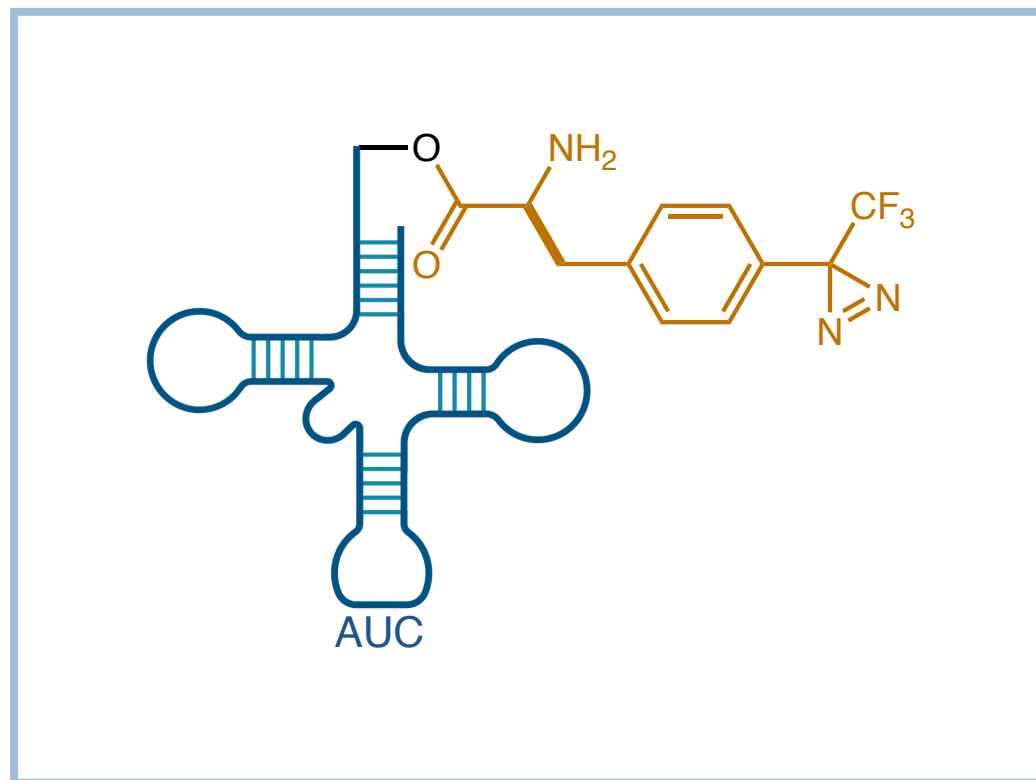


Genetic Code Expansion



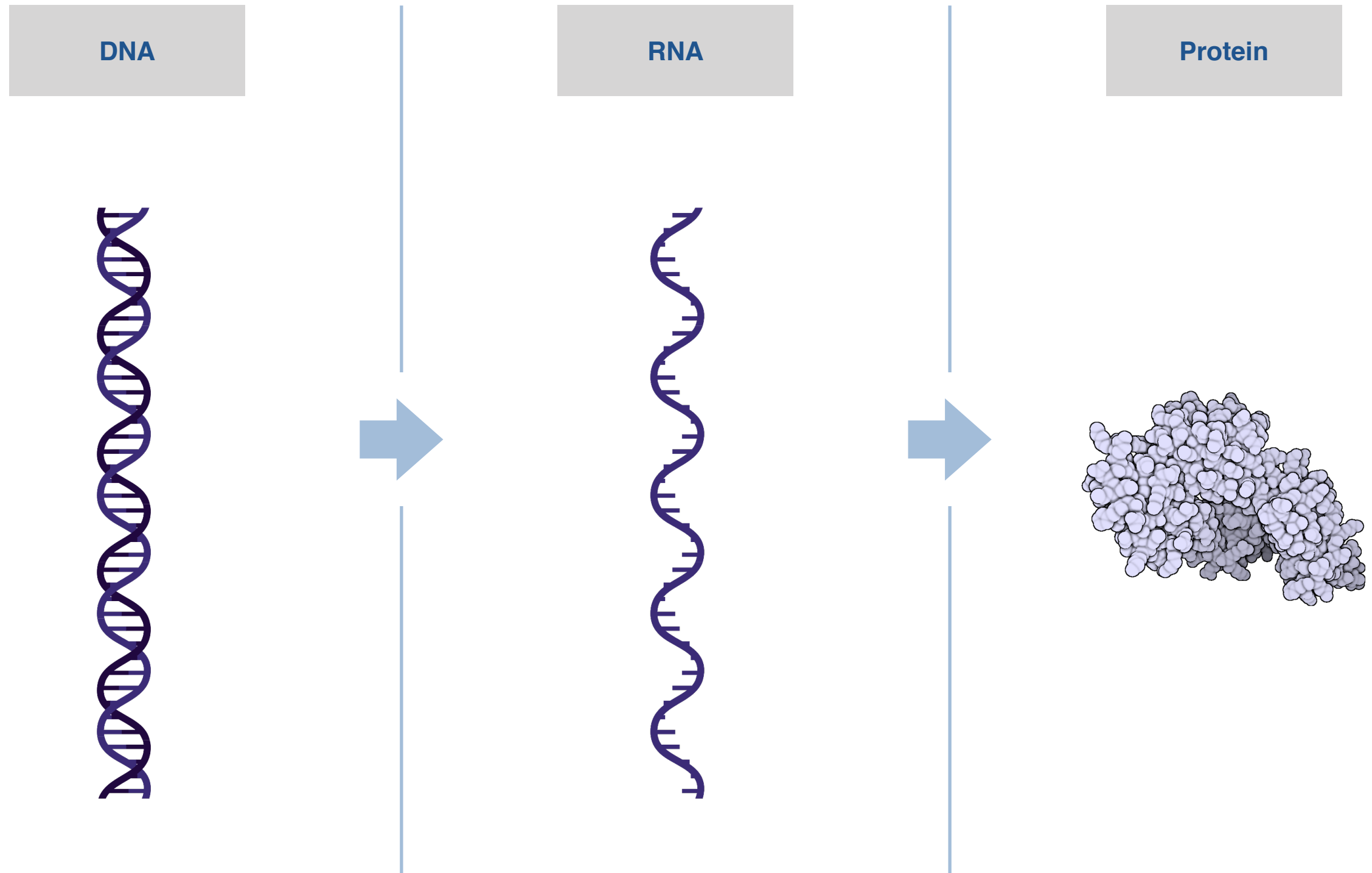
Benito Buksh

MacMillan Research Group

Group Meeting

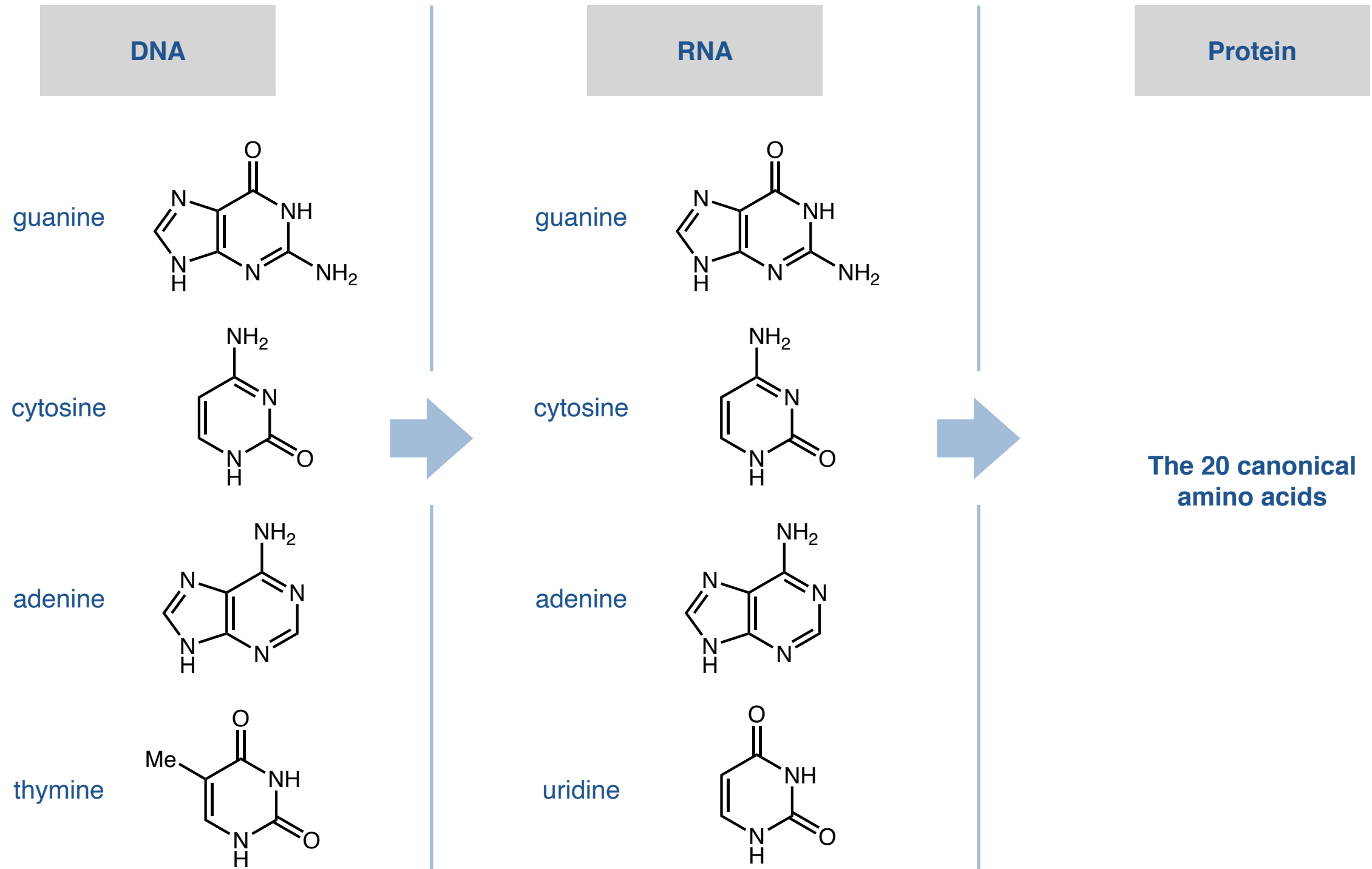
