

# Lost in Translation

Lecture 10

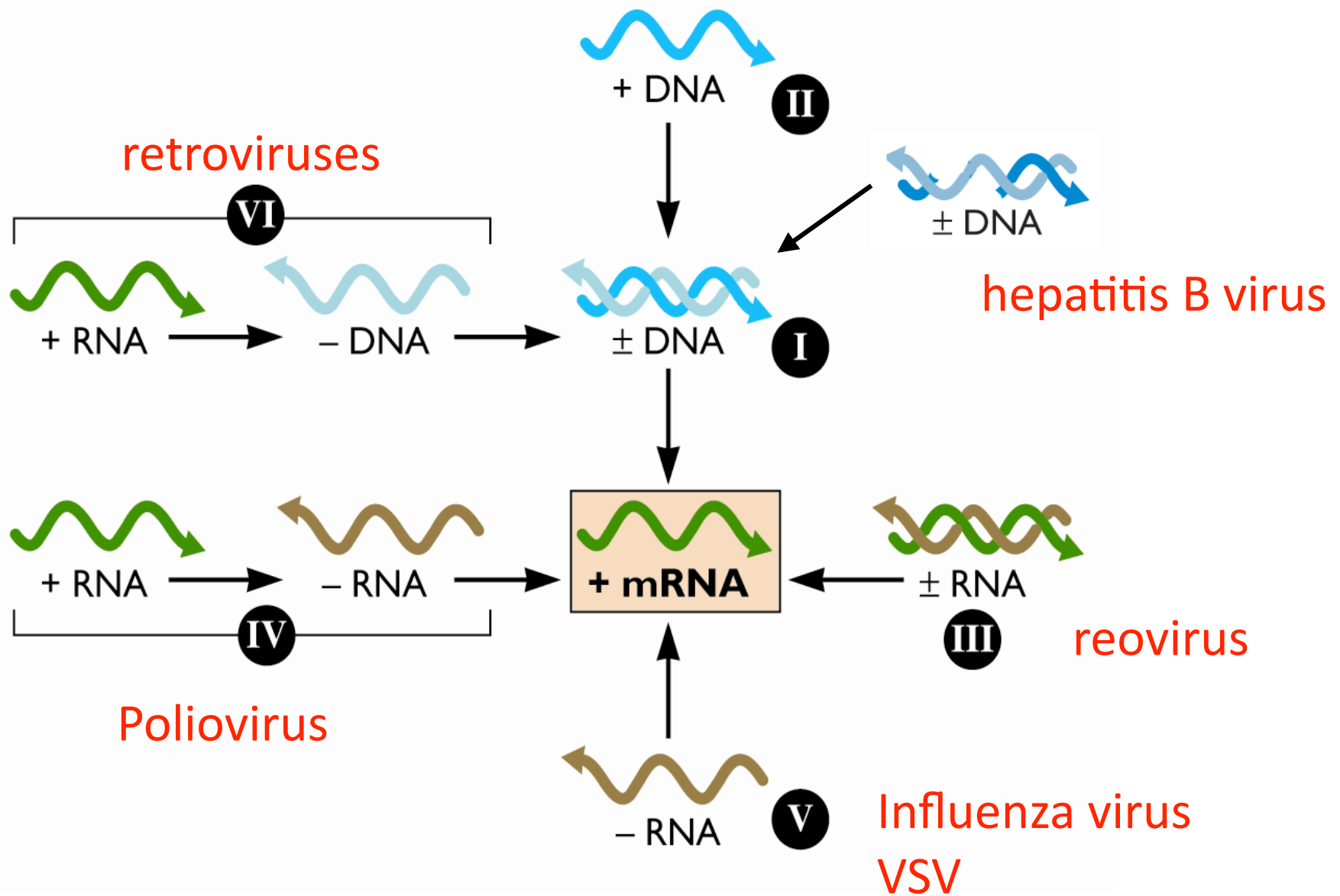
Biology W3310/4310

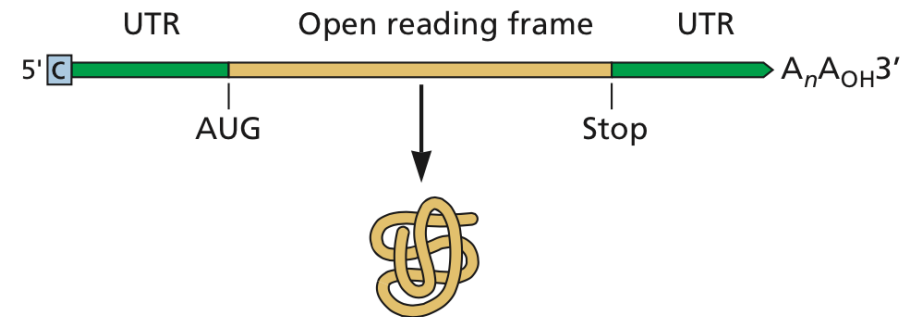
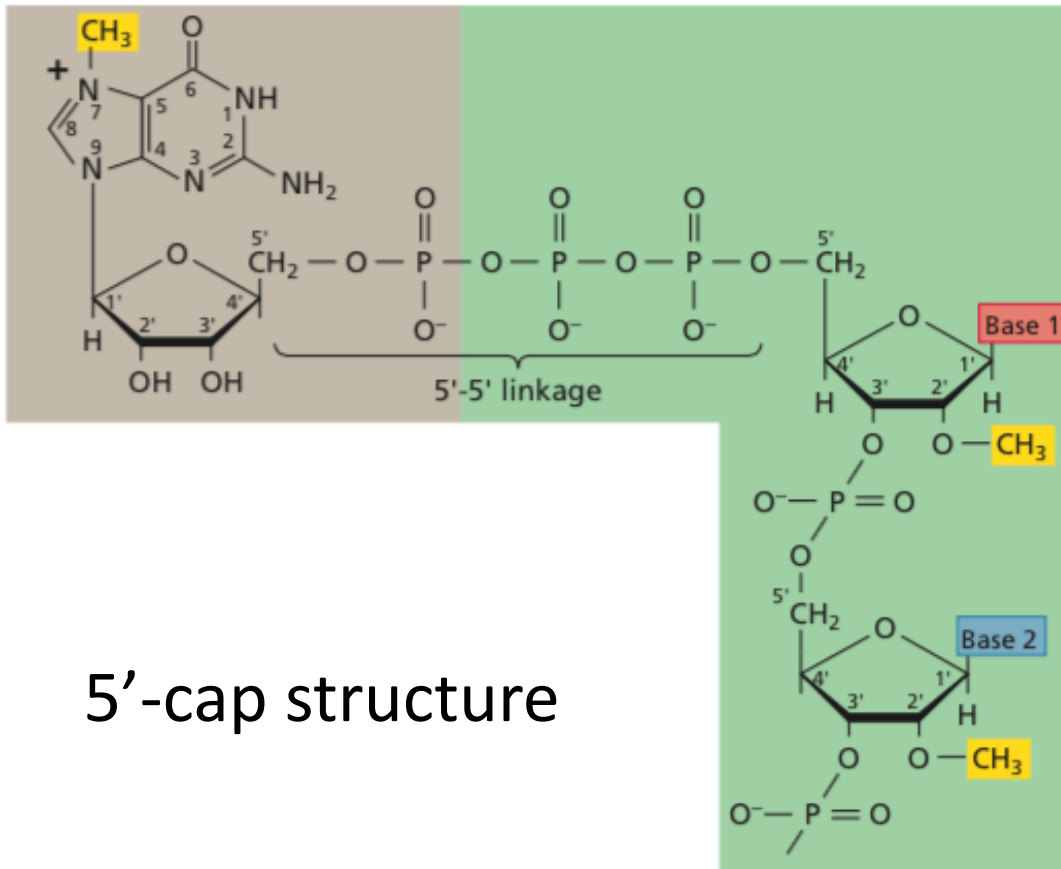
Virology

Spring 2016

*Translation is that which transforms everything  
so that nothing changes.*

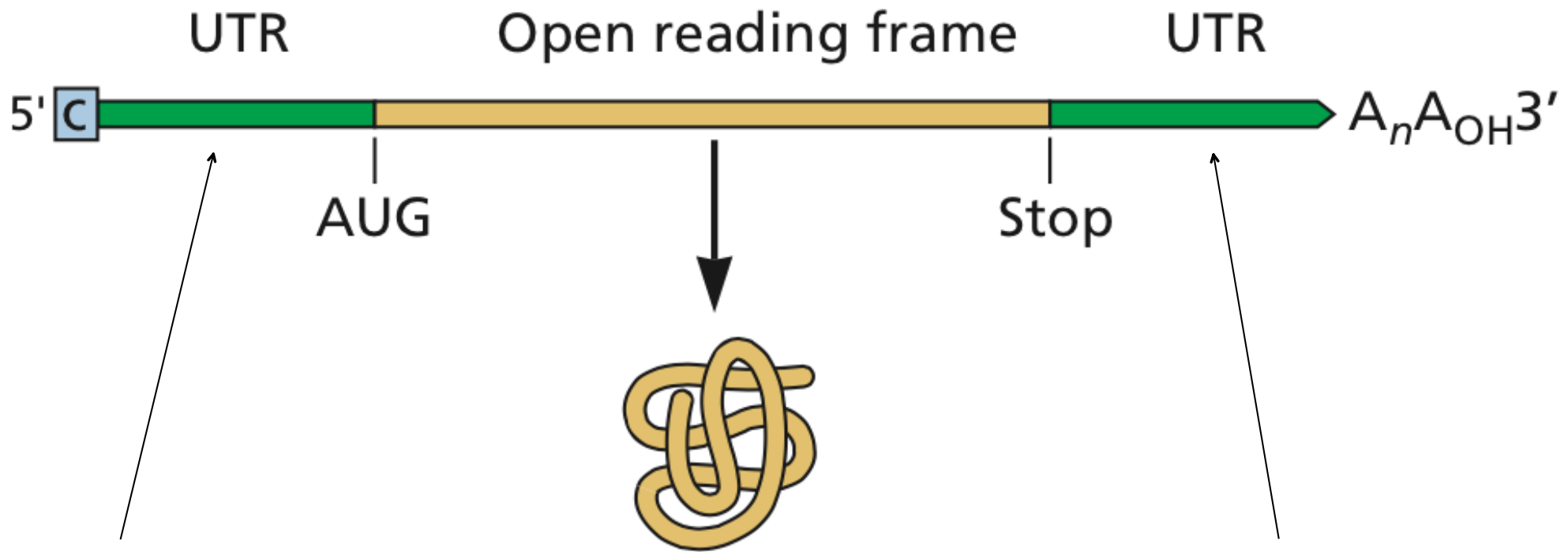
—GÜNTER GRASS





## 5'-cap structure

- Most eukaryotic mRNAs except organelle mRNAs and certain viral mRNAs
- 5'-7-methylguanosine (m7G) joined to second nucleotide of mRNA by 5'-5' phosphodiester linkage
- Directs pre-mRNAs to processing and transport pathways, regulates mRNA turnover, required for efficient translation by 5'-end dependent mechanism



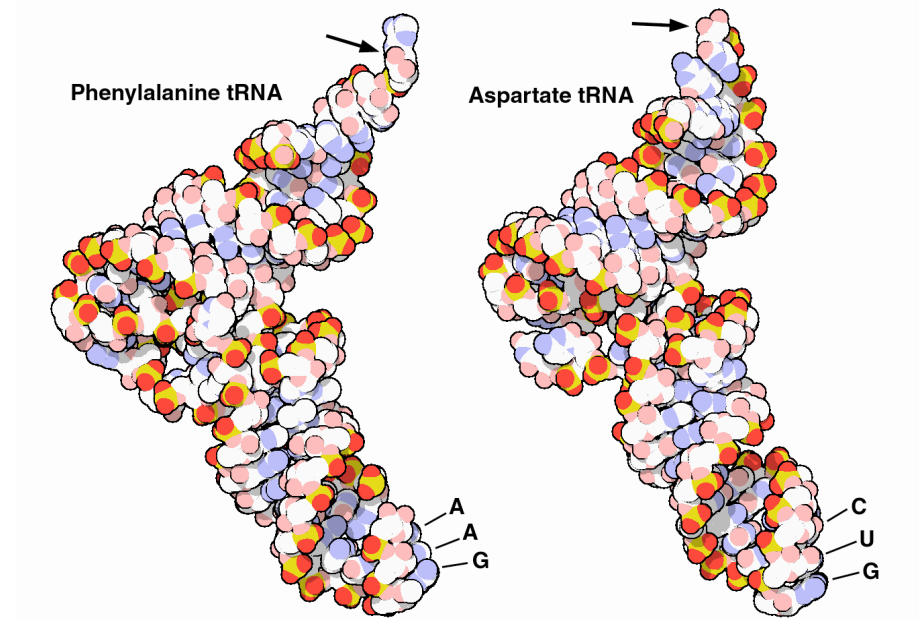
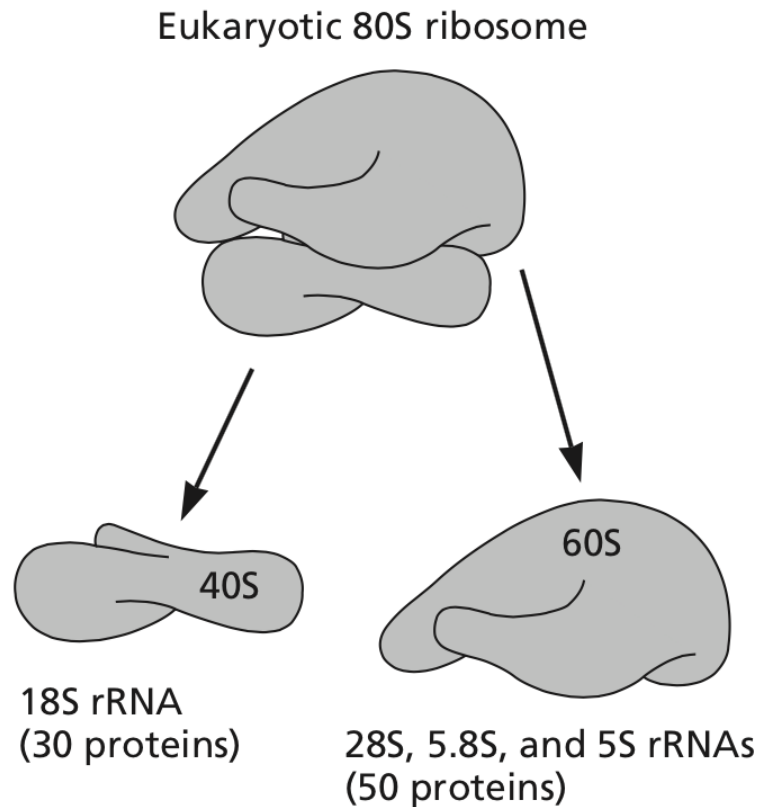
### 5'-untranslated region

- 3' – >1,000 nt in length, typically 50 – 70 nt
- Often contains RNA secondary structures; must be unwound to allow passage of ribosome
- Length and secondary structure influence translation efficiency

### 3'-untranslated region

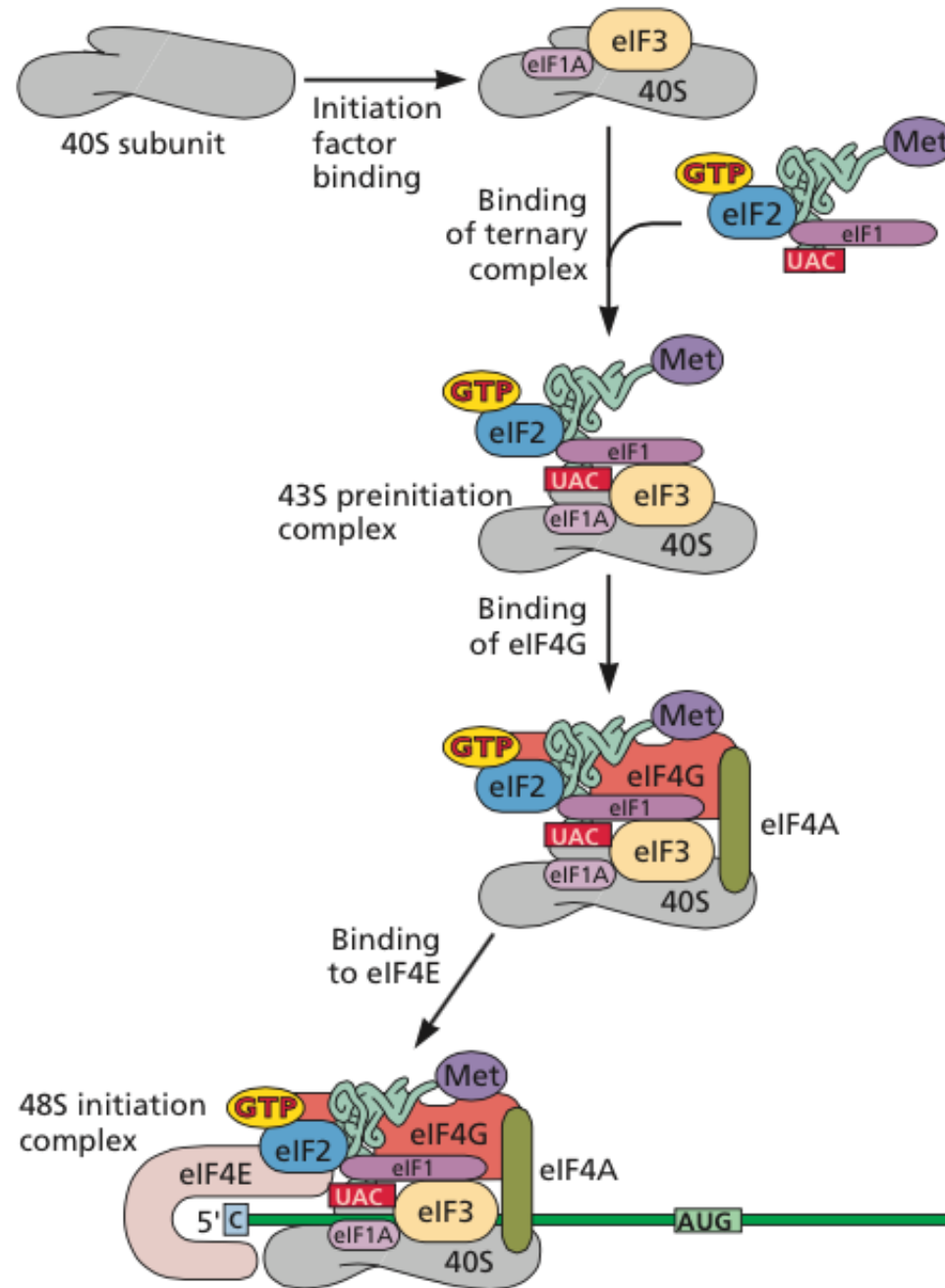
- Can regulate translation initiation, translation efficiency, mRNA stability
- **poly(A) tail**, necessary for efficient translation

