 Published, JBC Papers in Press, March 28, 2012, DOI 10.1074/jbc.M111.314468

Yoshihide Yamaguchi[‡1], Akiko Hayashi[‡], Celia W. Campagnoni[§†], Akio Kimura[¶], Takashi Inuzuka[¶], and Hiroko Baba[‡]

***Myelin protein zero** (P0 or MPZ) is a major myelin protein (**30 kDa**) expressed in the peripheral nervous system (PNS) in terrestrial vertebrates. Its main function is the formation and stabilization of the multilamellar membrane structure of compact myelin.

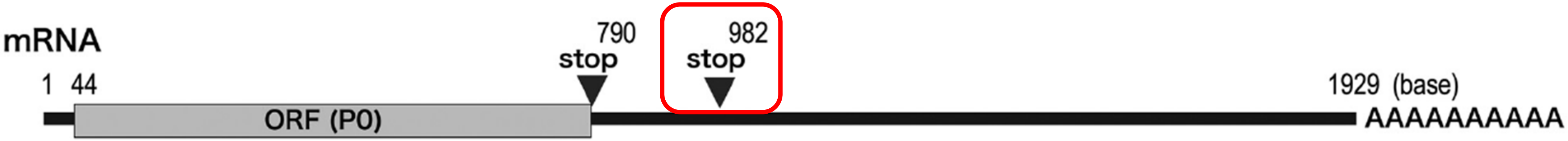
Stop codon readthrough is a process that increases the diversity of genomic information.

This mechanism is well documented with respect to viruses, yeast and *Drosophila,* but is believed to occur also in higher animals.

L-MPZ, a Novel Isoform of Myelin P0, Is Produced by Stop Codon Readthrough*

Received for publication, October 28, 2011, and in revised form, March 22, 2012 Published, JBC Papers in Press, March 28, 2012, DOI 10.1074/jbc.M111.314468

Yoshihide Yamaguchi[‡1], Akiko Hayashi[‡], Celia W. Campagnoni[§†], Akio Kimura[¶], Takashi Inuzuka[¶], and Hiroko Baba[‡]



***Myelin protein zero** (P0 or MPZ) is a major myelin protein (**30 kDa**) expressed in the peripheral nervous system (PNS) in terrestrial vertebrates. Its main function is the formation and stabilization of the multilamellar membrane structure of compact myelin.

A **36-kDa** isoform, named L-MPZ, has been detected under normal conditions in human, bovine, rat, and mouse PNS.

Stop codon readthrough is a process that increases the diversity of genomic information.

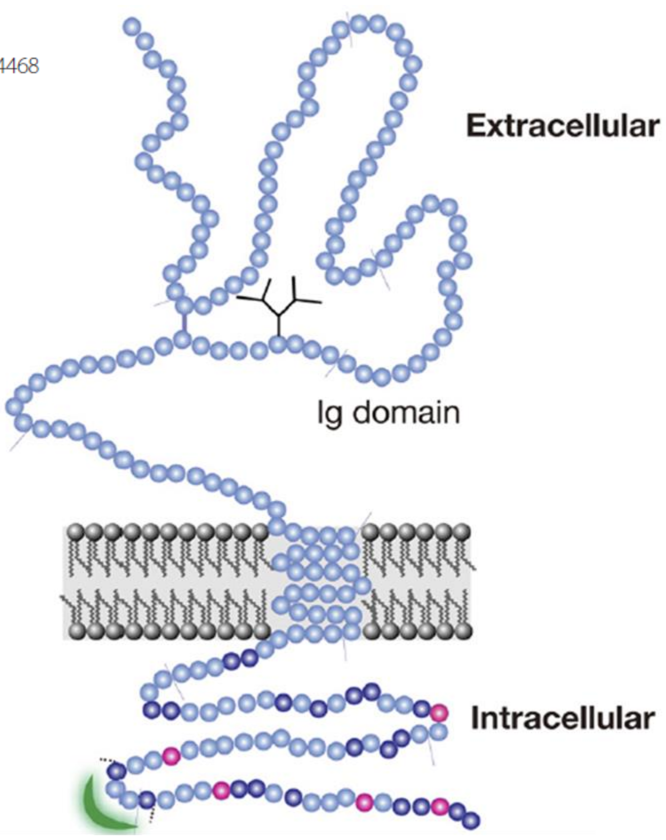
This mechanism is well documented with respect to viruses, yeast and *Drosophila,* but is believed to occur also in higher animals.