June 7th, 2022

The Central Dogma of Molecular Biology



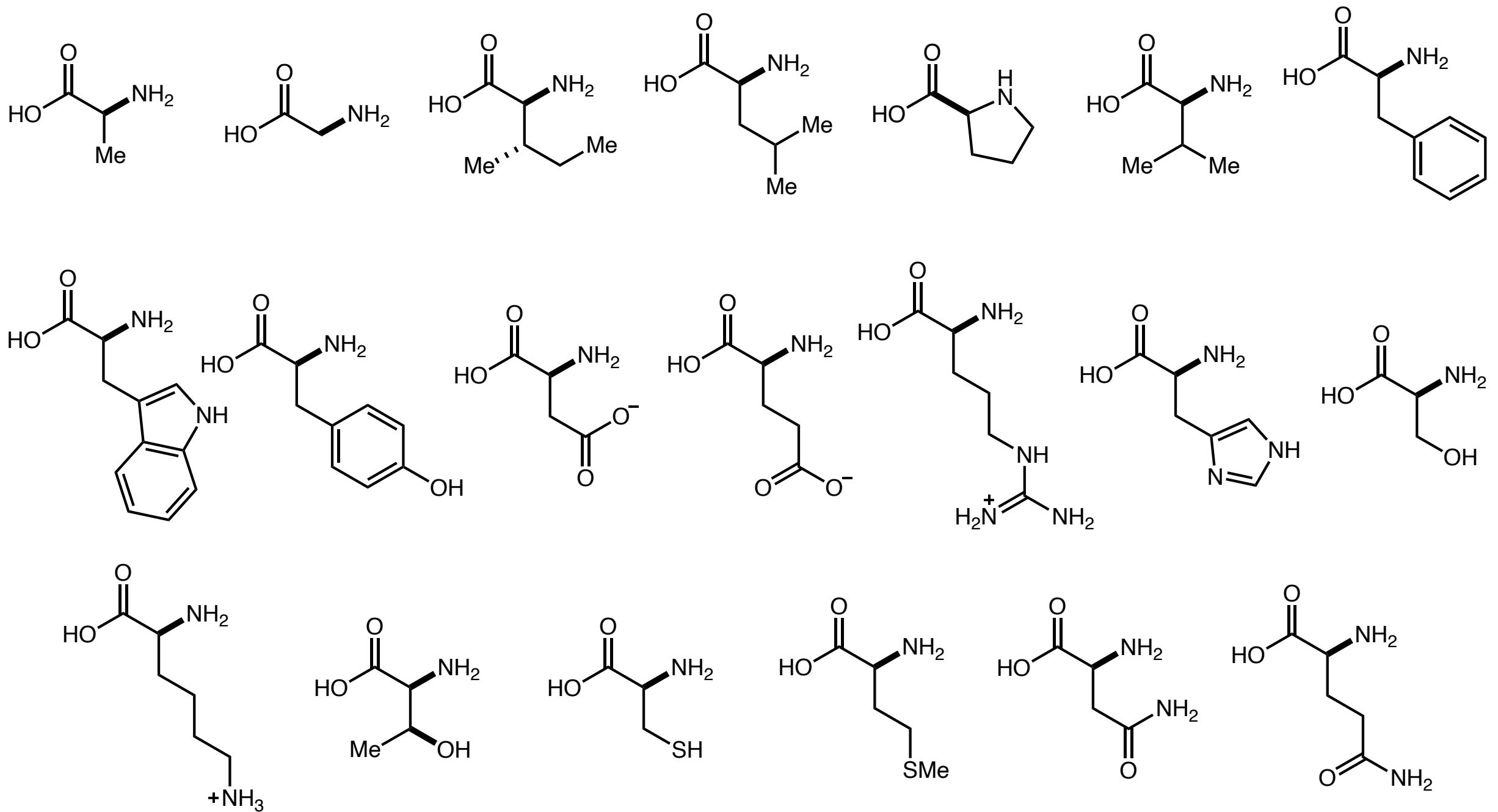
“DNA makes RNA makes protein”

The Central Dogma of Molecular Biology



“DNA makes RNA makes protein”