# Translational machinery

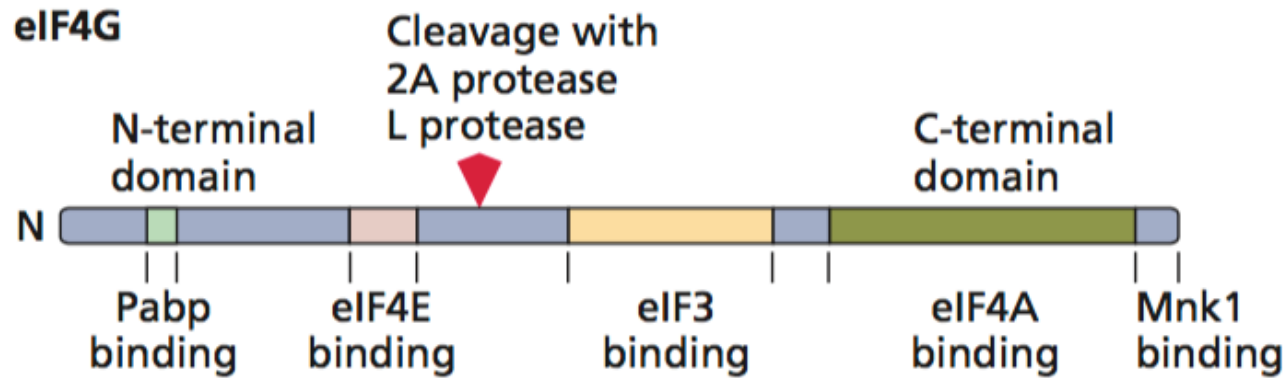


- Initiation proteins (eIF)
- Elongation proteins (eEF)
- Termination proteins (eRF)

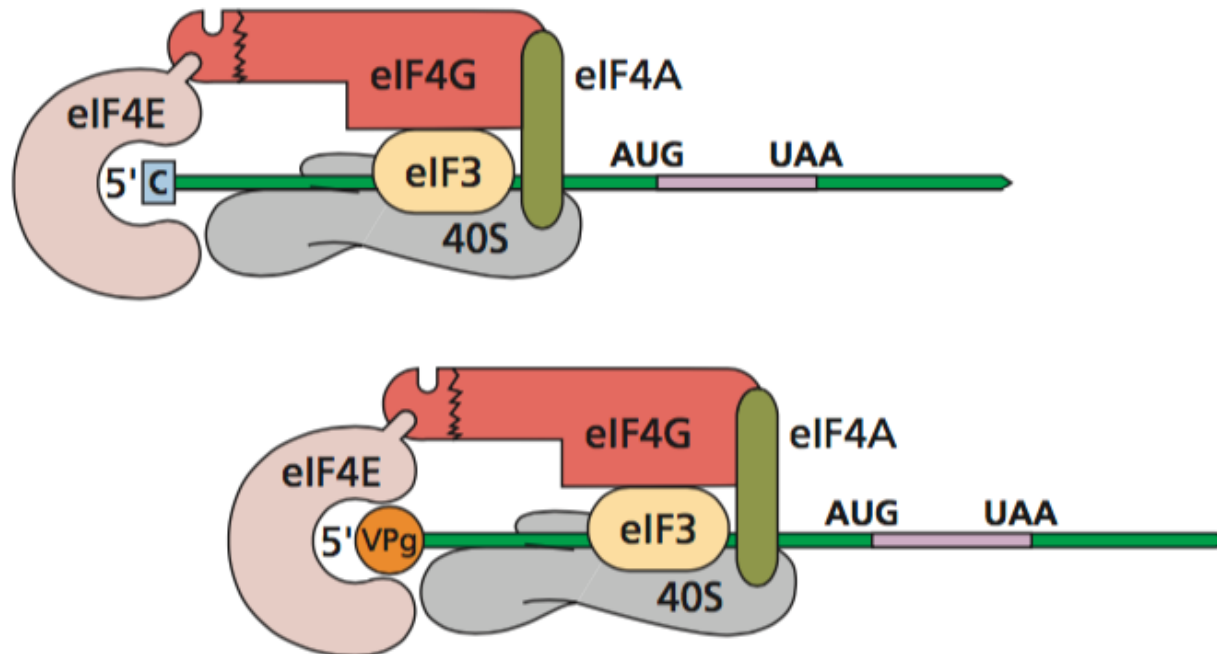
# 5'-end dependent initiation



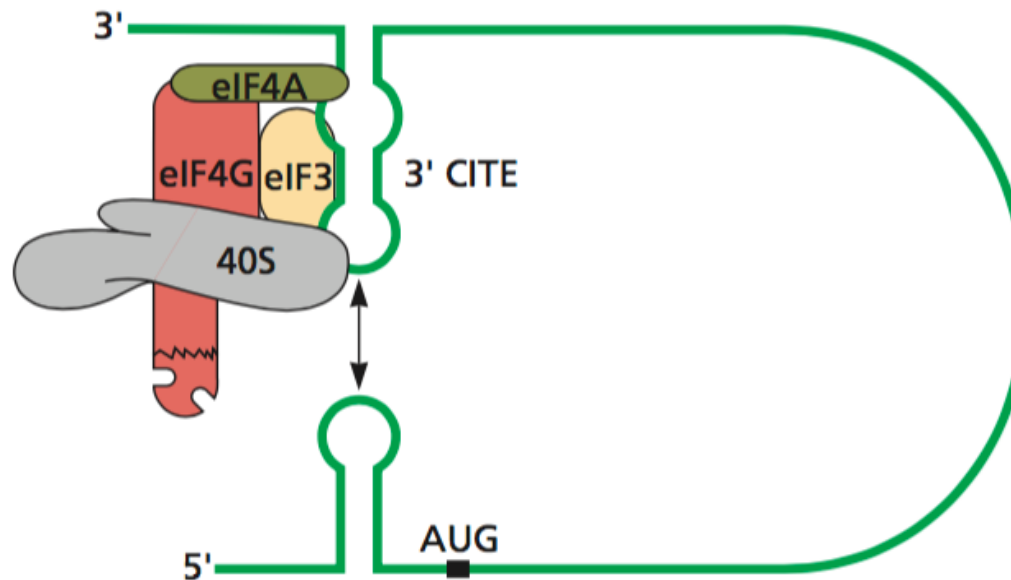
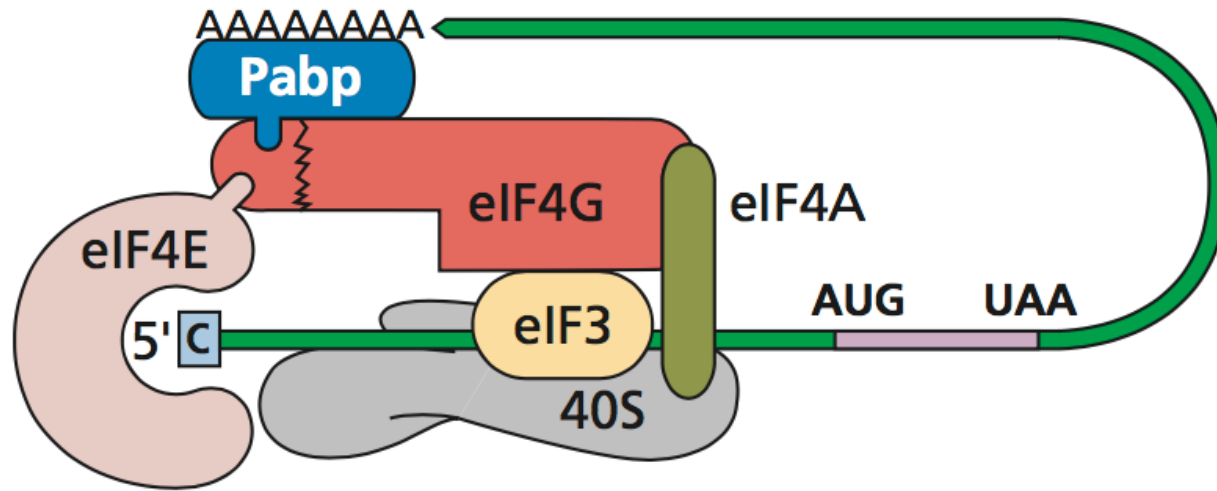
# 5'-end dependent initiation



## 5'-end-dependent initiation

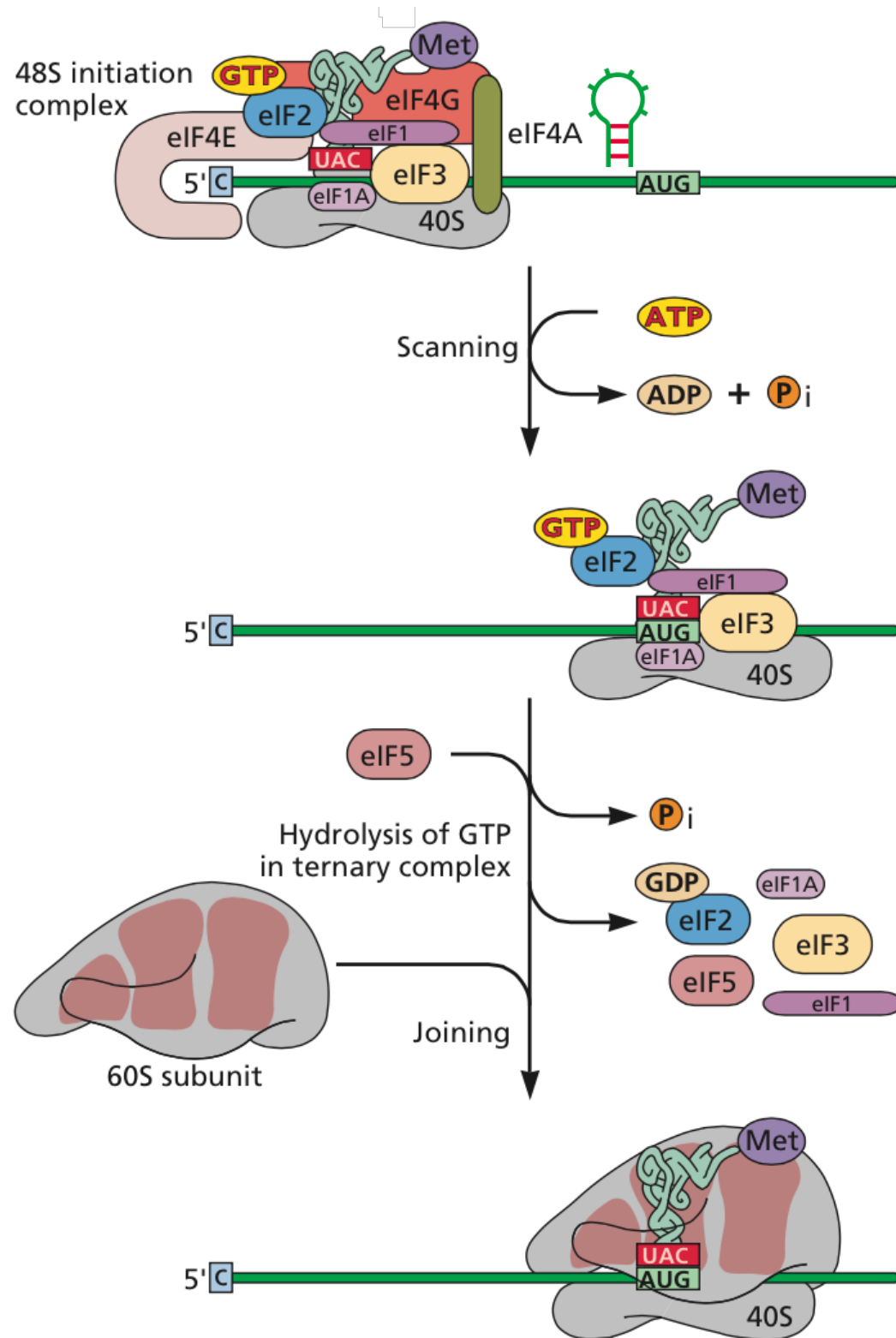


# Juxtaposition of mRNA ends



Pea enation mosaic virus  
Barley yellow dwarf virus





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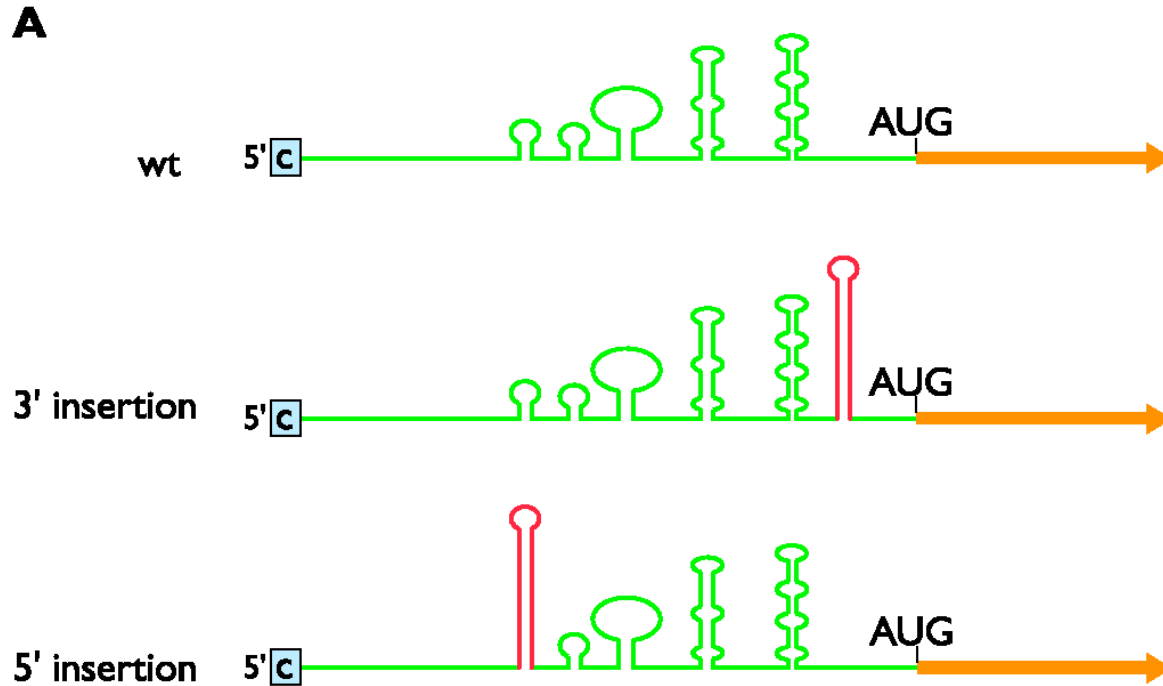
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room number: virus