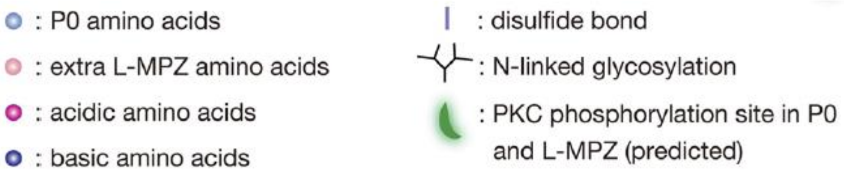
L-MPZ, a Novel Isoform of Myelin P0, Is Produced by Stop Codon Readthrough*

Received for publication, October 28, 2011, and in revised form, March 22, 2012 Published, JBC Papers in Press, March 28, 2012, DOI 10.1074/jbc.M111.314468

Yoshihide Yamaguchi‡1, Akiko Hayashi‡, Celia W. Campagnoni§†, Akio Kimura¶, Takashi Inuzuka¶, and Hiroko Baba‡

MPZ





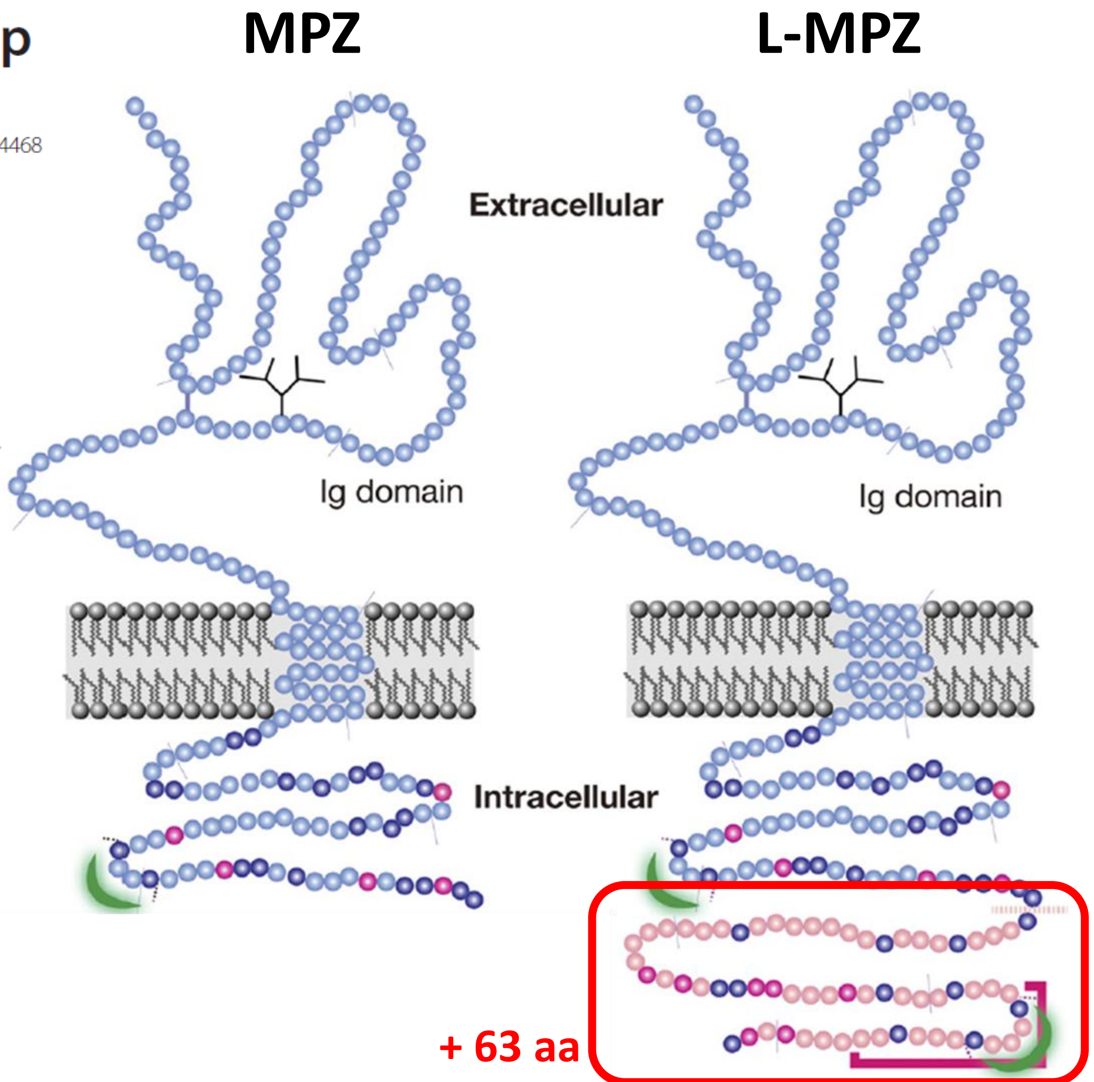
Stop codon readthrough is a process that increases the diversity of genomic information.

This mechanism is well documented with respect to viruses, yeast and *Drosophila,* but is believed to occur also in higher animals.