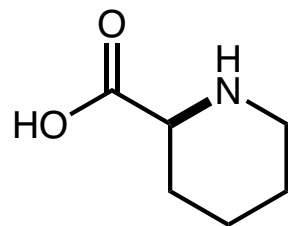
The 20 Canonical Amino Acids



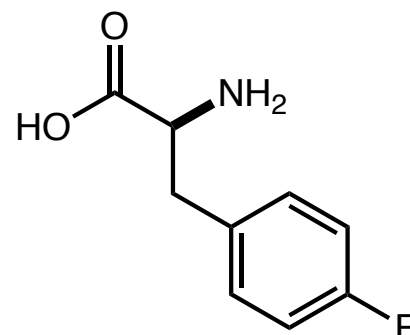
Outside of few exceptions, proteins are made up of the 20 canonical amino acids

Expanding the Genetic Code

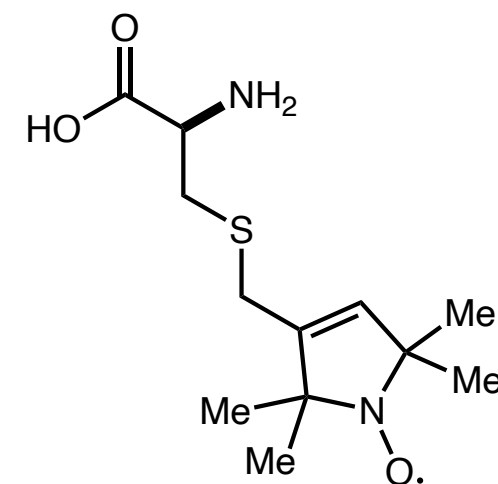
Synthetic organic chemistry allows us to make amino acids that are “noncanonical”



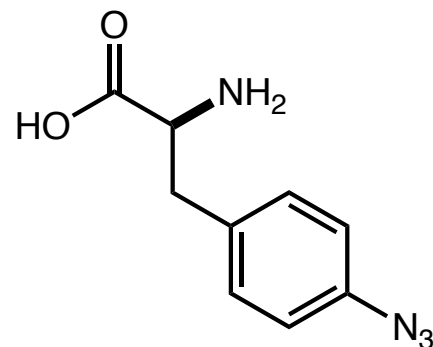
Proline analogue



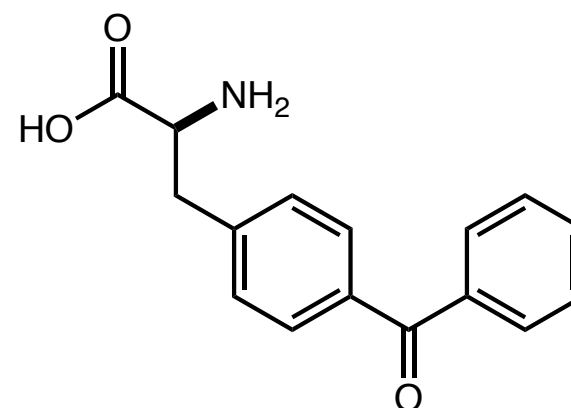
Tyrosine analogue



EPR probe



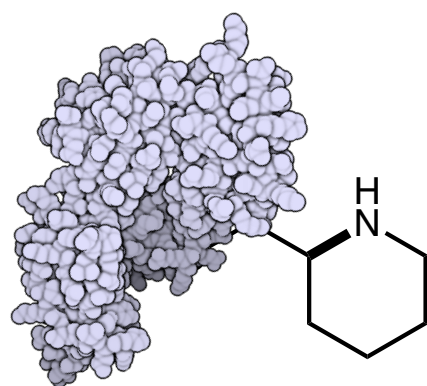
Bioorthogonal click handle



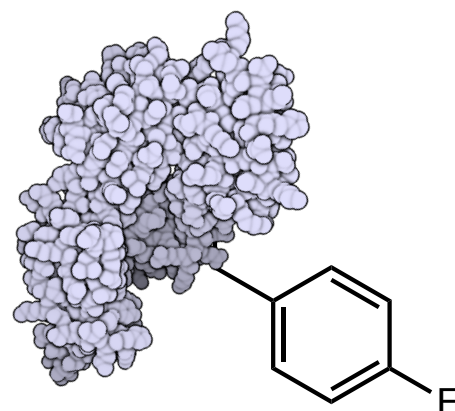
Photoaffinity label

Expanding the Genetic Code

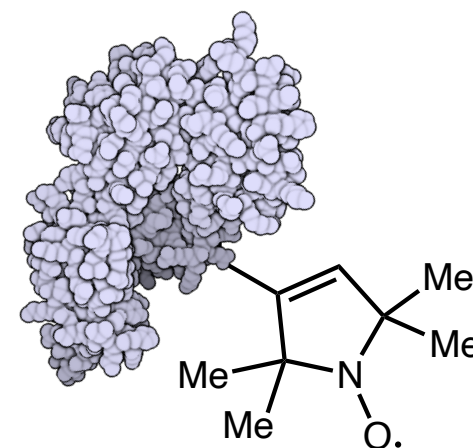
Synthetic organic chemistry allows us to make amino acids that are “noncanonical”