**Which statement about the 5'-cap on mRNA is incorrect?**

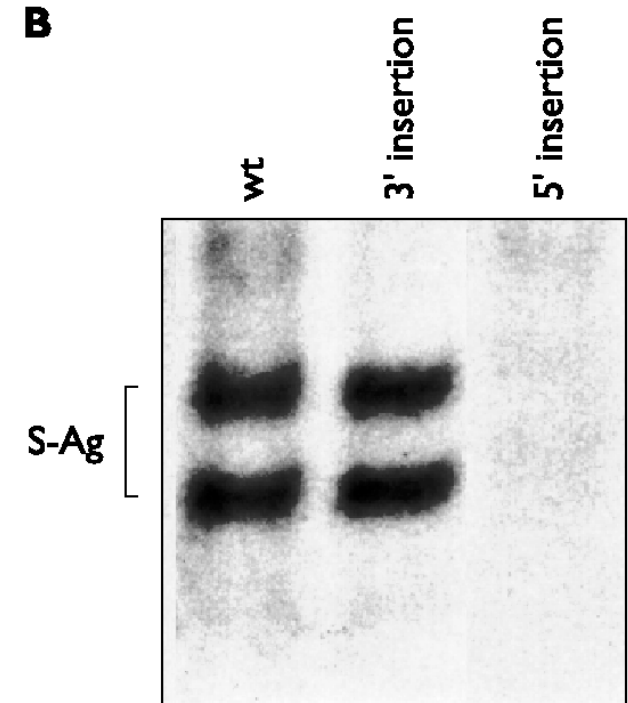
1. It consists of m<sup>7</sup>G joined to second nucleotide of mRNA by an unusual 5'-5' phosphodiester linkage
2. It is present on most cellular mRNAs
3. It is required for efficient translation by 5'-end dependent initiation
4. It binds the cap-binding protein eIF4E
5. It is found on mRNA but not pre-mRNA

**Other mechanisms for decoding have been discovered in virus-infected cells**

# Ribosome shunting

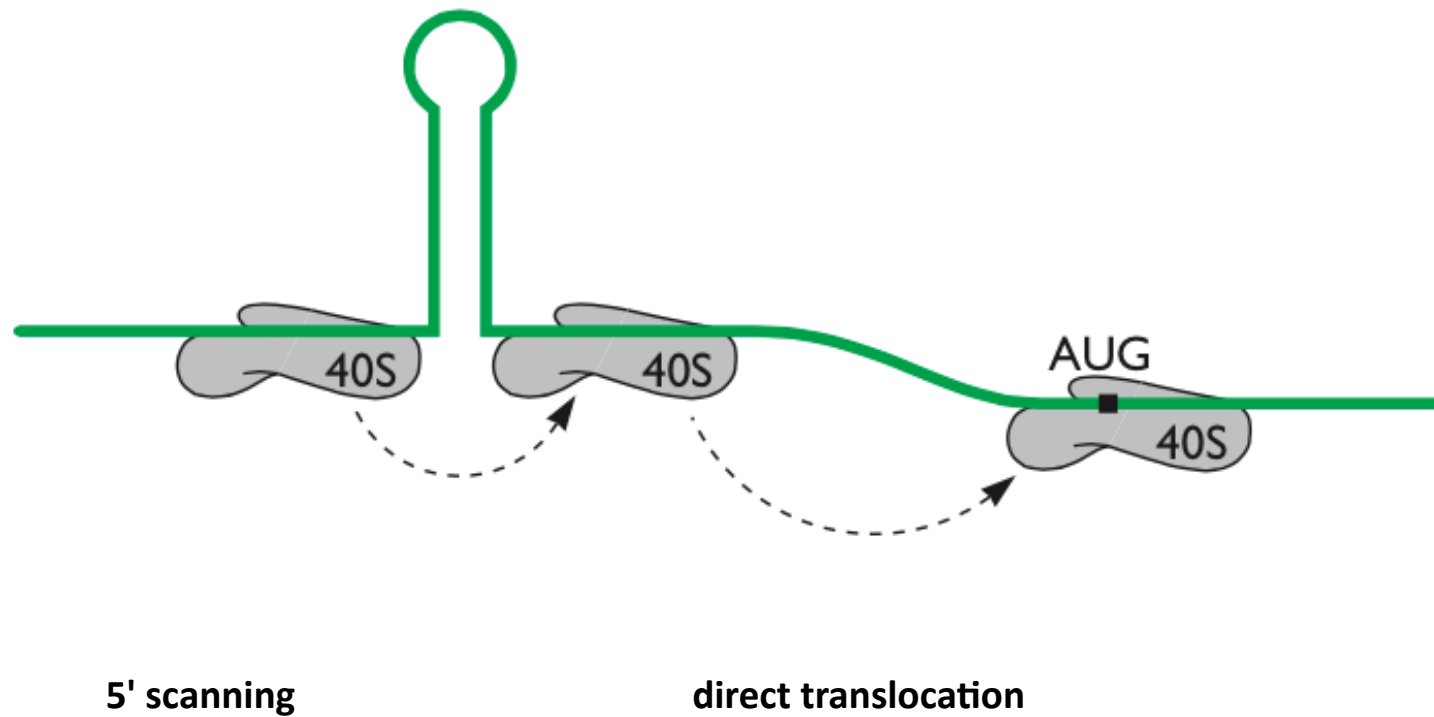


-80 kcal/mole



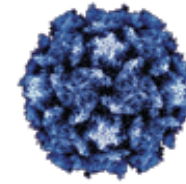
# Ribosome shunting

- 35s mRNAs of plant caulimoviruses
- Late adenovirus mRNAs
- P/C mRNA of Sendai virus



*Shunting is predicted to decrease dependence of mRNAs for eIF4F during initiation by reducing the need for mRNA unwinding*

# Internal initiation



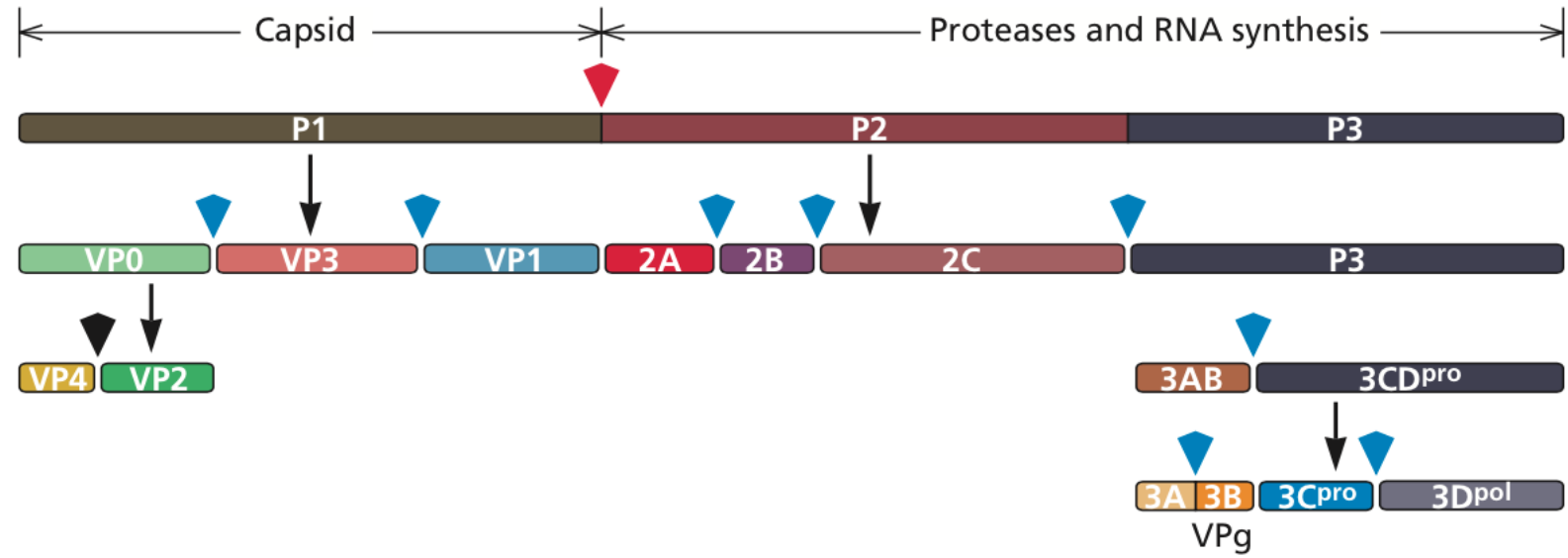
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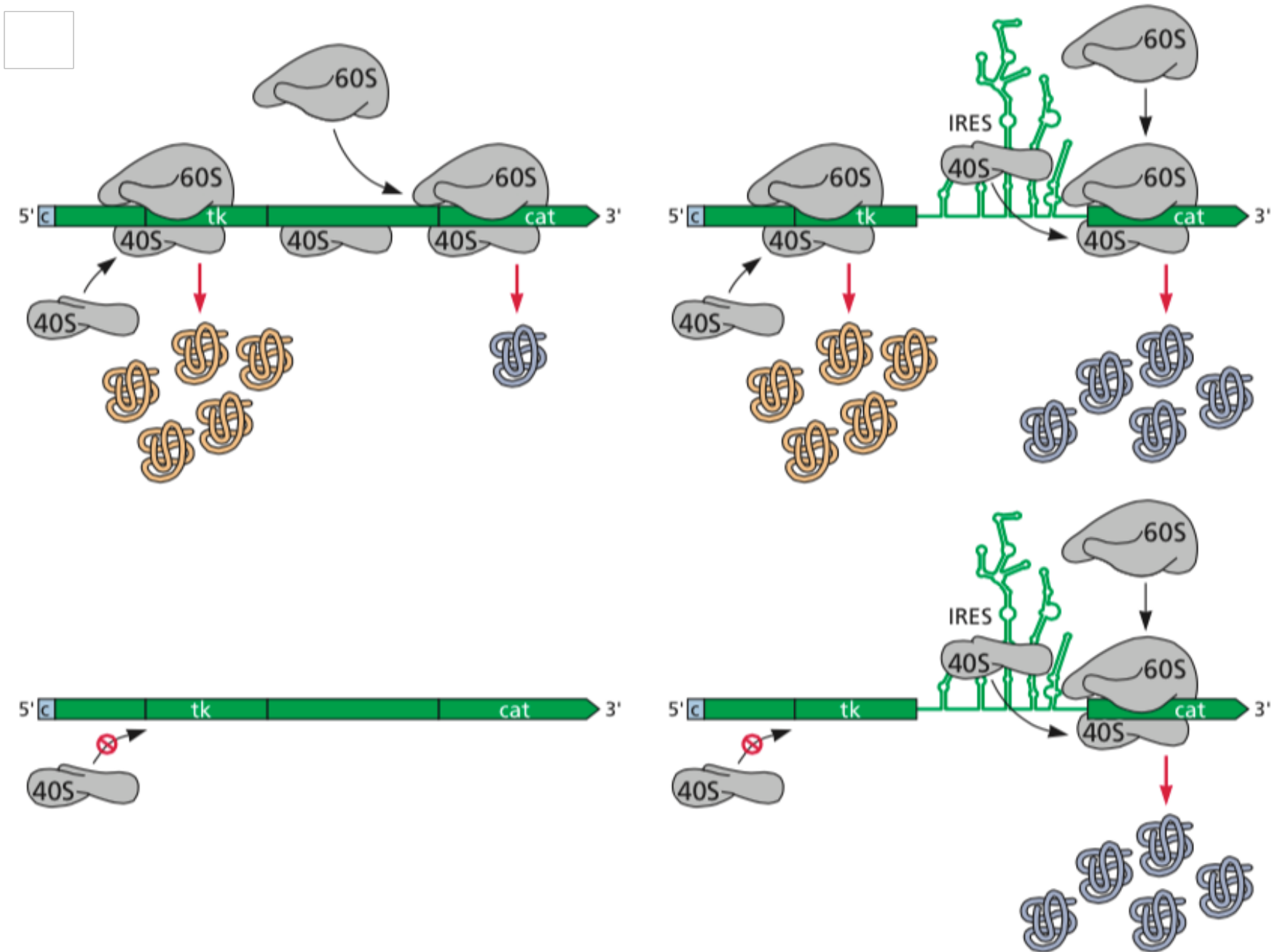
2*** 10      20      30      40      50      60      70      80      90      100 3*** 2110 120      130      140      150      160      170      180
TAAACACG TCTGGGTTG TACCCACCGC AGAGGCGCAC GTGGGGGCTA GTACTCGGTT ATTGCGGTAC CTTGTACGC CTGTTTATA CTGCGTTGCG GTAACTTAA GGCACAAAC CAAGTTCAAT AAGAGGGGGT ACAAACCACT ACCACCACGA ACAAGCACTT CTGTTGCGC
2*** 190 1*** 200      210 222 220      230      240      250      260      270      280      290      300 2310 1*** 2320 2332 330      340      350      360
GCTGATGTCG TATAAGCTGC TTGCGTGCTT GAAAGCGACG GATCCGTTAT CGCCTTATGT ACTTCGAGAA GCGCAGTACC ACCTCGGAAT KTTTCGATCG TTGCGCTCAG CACTCAACCC CAGAGTGTA CTTAAGGCTA TGAATCTGGA CATCCCTCAC GCGTACGCT GTCCAGGCT
2*** 370 2*** 380 2*** 390 2*** 400 2332 410 2332 420 2332 430 2332 440 2332 450 2332 460 2332 470 2332 480 2332 490 2332 500 2332 510 2332 520 2332 530 2332 540
GCCTTGGCGG CTTACCTATG GCTAACGCTA TGGACGCTA GTTGTGACA AGGTGTGAG ACGCTATTAG CCTACATAG AATCTCTGCG GCGCTGATG CCGCTAATCC CACCTTCGGA GCGCTGCTC ACAAACCACT CATTCGCTG TCGTACCGG CAGTCCGCTG GCGGACGGA
2*** 550 2*** 560 2*** 570 2*** 580 2*** 590 2*** 600 2332 610 2332 620 2332 630 2332 640 2332 650 2332 660 2332 670 2332 680 2332 690 2332 700 2332 710 2332 720
CTACTTTGCG TGTGCGTCTT TCGTTTATTT TATTGTGCGC TCGTTATGTT GAAATCACA GATTGTTATC TAAAGCGAA TTGATTTGCG KATCCGCTCA AATCAGACT CATTATCTAT CTGTTTCTG GATCGCTGC ATTGCTGCT TTTACTCTA GTACAATTTC AACAGTTATT
2*** 730 2*** 740 2*** 751 2*** 761 2*** 771 2*** 781 2*** 791 2*** 801 2*** 811 2*** 821 2*** 831 2*** 841 2*** 851 2*** 861 2*** 871 2*** 881 2*** 891 2*** 901
TCAATCAGAC AATTGTATCA TA ATG GGT GCT CAG GGT TCA TCA CAG AAA GTG GCG CCA CAT GAA AAC TCA AAT AGA GCG TAT GGT GGT TCT ACC ATT AAT TAC ACC ACC ATT AAT TAT TAT AGA GAT TCA GCT AGT AAC GCG GCT TCG AAA
Met Gly Ala Gln Val Ser Ser Gln Lys Val Gly Ala His Gln Asn Ser Asn Arg Ala Tyr Gly Gly Ser Thr Ile Asn Tyr Thr Thr Ile Asn Tyr Tyr Arg Asp Ser Ala Ser Asn Ala Ala Ser Lys
    