L-MPZ, a Novel Isoform of Myelin P0, Is Produced by Stop Codon Readthrough*

Received for publication, October 28, 2011, and in revised form, March 22, 2012 Published, JBC Papers in Press, March 28, 2012, DOI 10.1074/jbc.M111.314468

Yoshihide Yamaguchi[‡1], **Akiko Hayashi**[‡], **Celia W. Campagnoni**[§†], **Akio Kimura**[¶], **Takashi Inuzuka**[¶], **and Hiroko Baba**[‡]



● : P0 amino acids

● : extra L-MPZ amino acids

● : acidic amino acids

● : basic amino acids

| : disulfide bond

: N-linked glycosylation

: PKC phosphorylation site in P0 and L-MPZ (predicted)

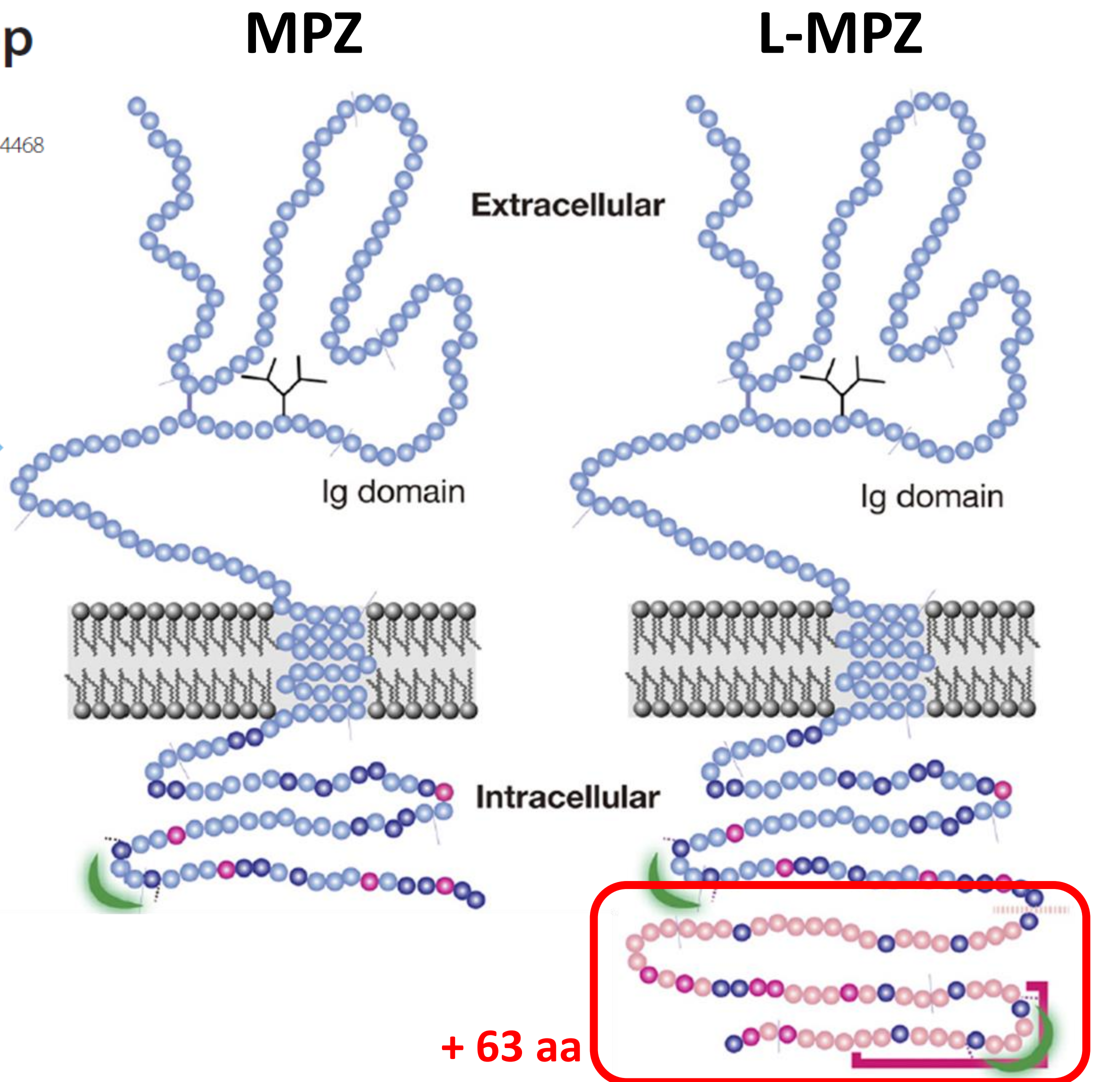
Stop codon readthrough is a process that increases the diversity of genomic information.

This mechanism is well documented with respect to viruses, yeast and *Drosophila,* but is believed to occur also in higher animals.

L-MPZ, a Novel Isoform of Myelin P0, Is Produced by Stop Codon Readthrough*

Received for publication, October 28, 2011, and in revised form, March 22, 2012 Published, JBC Papers in Press, March 28, 2012, DOI 10.1074/jbc.M111.314468

Yoshihide Yamaguchi[‡1], Akiko Hayashi[‡], Celia W. Campagnoni[§†], Akio Kimura[¶], Takashi Inuzuka[¶], and Hiroko Baba[‡]



Because the L-MPZ-specific region contains an additional putative phosphorylation site, it may have some unique roles in normal and pathological myelin conditions.