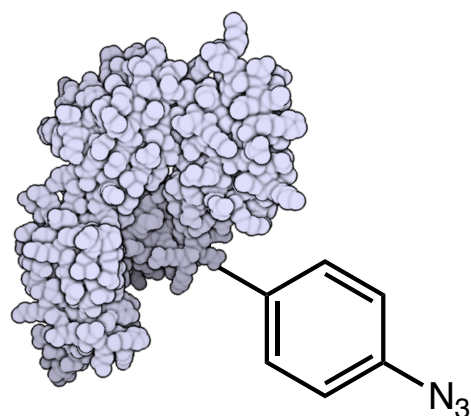
Proline analogue



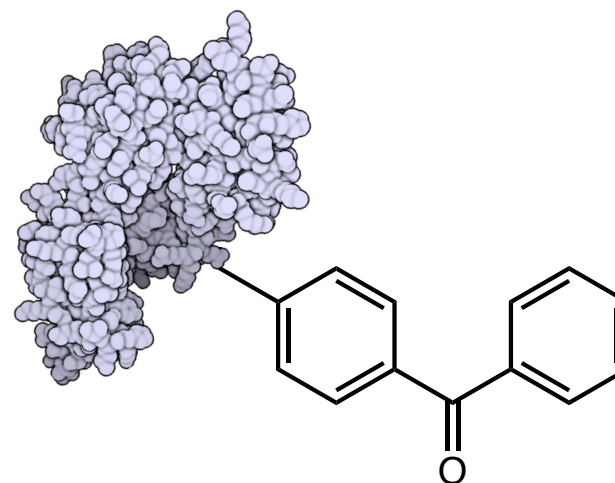
Tyrosine analogue



EPR probe



Bioorthogonal click handle

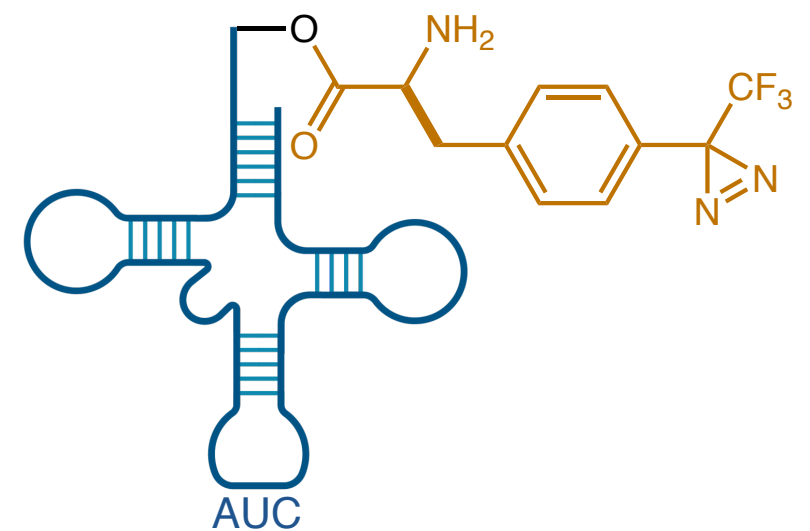


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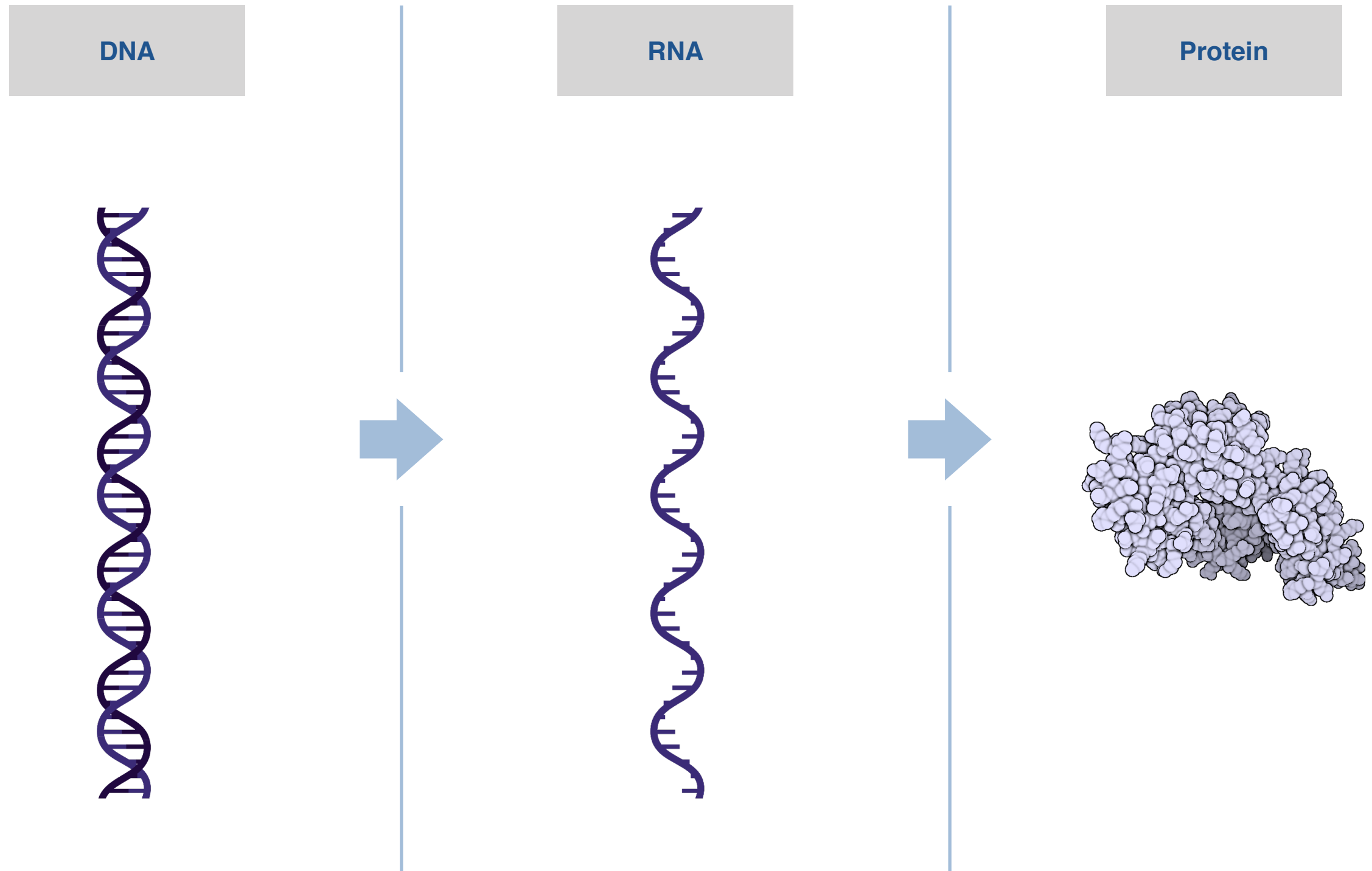
Is it possible to expand the genetic code to incorporate noncanonical amino acids into proteins?

Expanding the Genetic Code

- The traditional genetic code
- Expanding the genetic code
 - In vitro
 - In eukaryotes, prokaryotes, and mammalian cells
- Orthogonal ribosomes
- Genetically recoded organisms and synonymous codon compression
- Outlook



The Genetic Code



How does DNA / RNA sequence encode for protein sequence?