```

Viral (+) strand genome

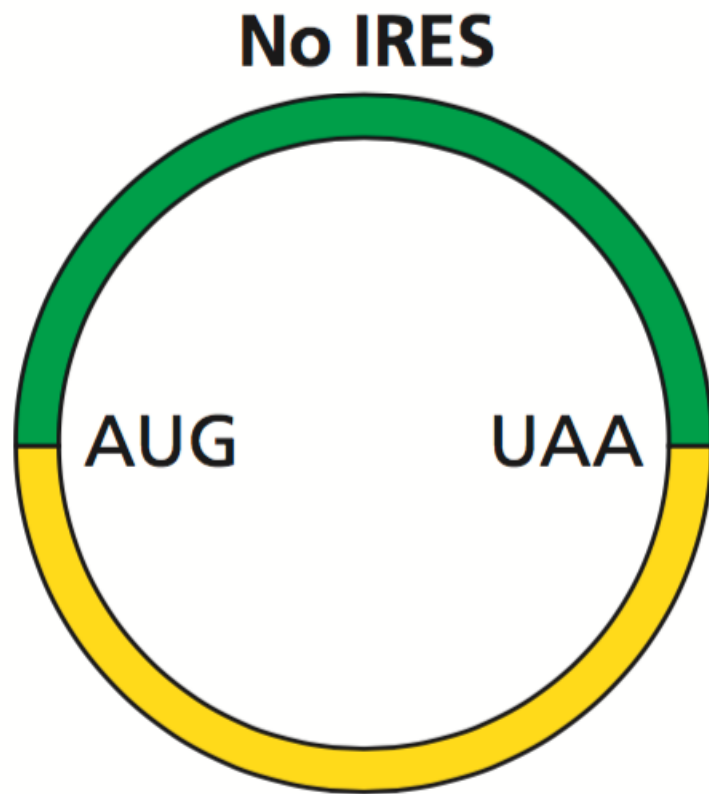


Translation, processing

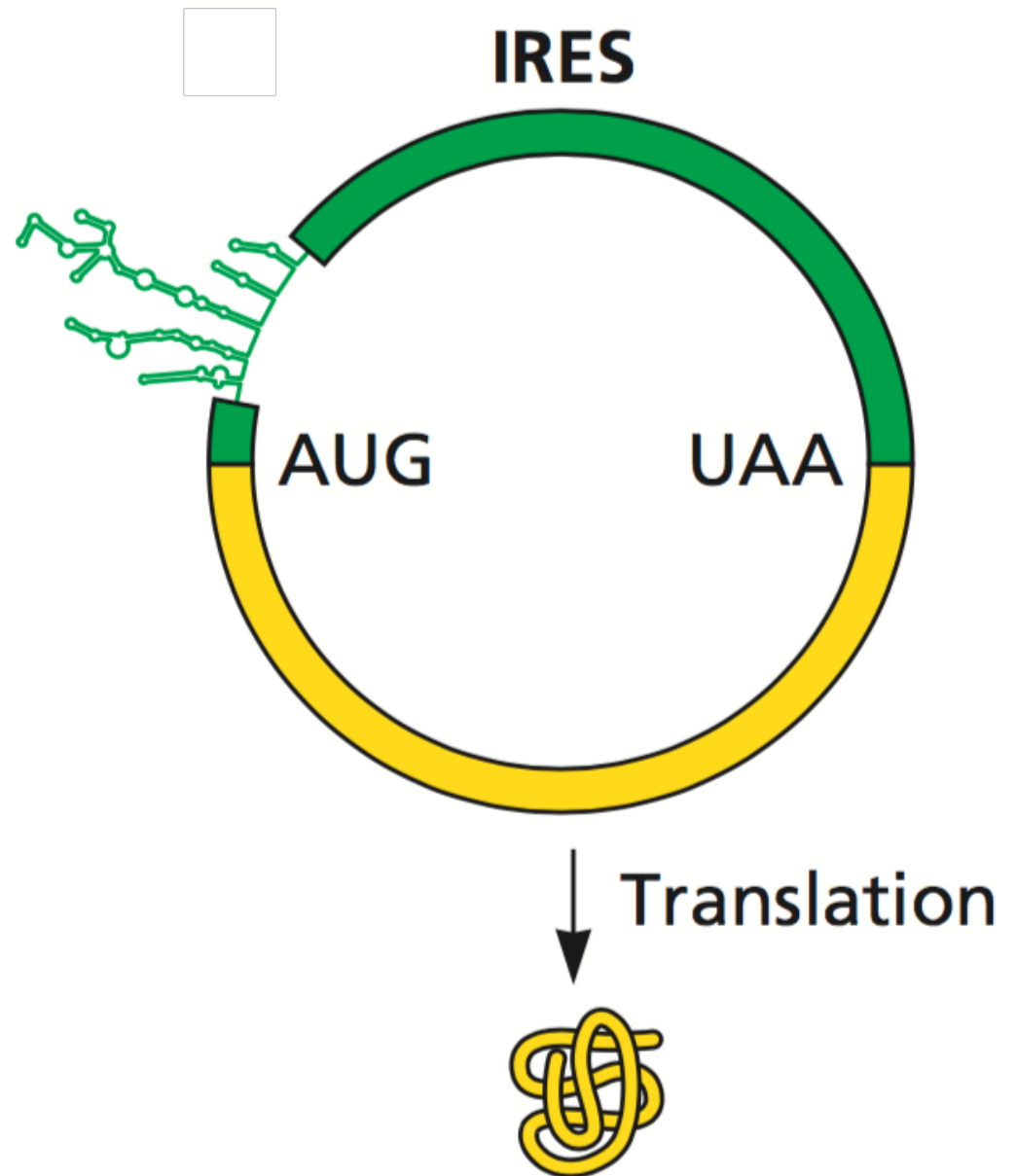




IRES = internal ribosome entry site

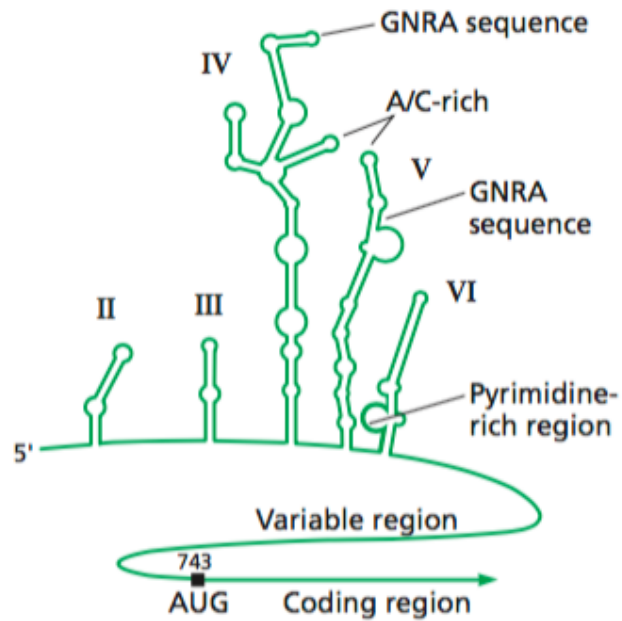


↓  
No protein

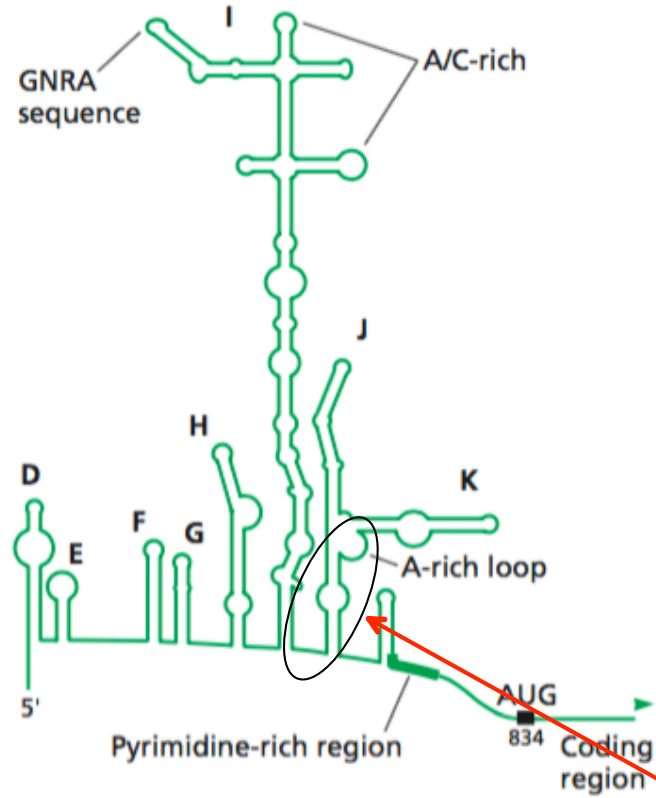




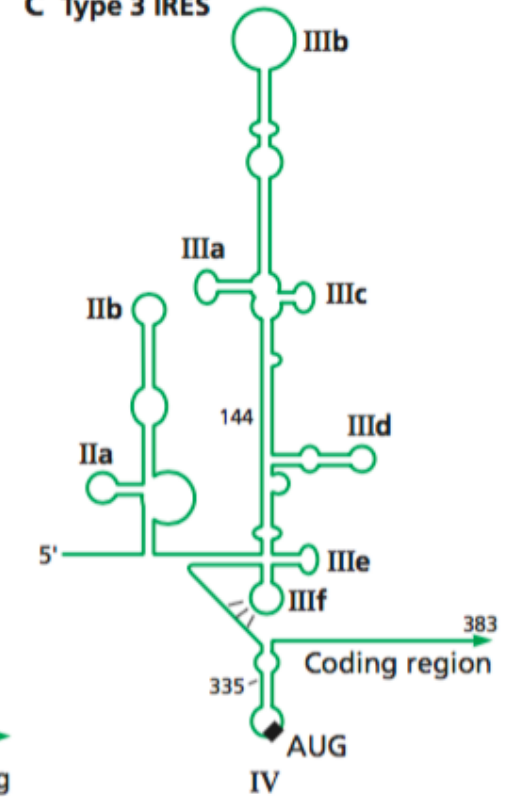
**A Type 1 IRES**



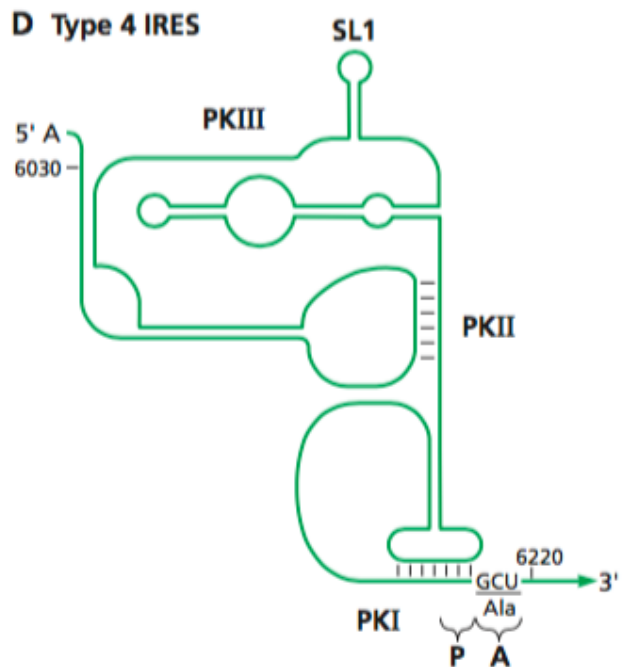
**B Type 2 IRES**



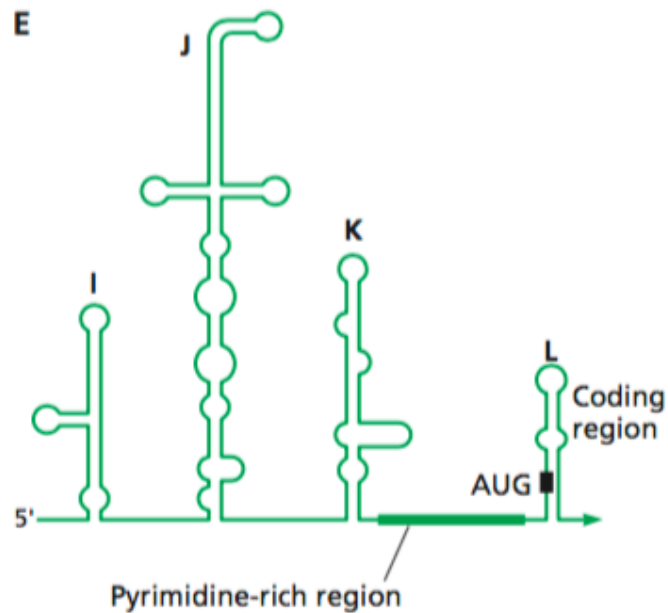
**C Type 3 IRES**



**D Type 4 IRES**

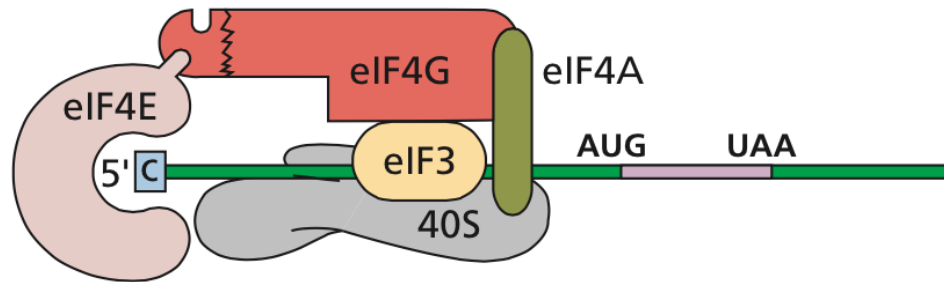


**E**



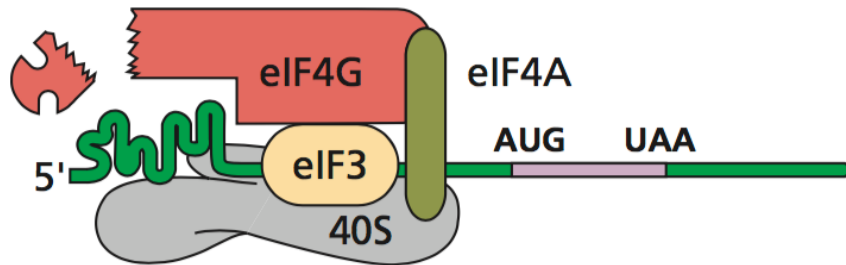
eIF4G footprint

### 5'-end-dependent initiation



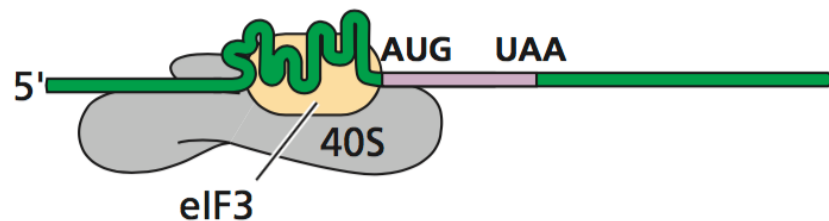
all eIFs

### Type 1 or 2 IRES



all eIFs except  
eIF4E

### Hepatitis C virus IRES



eIF2, eIF3

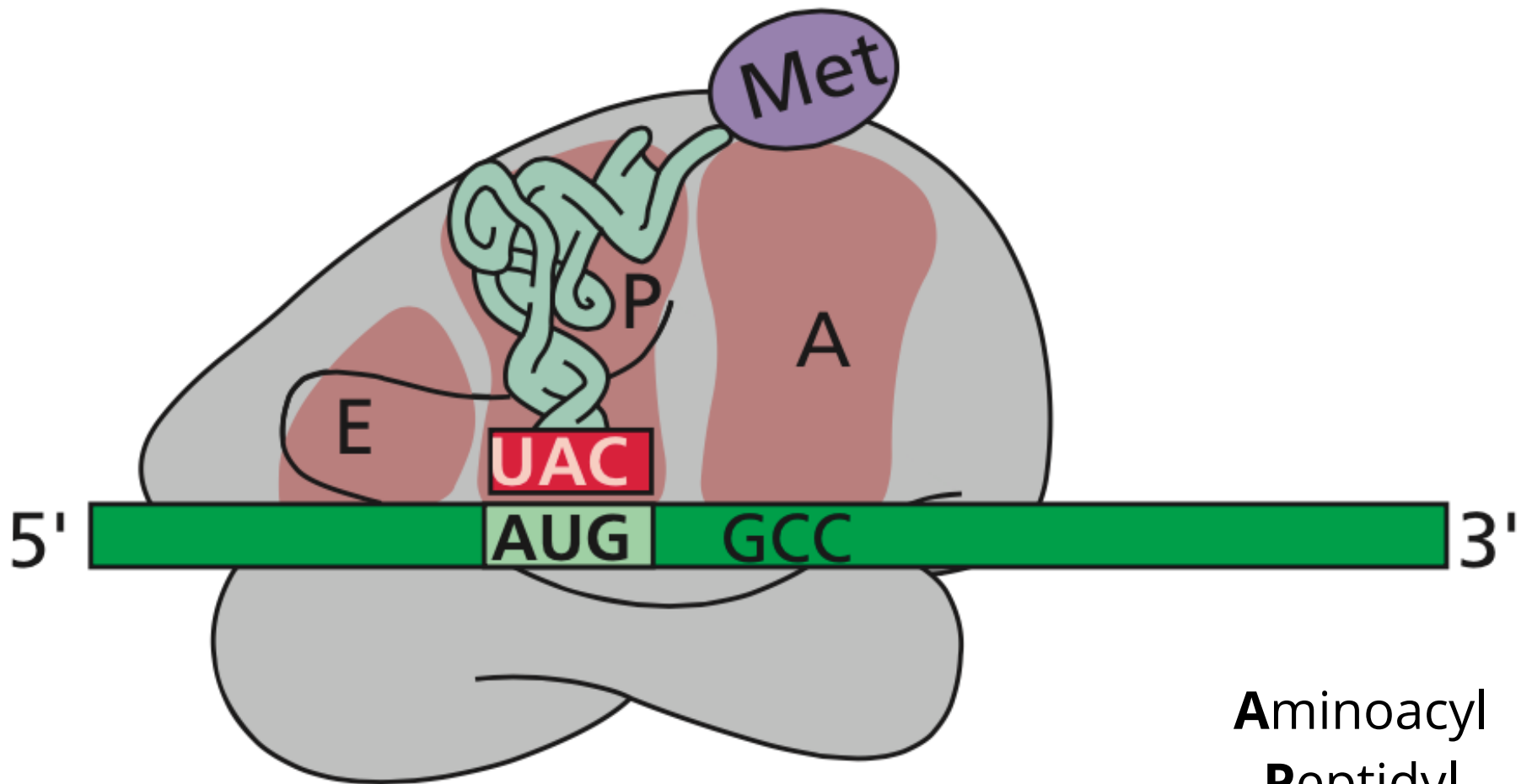
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**What do ribosome shunting and internal ribosome initiation have in common?**

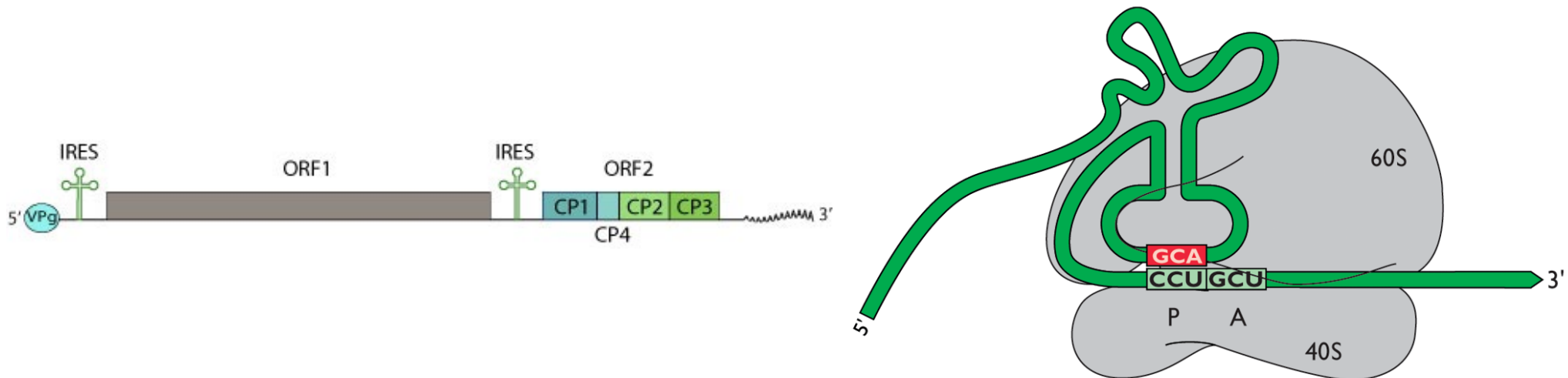
1. Cap recruitment of 40S subunit
2. Both involve RNA secondary structures
3. Ribosome scanning through the entire 5'-UTR
4. Both require cap-binding protein eIF4E
5. All of the above



**A**minoacyl  
**P**eptidyl  
**E**xit

# Methionine-independent initiation

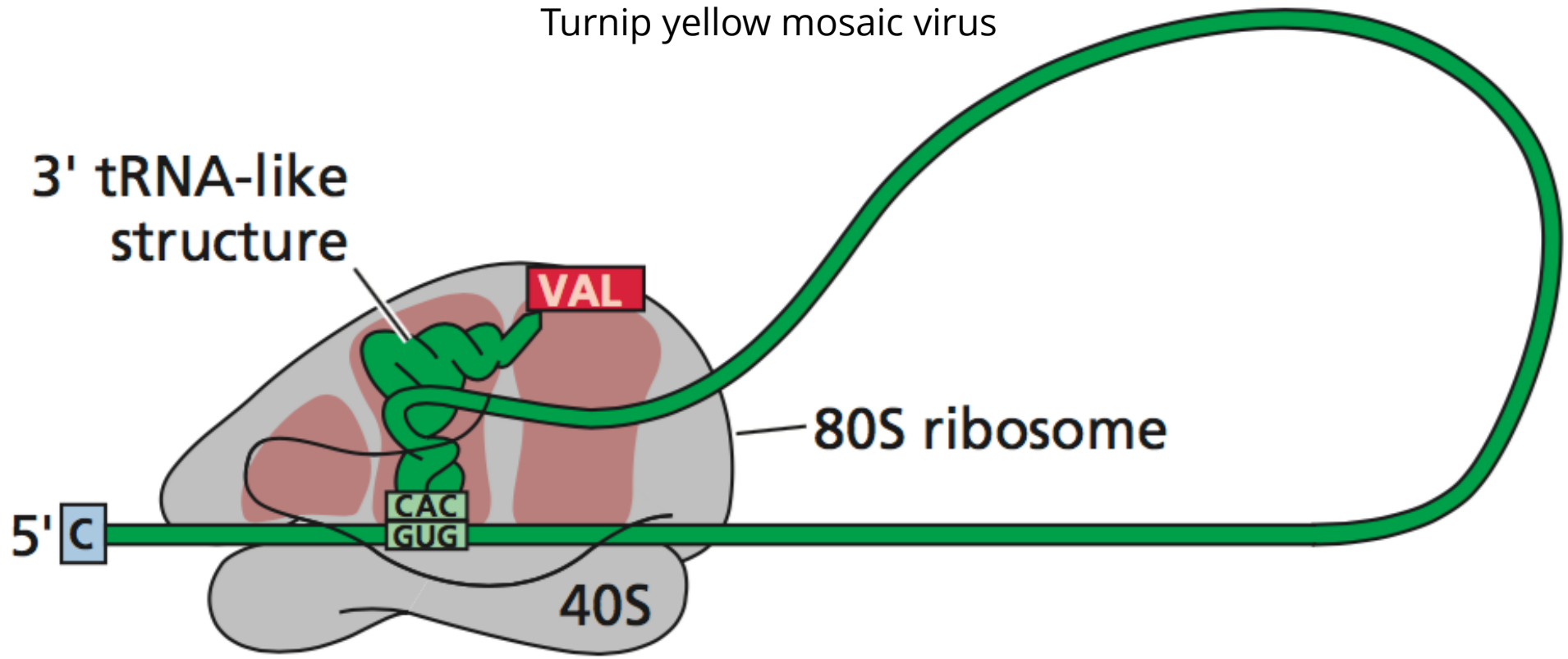
Cricket paralysis virus



- Can assemble 80S ribosomes without any eIFs or Met-tRNAi
- RNA mimics tRNAi

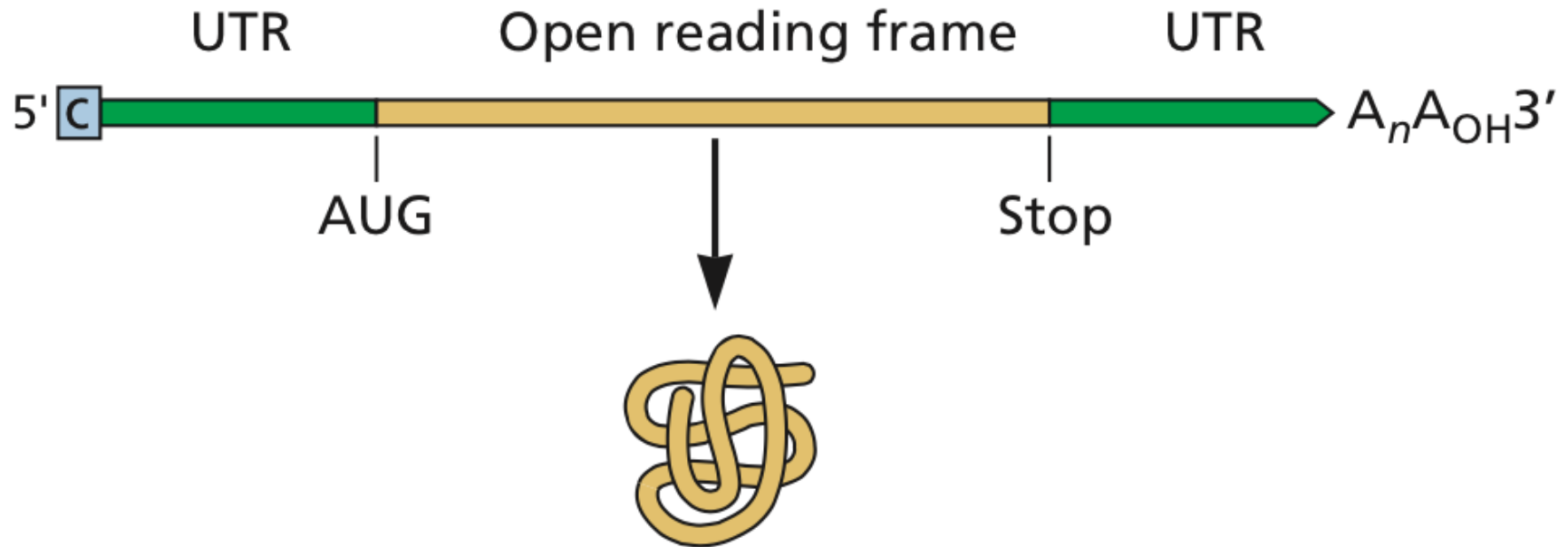
# Methionine-independent initiation

Turnip yellow mosaic virus

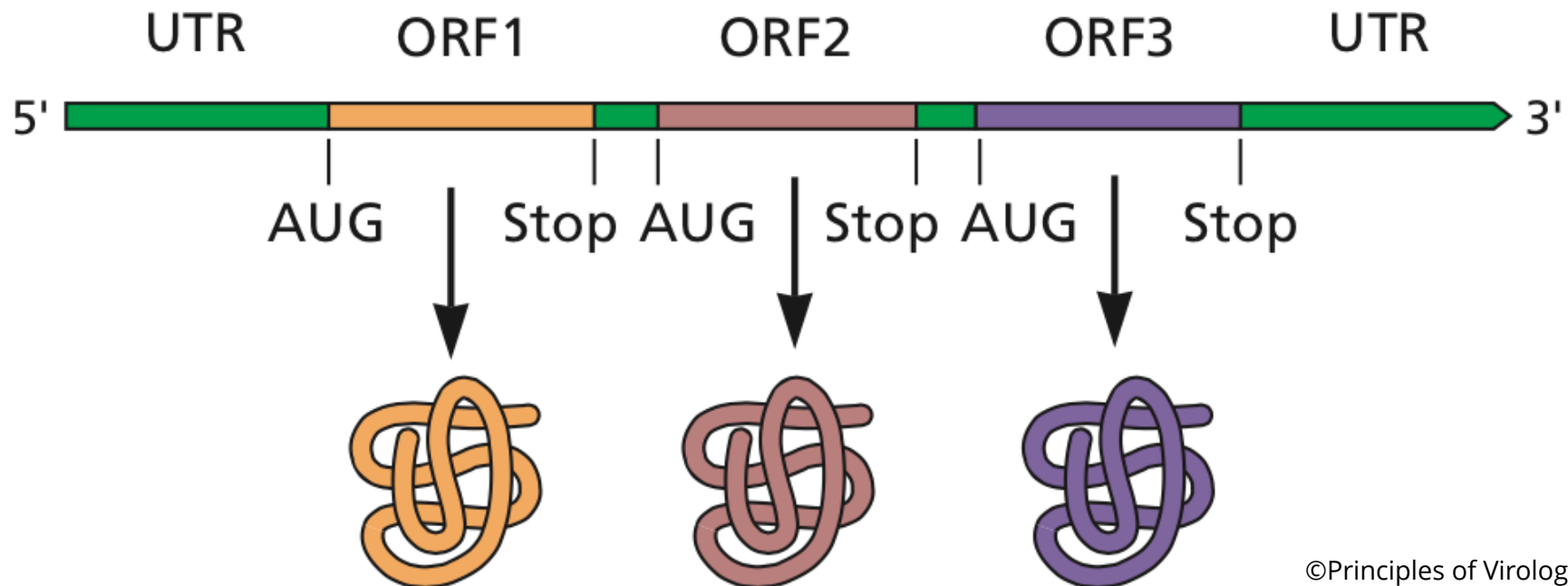


- Can assemble 80S ribosomes without any eIFs or Met-tRNA<sub>i</sub>
- RNA mimics tRNA<sub>i</sub>

## Eukaryotic mRNA (monocistronic)



## Bacterial and archaeal mRNA (polycistronic)



# Maximizing coding capacity of the viral genome

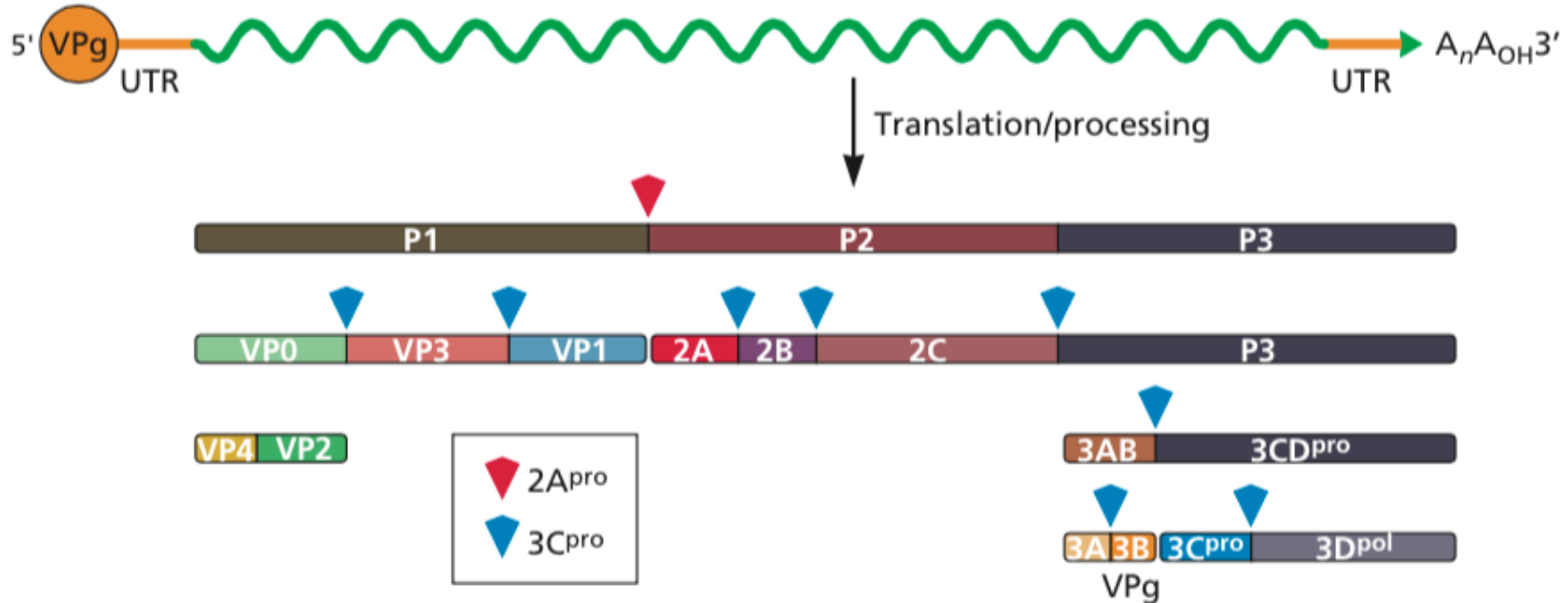