The Genetic Code

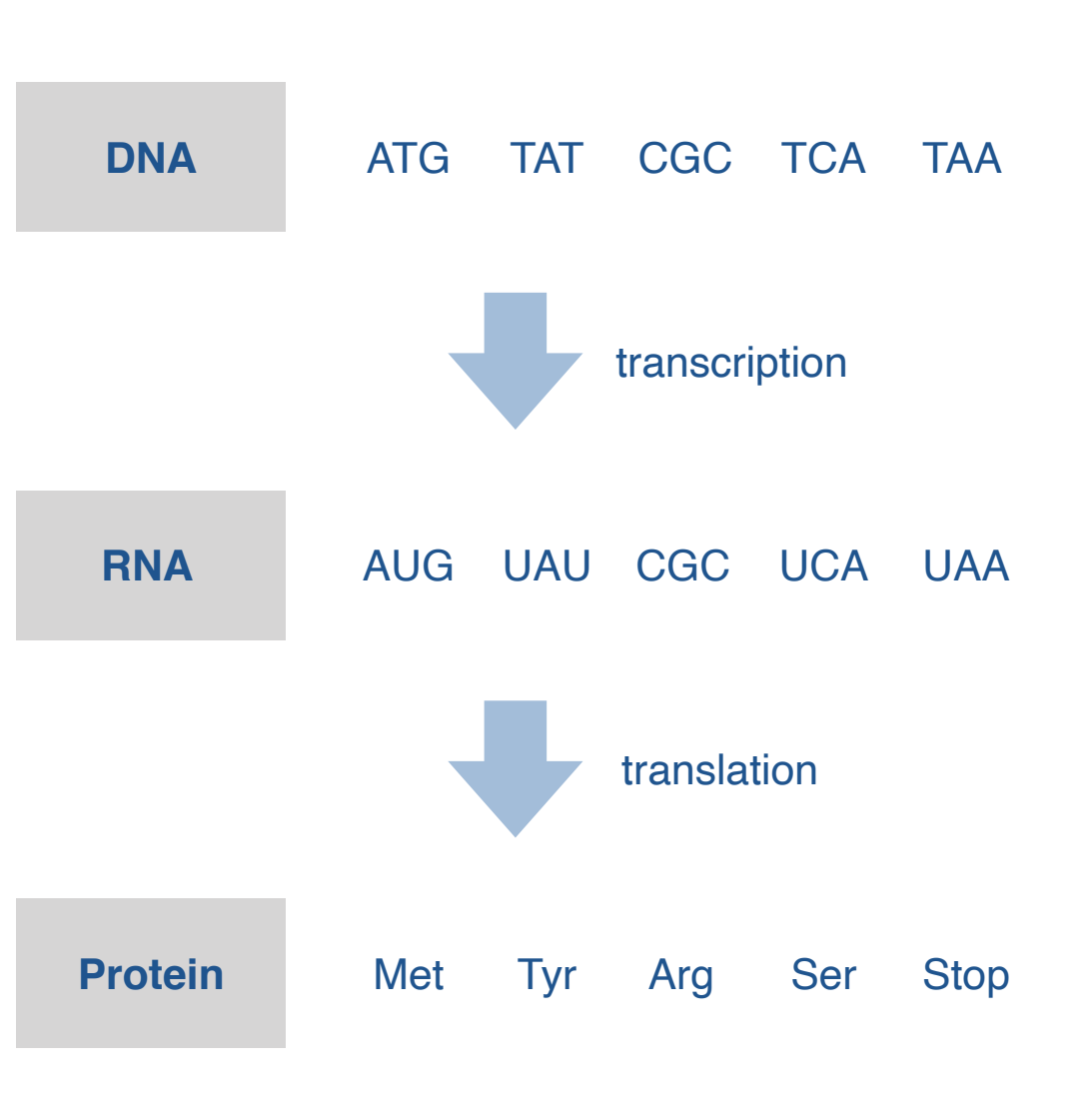
Codon: Sequence of three nucleotides

- 61 codons encode for amino acids
- 3 codons encode for stop codons

		Second Position				
		T	C	A	G	
First Position	T	TTT } Phe TTC } TTA } Leu TTG }	TCT } TCC } Ser TCA } TCG }	TAT } Tyr TAC } TAA STOP TAG STOP	TGT } Cys TGC } TGA STOP TGG Trp	T C A G
	C	CTT } CTC } Leu CTA } CTG }	CCT } CCC } Pro CCA } CCG }	CAT } His CAC } CAA } Gln CAG }	CGT } CGC } Arg CGA } CGG }	T C A G
	A	ATT } ATC } Ile ATA } ATG Met	ACT } ACC } Thr ACA } ACG }	AAT } Asn AAC } AAA } Lys AAG }	AGT } Ser AGC } AGA } Arg AGG }	T C A G
	G	GTT } GTC } Val GTA } GTG }	GCT } GCC } Ala GCA } GCG }	GAT } Asp GAC } GAA } Glu GAG }	GGT } GGC } Gly GGA } GGG }	T C A G

Codons specify which amino acid will be added during protein synthesis

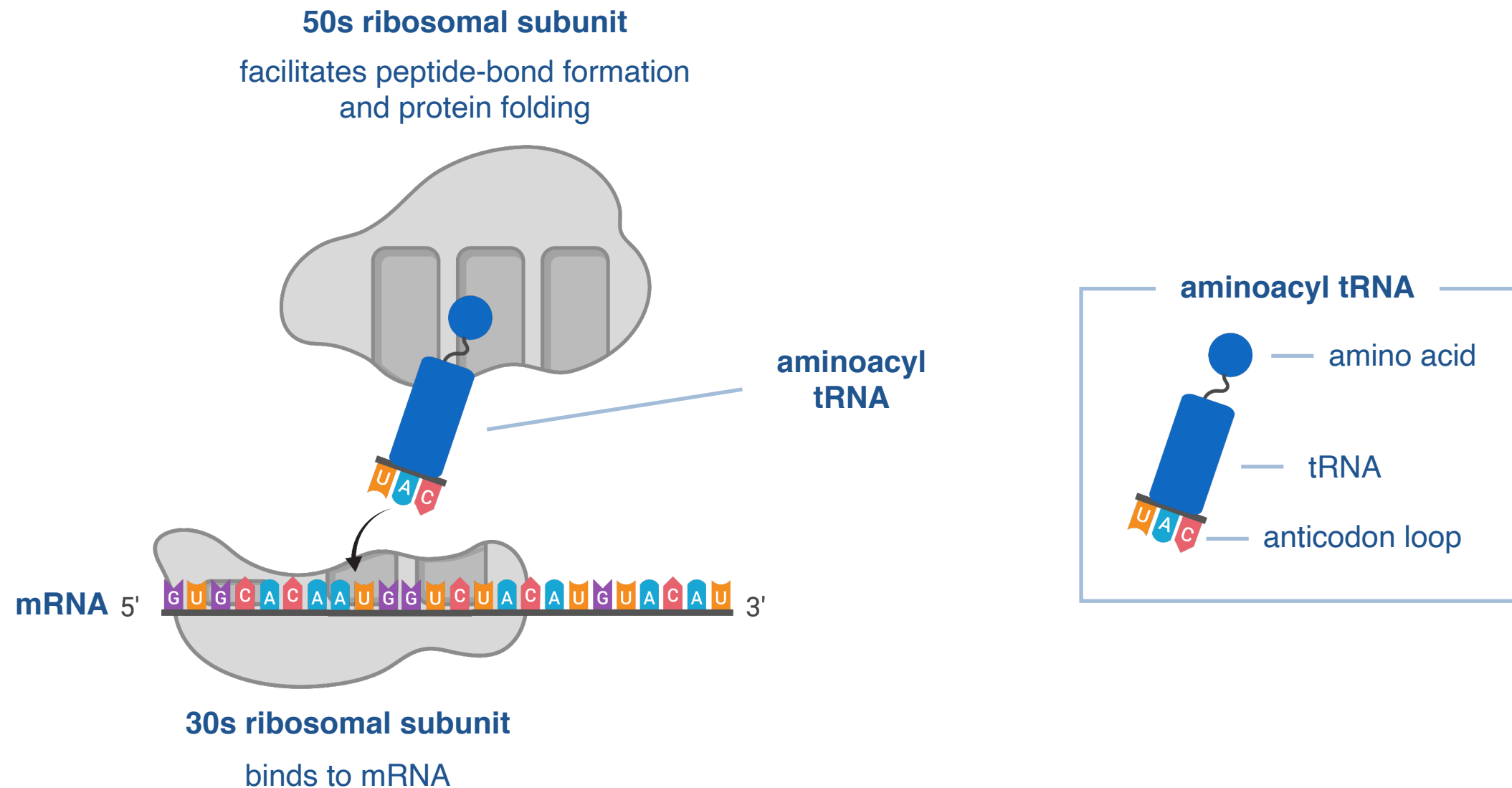
The Genetic Code



		Second Position				Third Position
		T	C	A	G	
First Position	T	TTT } Phe TTC } TTA } Leu TTG }	TCT } TCC } Ser TCA } TCG }	TAT } Tyr TAC } TAA STOP TAG STOP	TGT } Cys TGC } TGA STOP TGG Trp	
	C	CTT } CTC } Leu CTA } CTG }	CCT } CCC } Pro CCA } CCG }	CAT } His CAC } CAA } Gln CAG }	CGT } CGC } Arg CGA } CGG }	
	A	ATT } ATC } Ile ATA } ATG Met	ACT } ACC } Thr ACA } ACG }	AAT } Asn AAC } AAA } Lys AAG }	AGT } Ser AGC } AGA } Arg AGG }	
	G	GTT } GTC } Val GTA } GTG }	GCT } GCC } Ala GCA } GCG }	GAT } Asp GAC } GAA } Glu GAG }	GGT } GGC } Gly GGA } GGG }	