- Polyprotein (*Picornaviridae*, *Flaviviridae*, *Togaviridae*, *Arenaviridae*, *Bunyaviridae*, *Retroviridae*)
- Subgenomic mRNAs (*Rhabdoviridae*, *Paramyxoviridae*, *Togaviridae*)
- Segmented genome (*Orthomyxoviridae*, *Reoviridae*)
- RNA Splicing (*Orthomyxoviridae*, *Adenoviridae*, *Polyomaviridae*)
- Internal initiation (IRES) (*Picornaviridae*, *Flaviviridae*)
- Leaky scanning (*Retroviridae*, *Paramyxoviridae*)
- Re-initiation of translation (*Orthomyxoviridae*, *Herpesviridae*)
- Suppression of termination (*Retroviridae*, *Togaviridae*)
- Ribosomal frameshifting (*Retroviridae*)



# Polyprotein synthesis

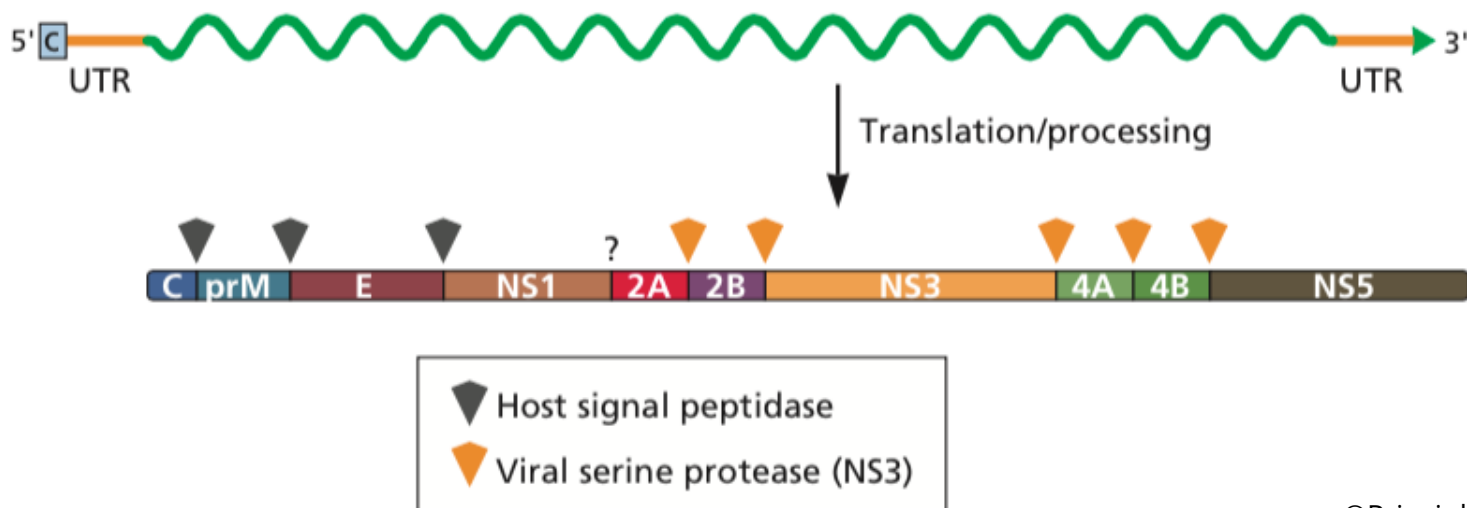
**A**

Viral (+) strand genome

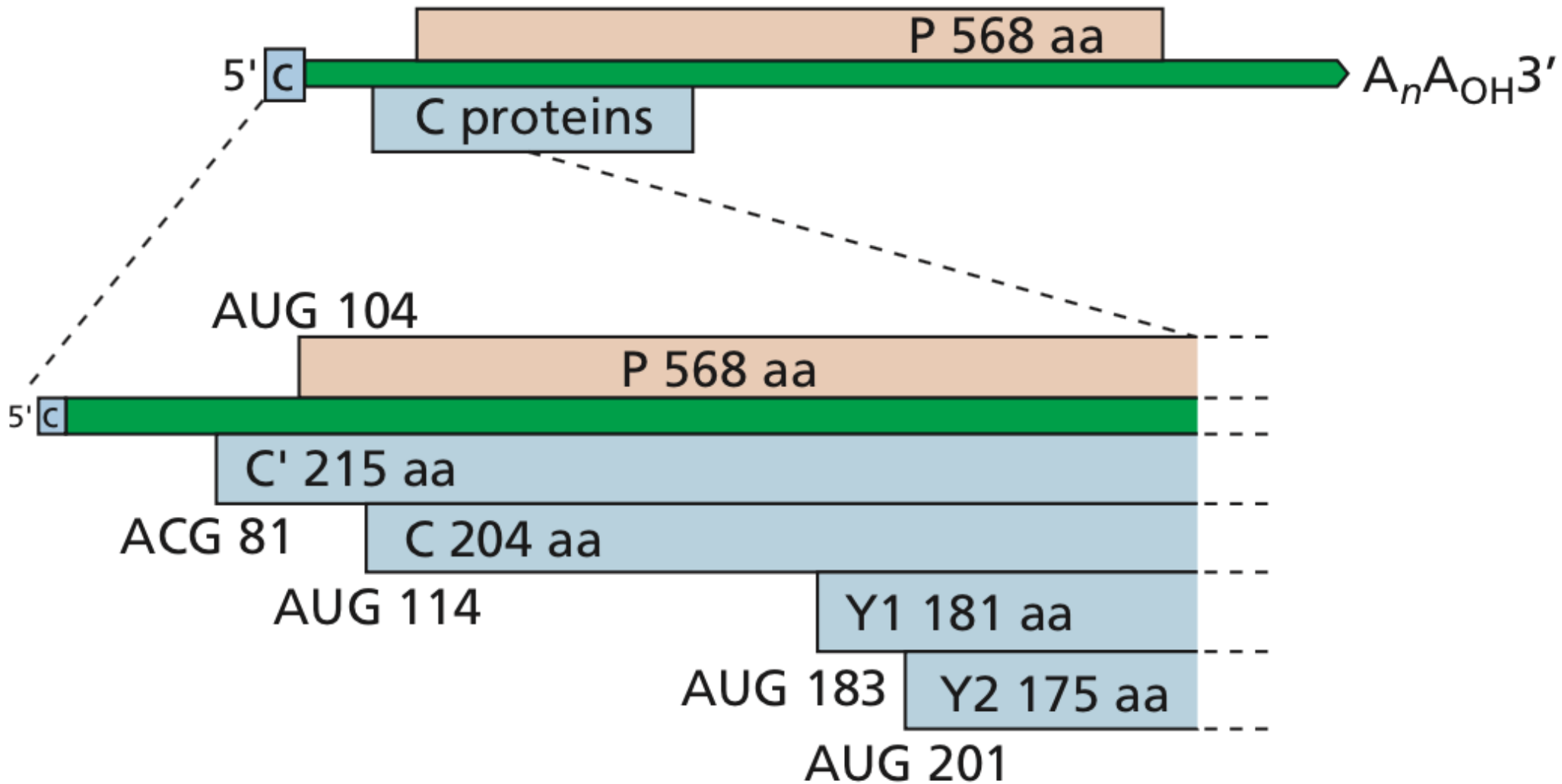


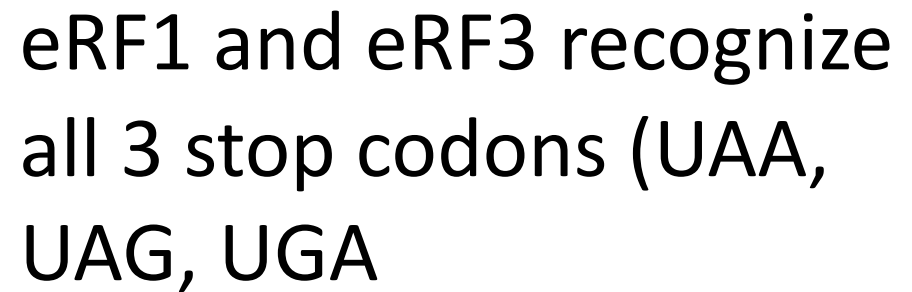
**B**

Viral (+) strand genome



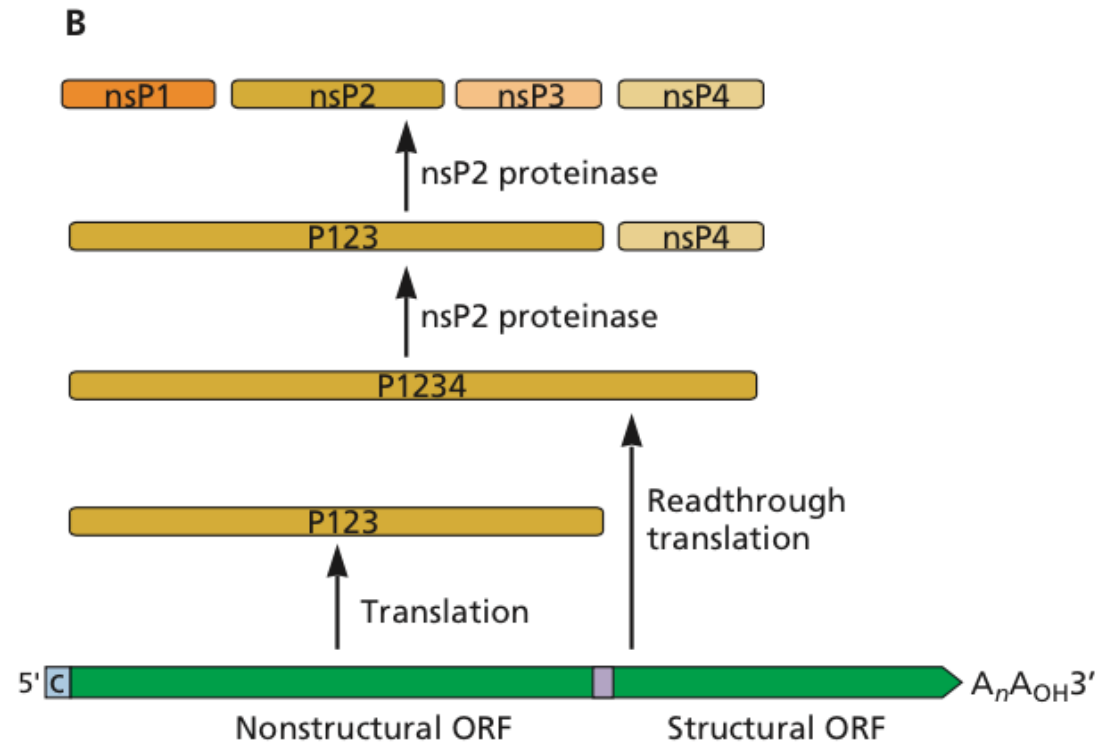
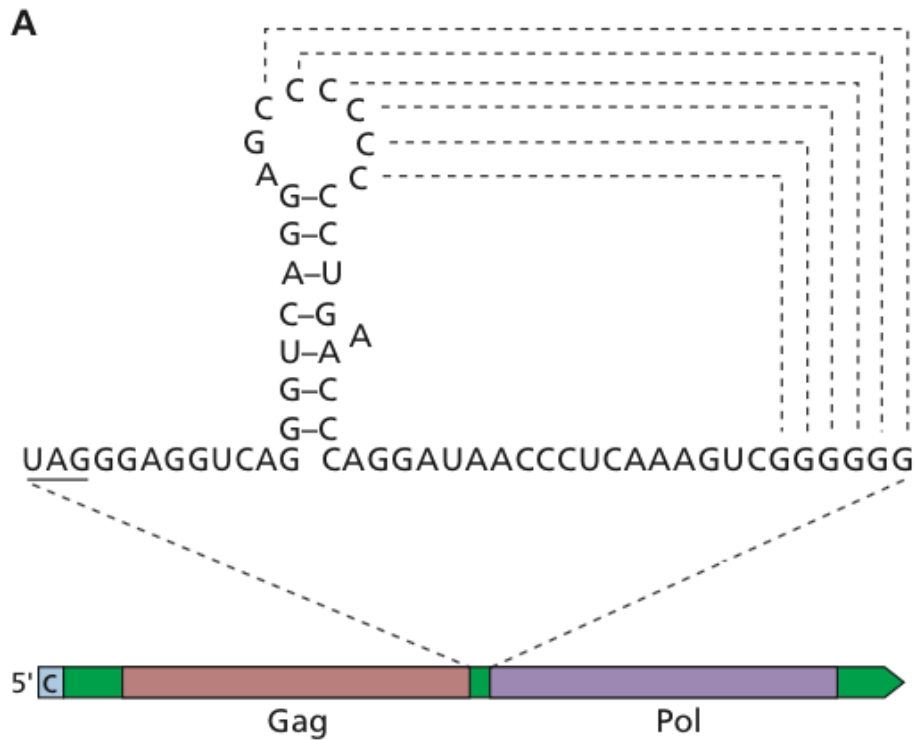
# Leaky scanning



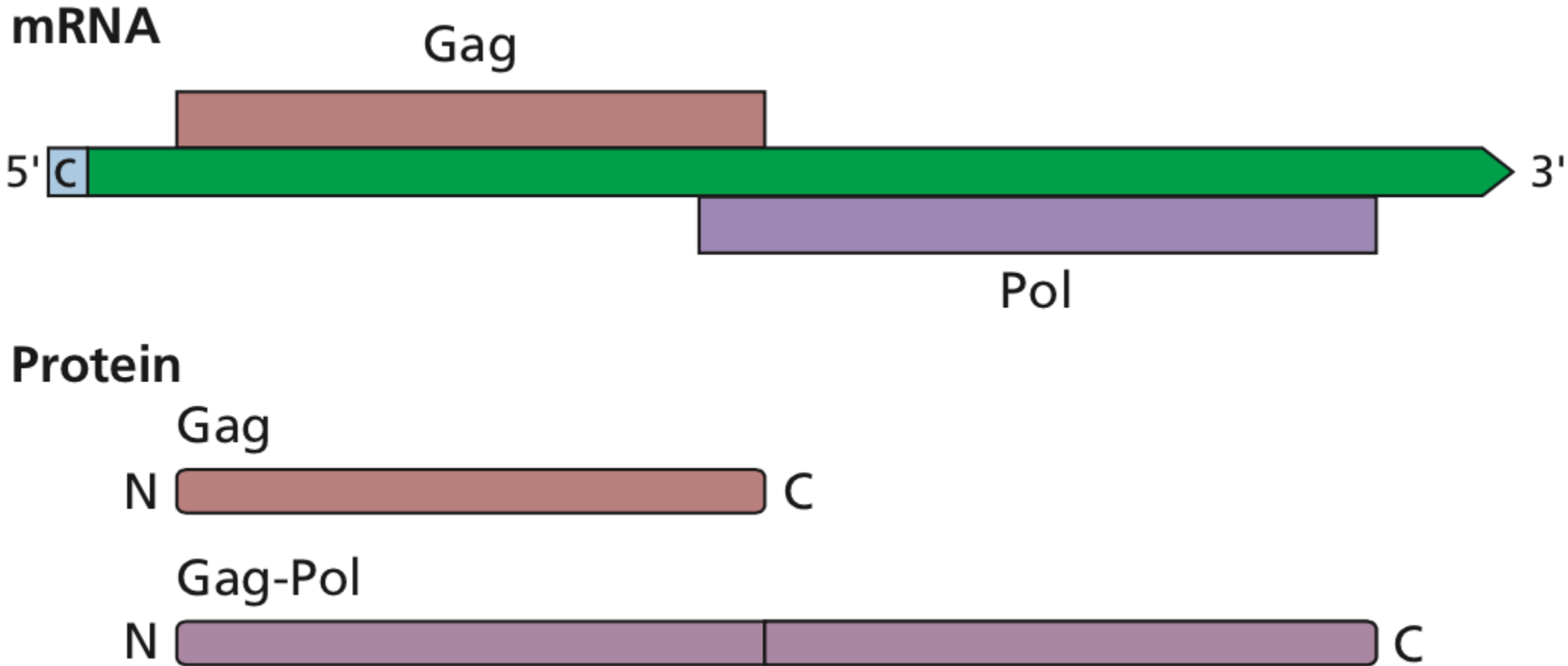


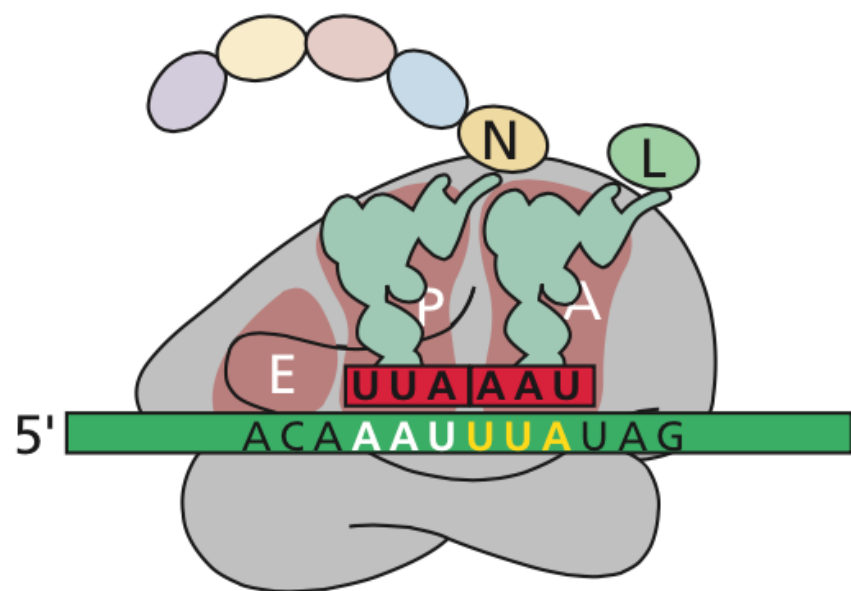
Stop codons may be recognized by charged tRNA - misreading, or charged suppressor tRNA (e.g. selenocysteine for UGA)

# Suppression of termination

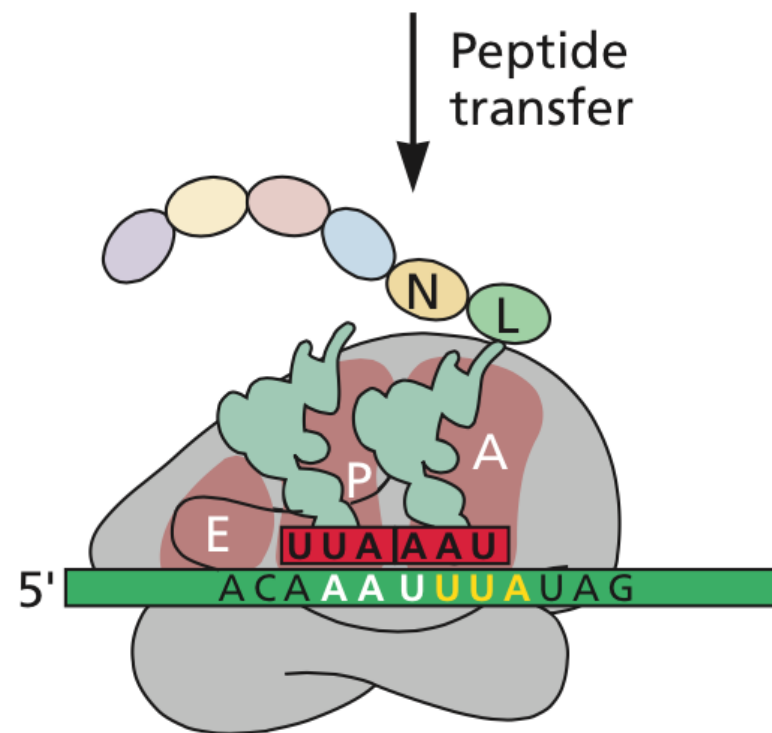
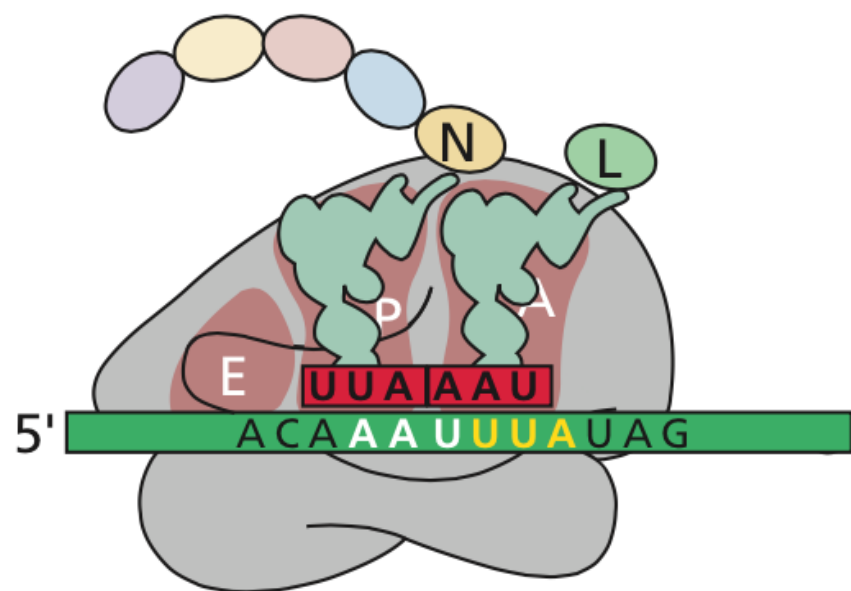


# Ribosomal frameshifting

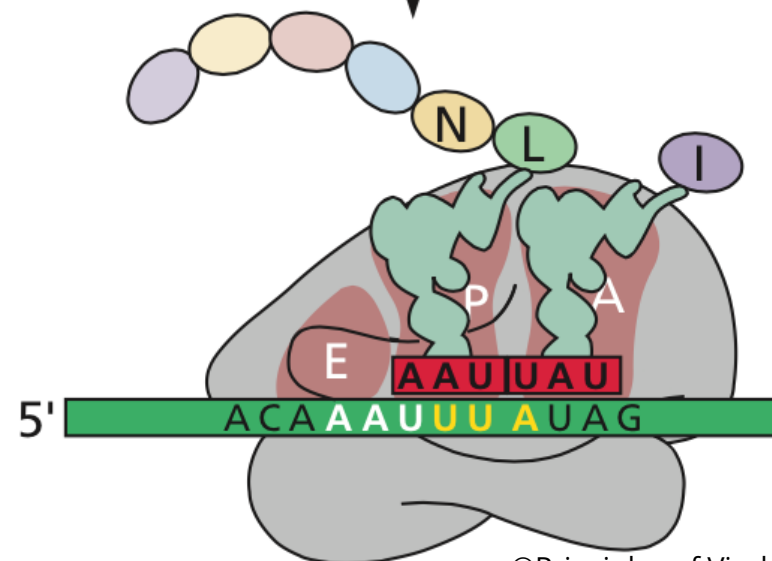




tRNA slippage



First -1  
frame tRNA



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**Compared with a polycistronic mRNA, a monocistronic mRNA:**

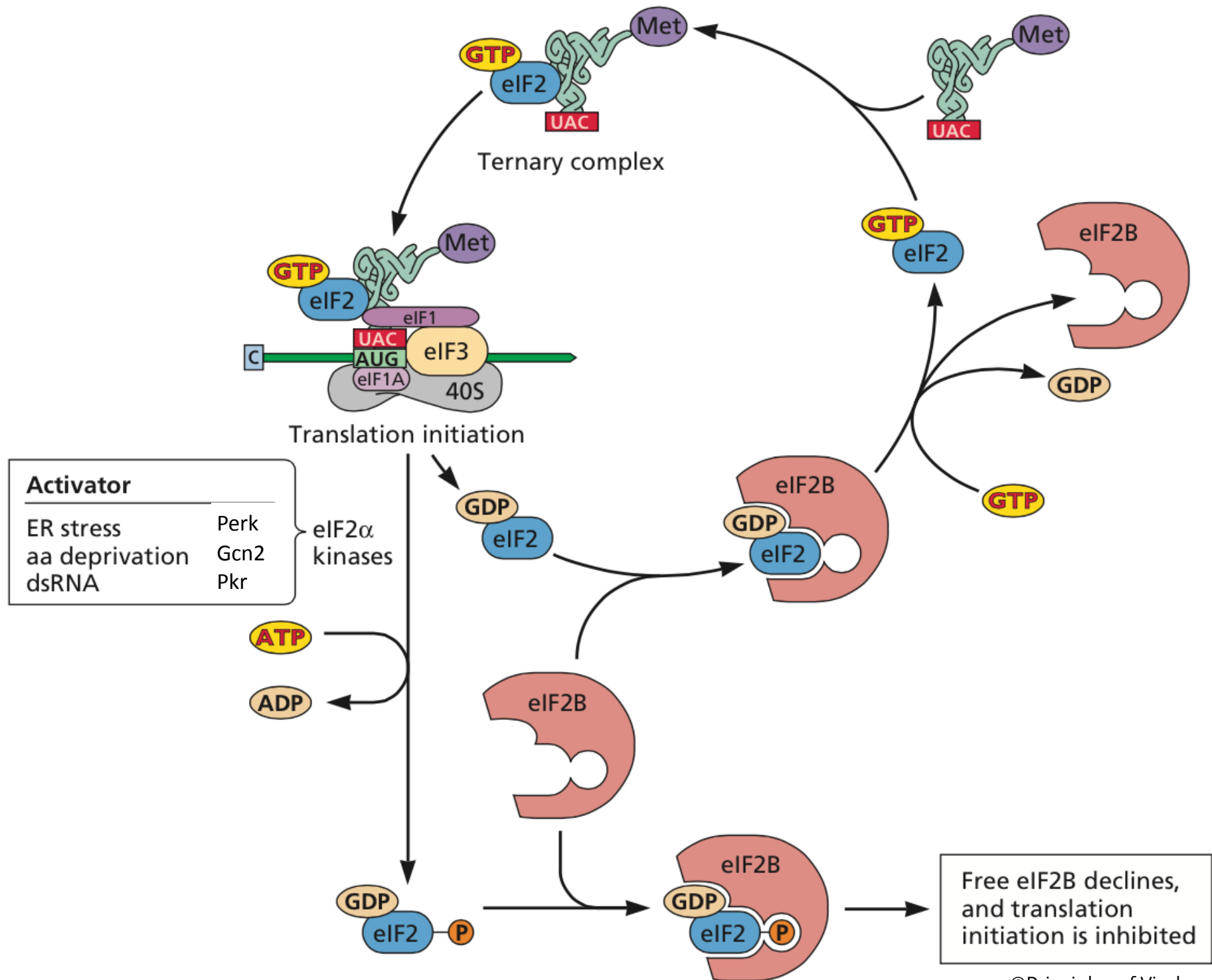
1. Does not require an AUG start codon
2. Does not bind the 40S ribosomal subunit
3. Has only one open reading frame
4. Is only found in viruses and bacteria
5. All of the above