Codons specify which amino acid will be added during protein synthesis

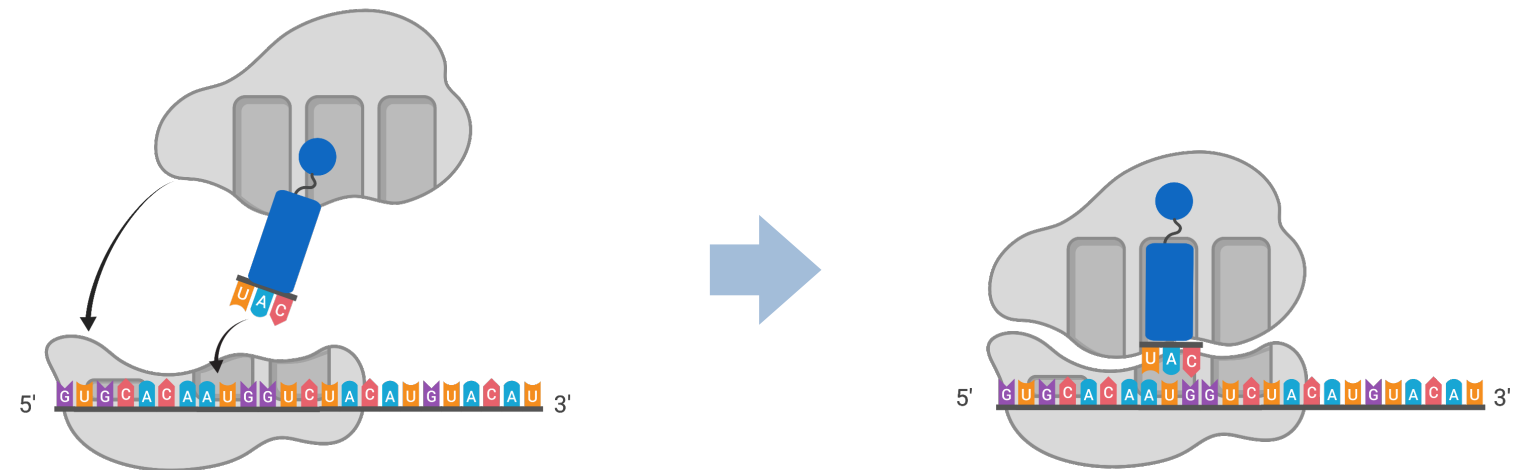
Translation of RNA to Protein via the Ribosome



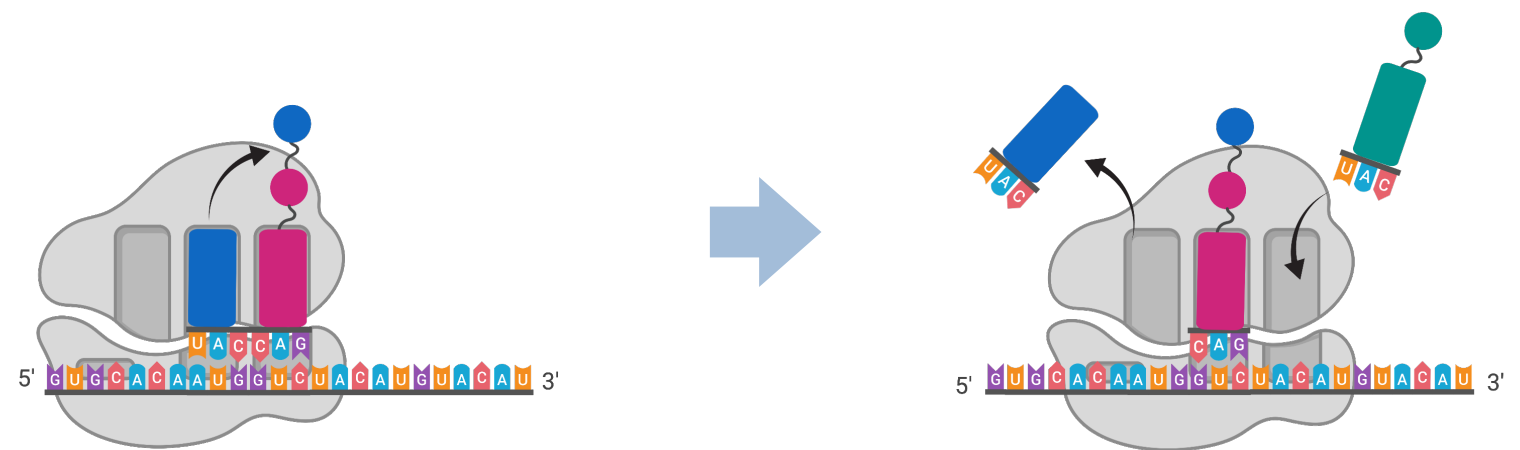
Aminoacyl tRNA charged with an amino acid through its anticodon loop binds to a complementary codon