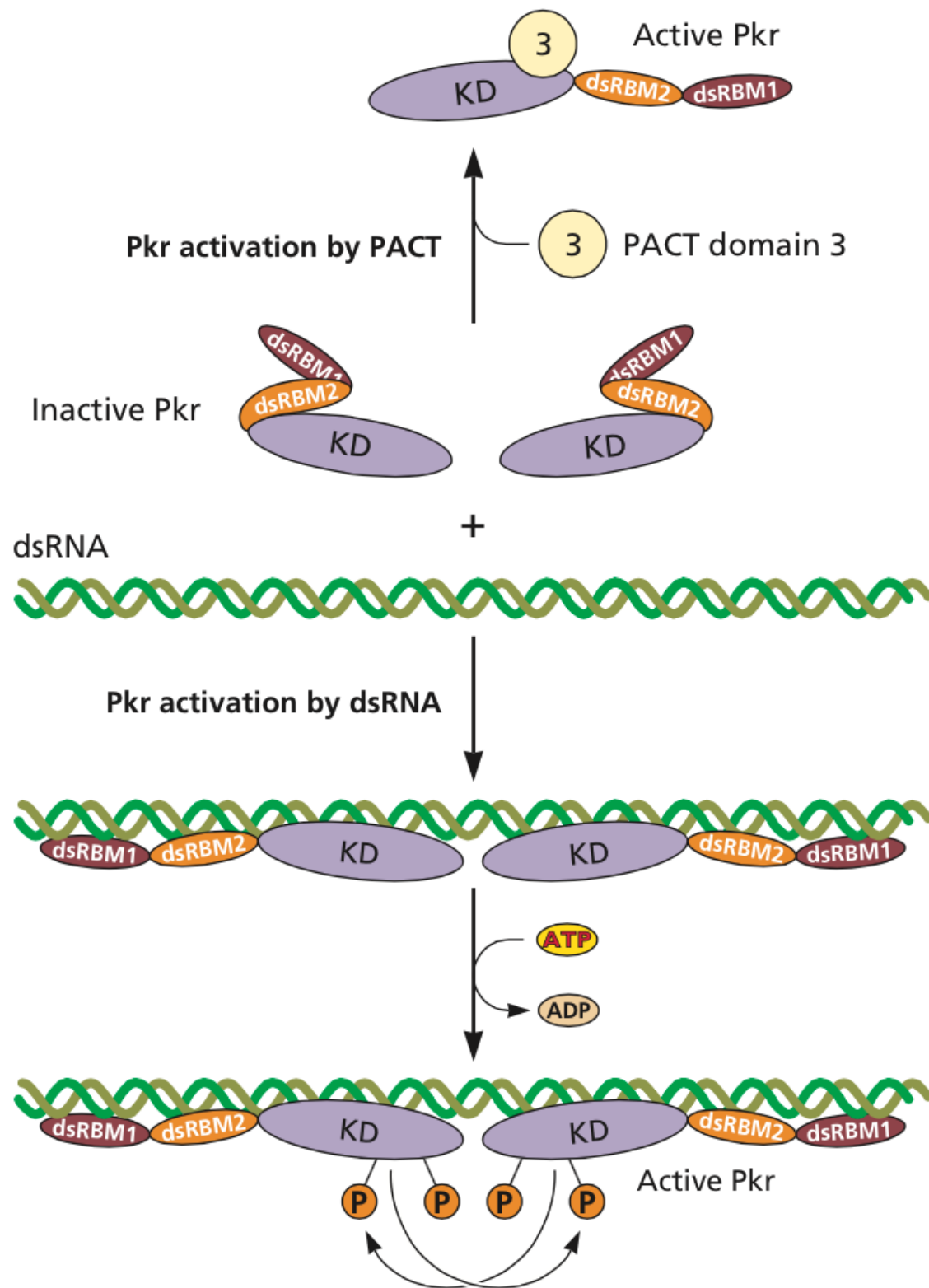
# Regulation of translation in virus-infected cells

- Initiation
- Elongation
- Termination

	Viruses	Viral functions	Effects on target
eIF4E	Caliciviruses and TMV	VPg	Binds eIF4E and recruits factors to viral mRNA
	Enteroviruses	Unknown	Induces host miR-141 and suppresses eIF4E mRNA translation
4EBP1	VSV	M protein	Dephosphorylate 4EBP1 (via inactivation of AKT-mTOR)
	Reoviruses	p17	
	SV40	Small t antigen	Dephosphorylates 4EBP1 (PP2A dependent)
	HSV-1	US3	Phosphorylate 4EBP1 (via TSC2 inactivation)
	HCMV	UL38	
	KSHV	v-GPCR	Phosphorylate 4EBP1 (via PI3K-AKT-mTOR pathway activation)
	EBV	LMP2A	
	Adenoviruses	E4 ORF1 and E4 ORF4	
	HCV	NS5A	Phosphorylates 4EBP1 (via FKBP38 binding to activate mTOR)
	HPV	E6	Phosphorylates 4EBP1 (via PDK1 activation and TSC2 degradation)
eIF4G	Enteroviruses	2A protease	Cleave eIF4G
	Caliciviruses	3C protease	
	Retroviruses	Protease	
	FMDV	Leader protease	
	Influenza viruses	Polymerase NS1	Binds eIF4G and promotes viral-mRNA translation
	Adenoviruses	100K	Binds eIF4G, dephosphorylates eIF4E (via competitive displacement of MNK1) and promotes ribosome shunting on viral mRNAs
	Rotaviruses	NSP3	Binds eIF4G and competitively displaces PABP
	HSV-1	ICP6	Binds eIF4G and increases its interaction with eIF4E
	Enteroviruses	IRES	Interacts with eIF4G to recruit the 40S ribosomal subunit
eIF4A	HSV-1	vhs	Binds eIF4A and either eIF4H or eIF4B, and this targets vhs endoribonuclease activity to mRNAs, accelerating mRNA turnover
	HCMV	UL69	Binds eIF4A (consequence unknown)
eIF5B	Enteroviruses	3C protease	Cleaves eIF5B
PABP	Enteroviruses	3C and 2A proteases	Cleave PABP
	Caliciviruses	3C-like protease	
	Lentiviruses	Protease	
	Rubella virus	Capsid	Binds PABP and suppresses translation