Translation of RNA to Protein via the Ribosome

1. Initiation



2. Elongation



3. Termination

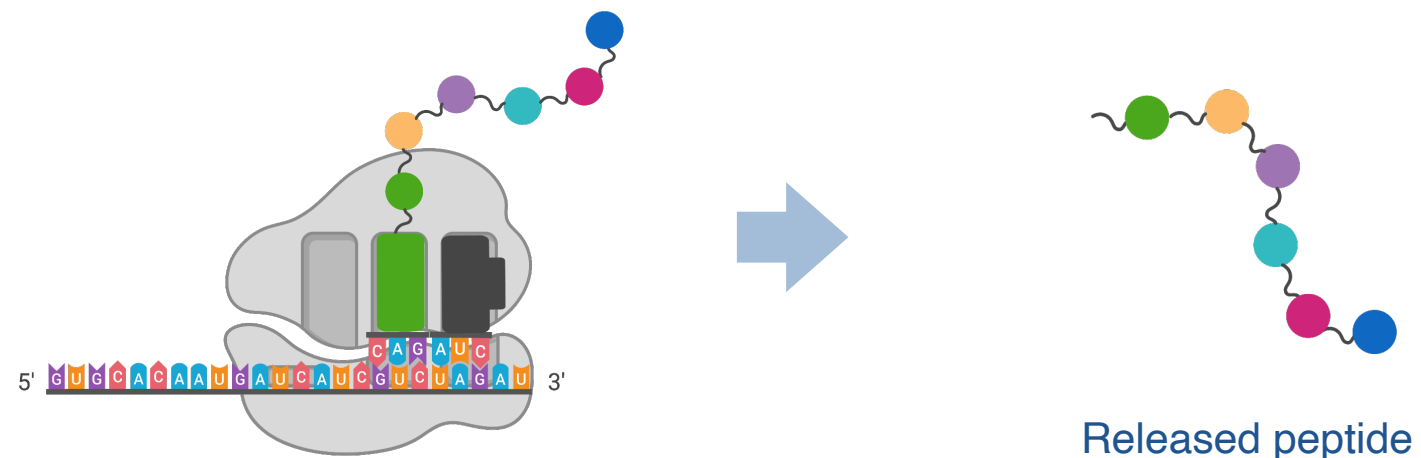
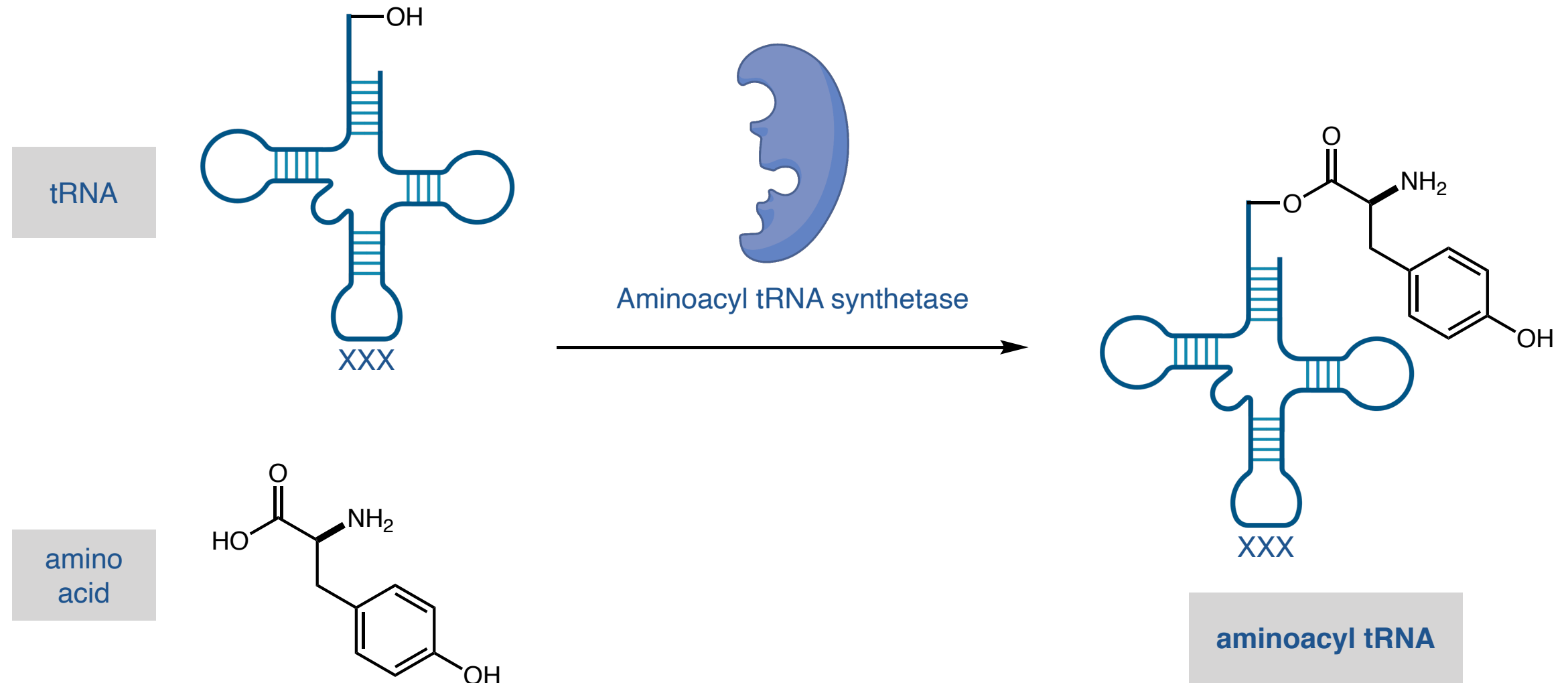