	Influenza viruses	NS1	Binds PABP (consequence unknown)
	HSV-1	ICP27	Binds PABP and stimulates translation of a viral mRNA subset
		ICP27 and UL47	Cause nuclear PABP accumulation
	HCMV	UL69	Binds PABP (consequence unknown)
	KSHV	SOX and K10	Bind PABP and causes its nuclear accumulation
	Bunyaviruses	NS5 protein	Causes nuclear PABP accumulation
eIF3	Rotaviruses	NSP3	Displaces PABP from eIF4G, and interacts with RoXaN to cause nuclear PABP accumulation
	Measles virus	N protein	Binds eIF3g and impairs translation
	Rabies virus	M protein	Binds eIF3h and impairs translation
	SARS CoV and IBV	Spike protein	Binds eIF3f and impairs translation
	Caliciviruses (including noroviruses)	VPg	Binds eIF3 and recruits factors to viral mRNA
	CaMV	RISP	Binds eIF3a and eIF3c, binds the 60S ribosomal subunit L24 and recruits ribosomes for re-initiation
		TAV	Binds and activates TOR, and recruits RISP
	HCV, CSFV and HIV	IRES	Interacts with eIF3 and recruits translation machinery
eIF2	HSV-1	US11	Inhibits PKR
		gB	Inhibits PERK
		γ34.5	Regulates eIF2α phosphatase
	EBV	SM	Inhibits PKR
		EBER RNAs	Bind PKR and prevent its activation
	HCMV	TRS1 and IRS1	Bind dsRNA and prevent PKR activation
	KSHV	v-IRF2	Binds PKR and prevents its activation
	VacV	E3L	Binds dsRNA and PKR
		K3L	Acts as a pseudosubstrate for PKR and PERK
	Adenoviruses	VA RNA	Binds PKR and prevents its activation
	ASFV	DP17L	Dephosphorylates eIF2α by recruiting PP2A
	HCV	NS5A	Inhibits PKR
		E2	Acts as a pseudosubstrate for PKR and PERK
		IRES	Inhibits PKR
	Influenza viruses	NS1	Sequesters dsRNA and prevents PKR activation
	Reoviruses	σ3	
	HPV	E6	Binds GADD34-PP1α to dephosphorylate eIF2α
eEF1A and eEF1B	TMV	VPg	Binds eEF1A so that it is redistributed to viral replication compartments
	SARS CoV	N protein	Binds eEF1A and impairs translation
	HIV-1	Gag	Binds eEF1A and impairs viral mRNA translation to stimulate packaging
	HSV-1	UL13	Phosphorylate eEF1Bα
	HCMV	UL97	
	EBV	BGLF4	
eRF1	HIV-1	Reverse transcriptase	Binds eRF1, modulates termination and re-initiation, and protects viral mRNAs from nonsense-mediated decay
	HCMV	uORF2	Binds eRF1 and inhibits translation at its own stop codon to regulate translation of the downstream HCMV ORF
Ribosome	HCV, CSFV and HIV	IRES	Binds the 40S ribosome in conjunction with eIF3
	CrPV	IRES	Binds the 40S ribosome to mediate initiation factor-independent translation
	FCV and Influenza B virus	TURBS	Base-pairs with 18S ribosomal RNA to promote re-initiation
	KSHV	ORF57	Binds PYM to recruit 40S ribosomes to viral mRNAs



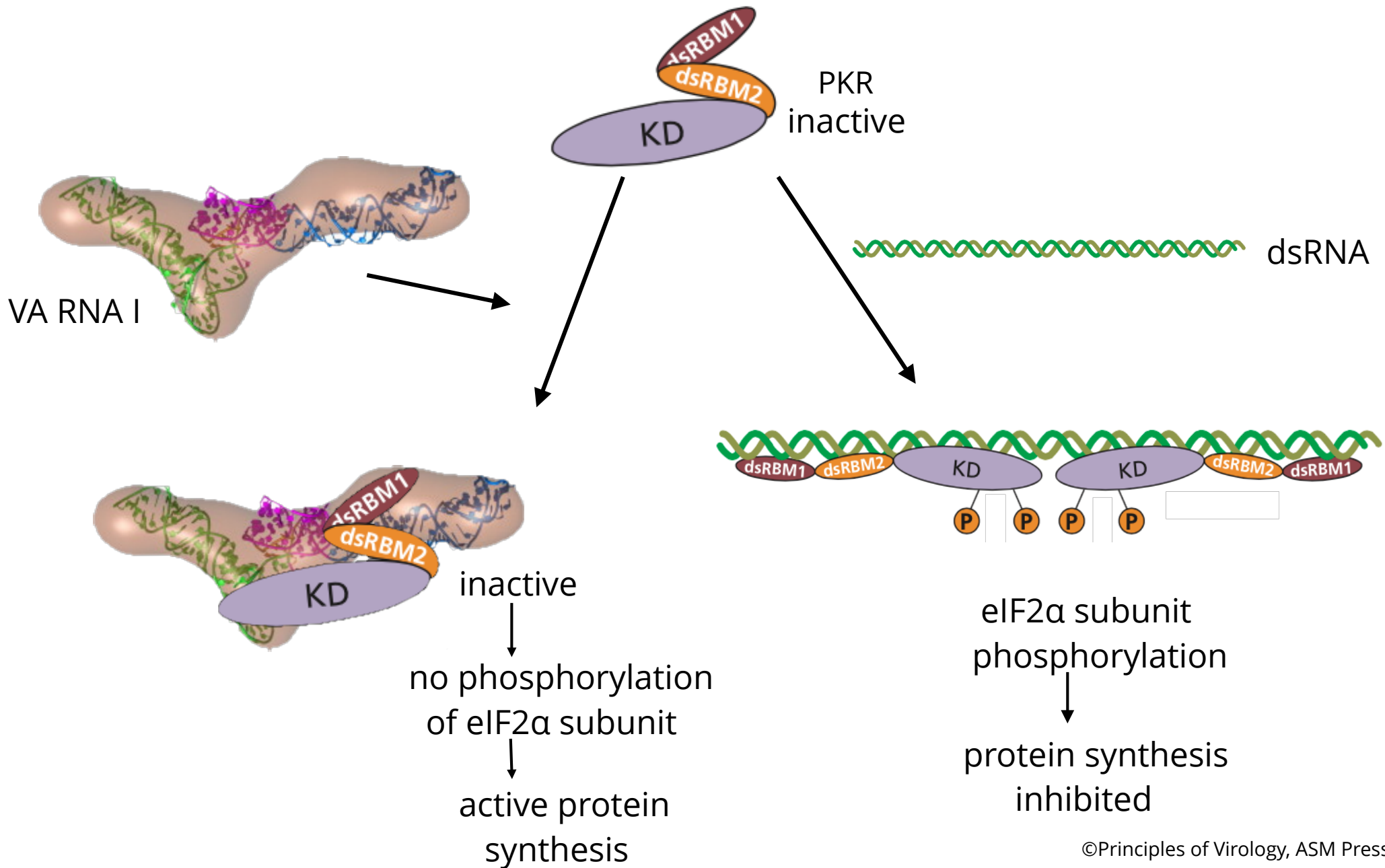




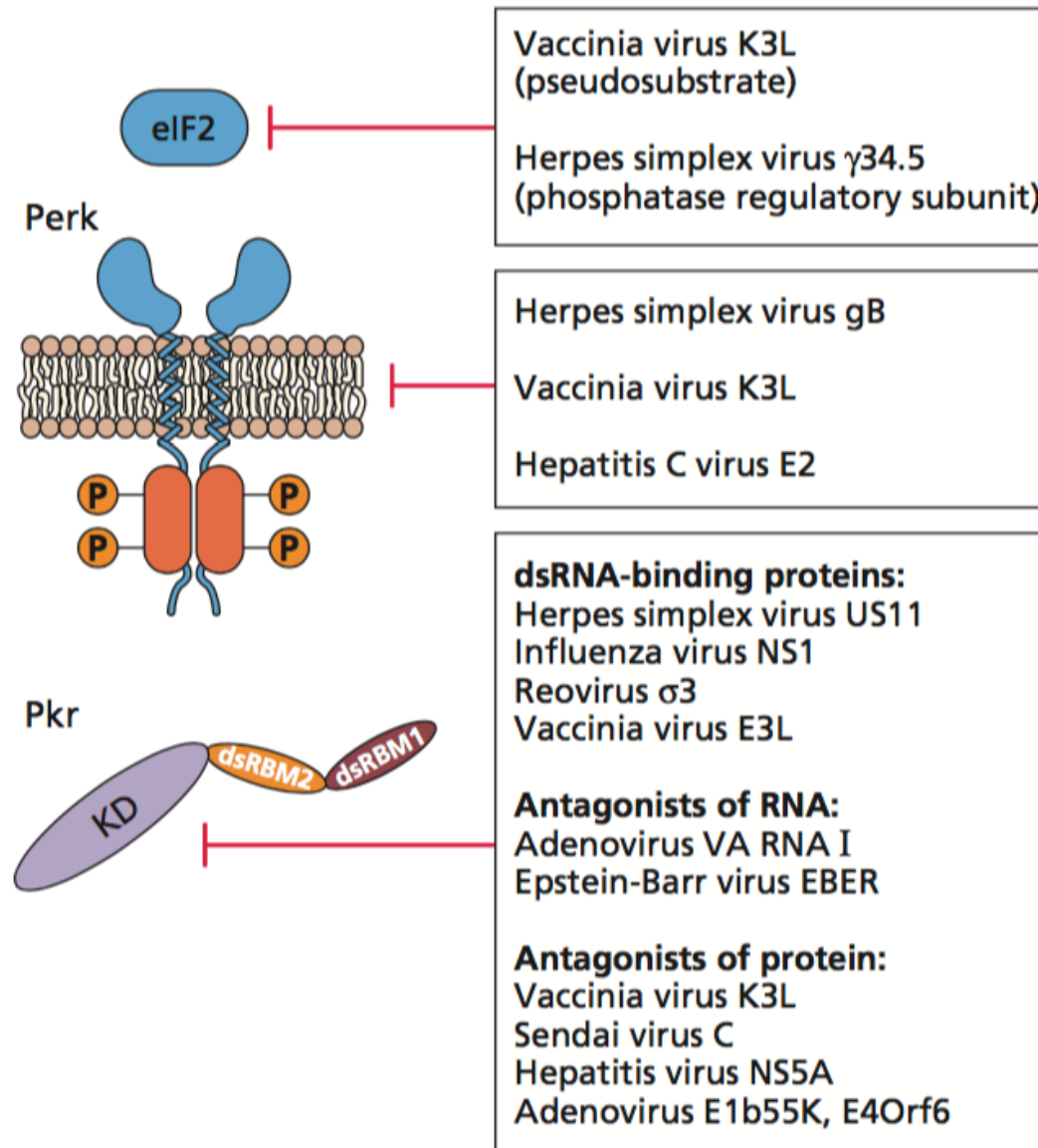
# PKR and cellular antiviral response

- PKR induced and activated by virus infection
- Leads to inhibition of host translation, apoptosis
- Different viral mechanisms have evolved to inactivate the PKR pathway

# Adenovirus VA RNA I prevents activation of PKR



# Viral proteins and RNAs that counter inactivation of eIF2



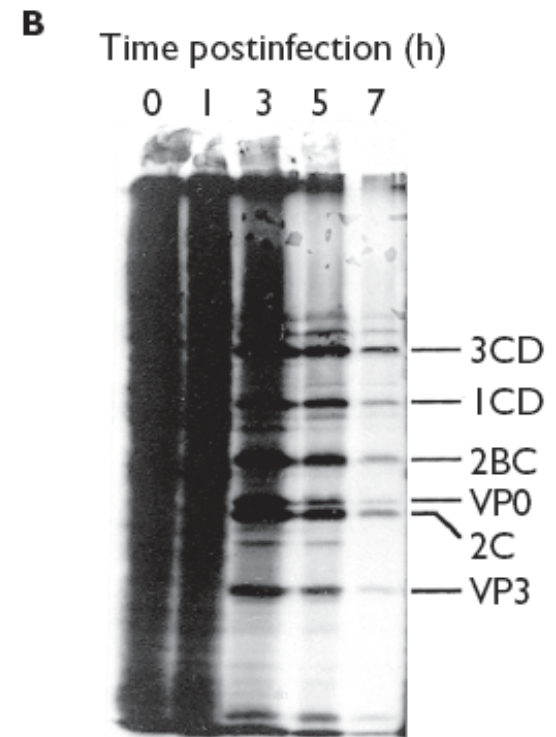
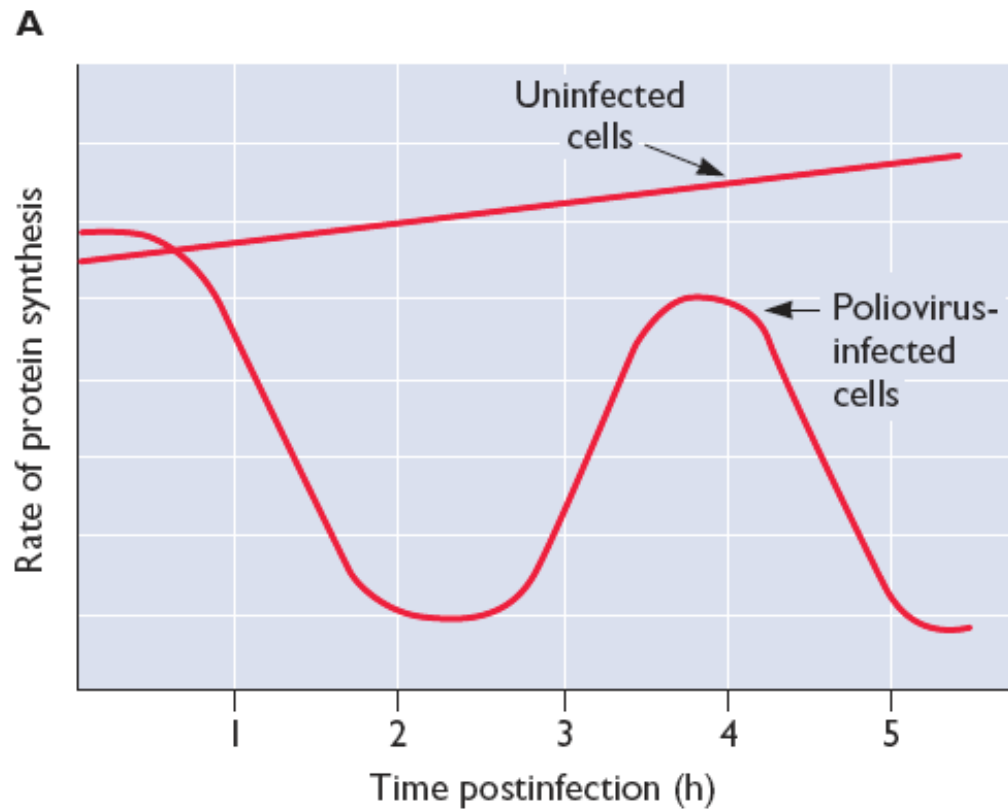
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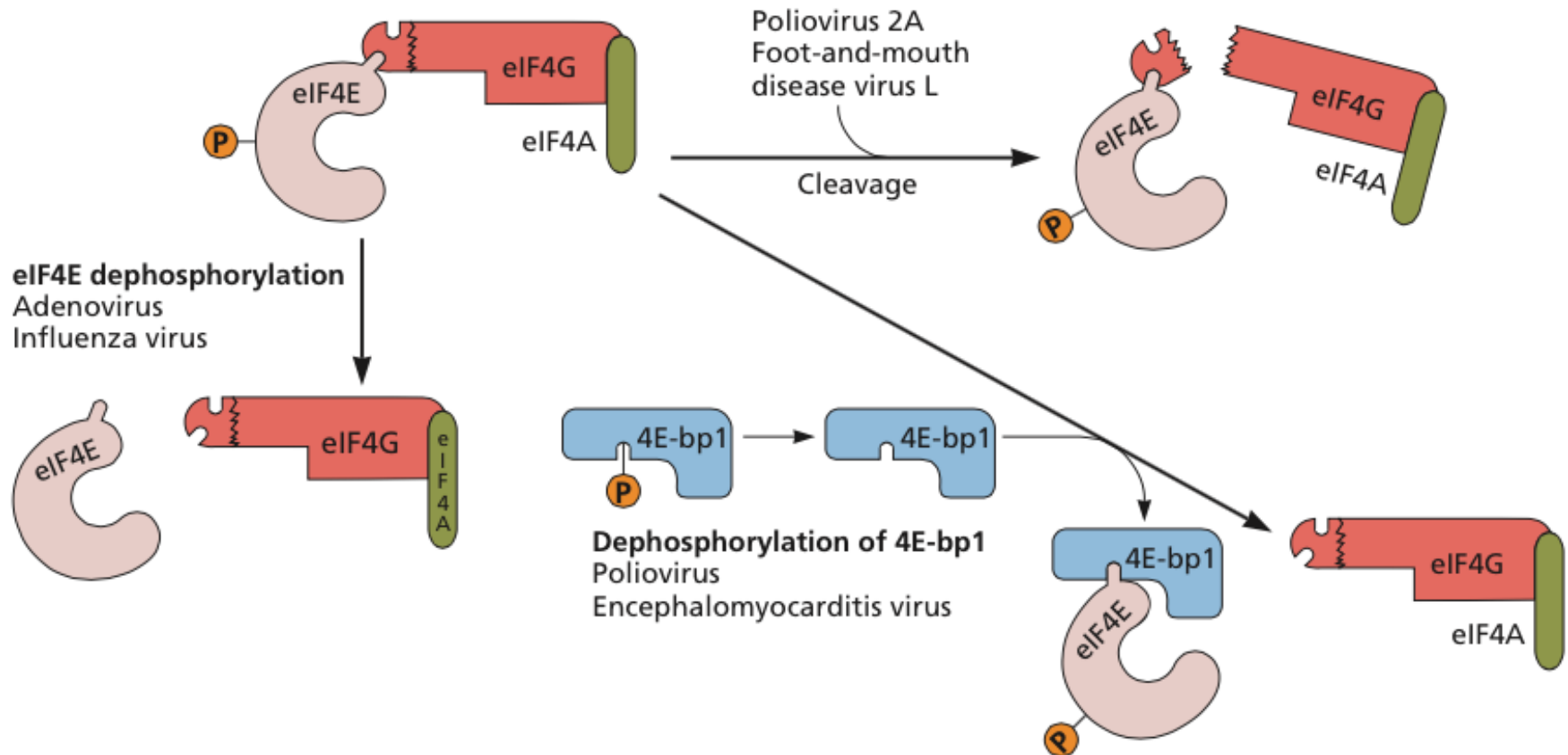
room number: virus

**PKR is an interferon-induced enzyme that is activated by \_\_\_\_, leading to phosphorylation of \_\_\_\_ and inhibition of translation.**

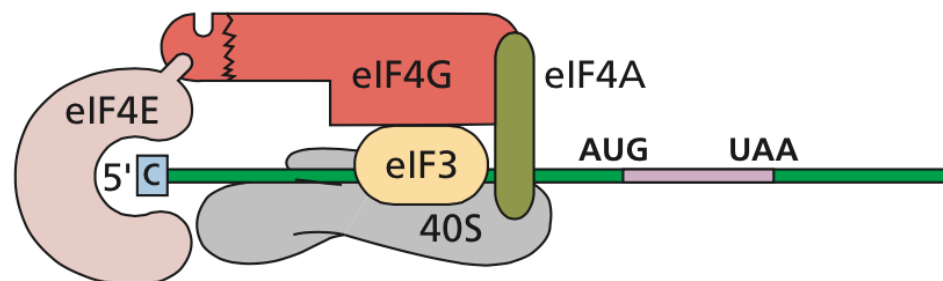
1. GDP, eIF2alpha
2. dsRNA, eIF2alpha
3. dsRNA, eIF2B
4. ssRNA, eIF2alpha
5. None of the above



# Modulation of cap recognition



## 5'-end-dependent initiation





# Stress granules