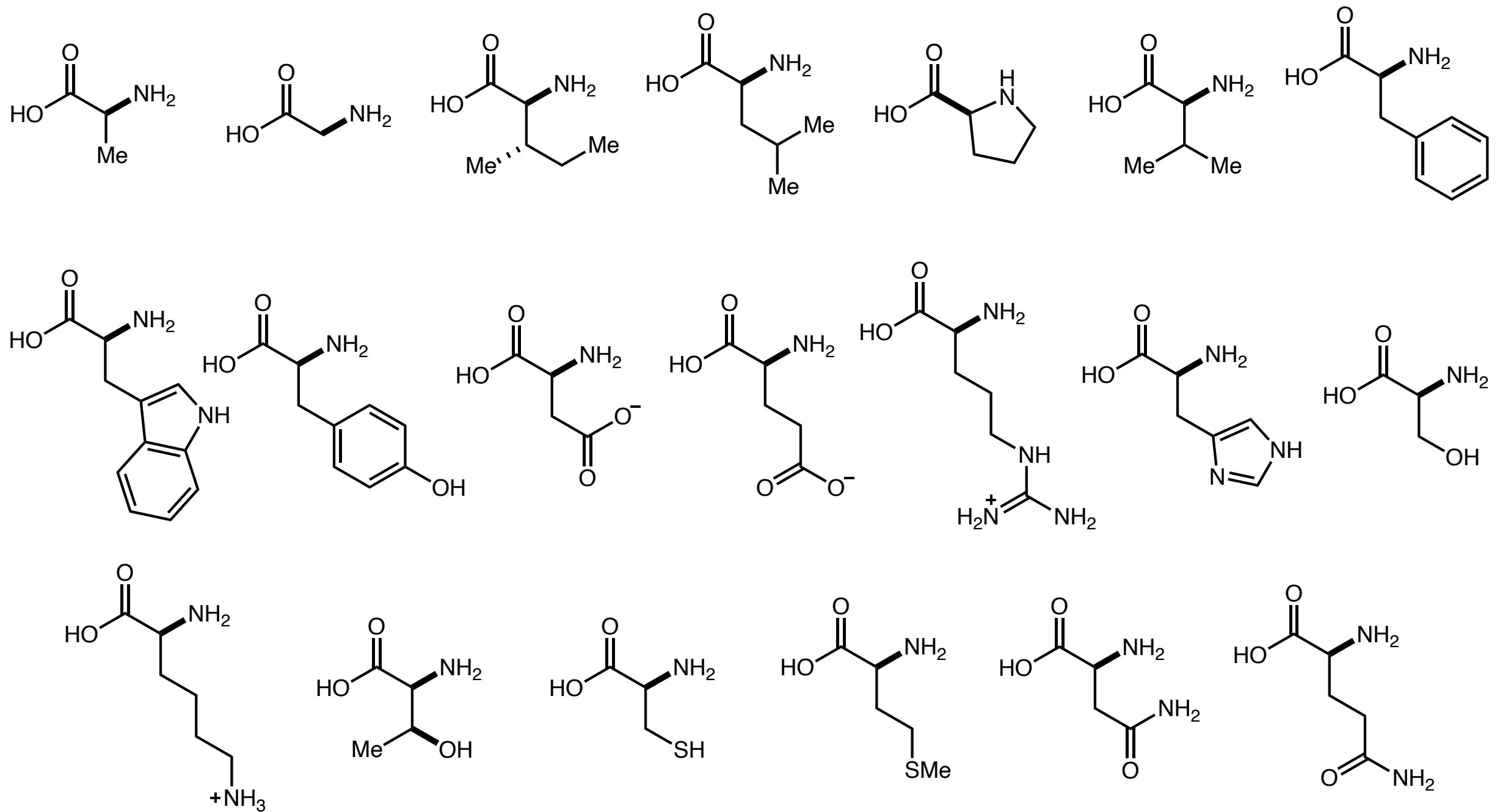
Image source: Biorender

Production of Aminoacylated tRNAs

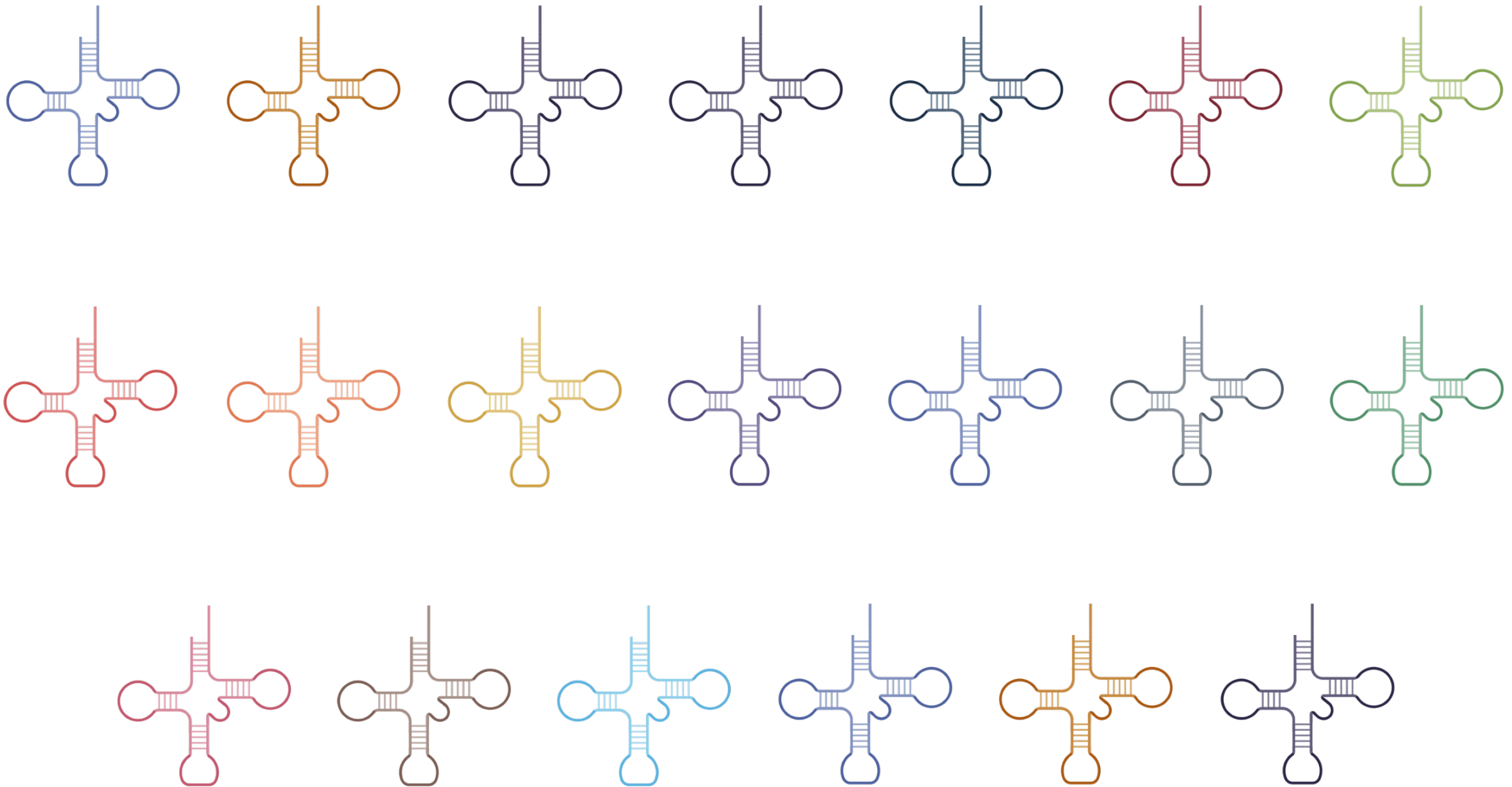


The aminoacyl tRNA synthetase is responsible for “charging” the tRNA with amino acid to form an aminoacyl tRNA

Production of Aminoacylated tRNAs

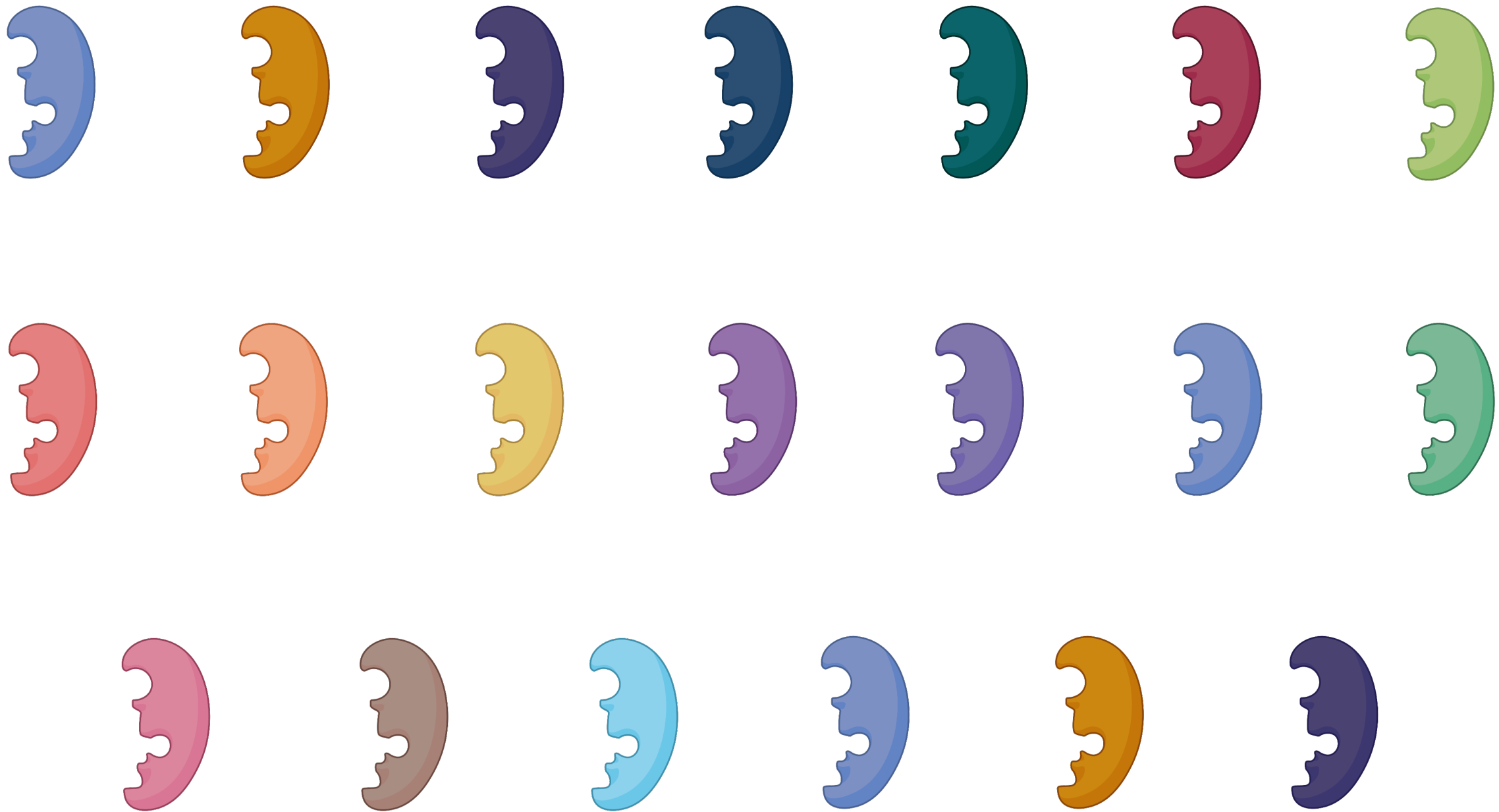


Production of Aminoacylated tRNAs



For each amino acid, there is at least one unique aminoacyl tRNA

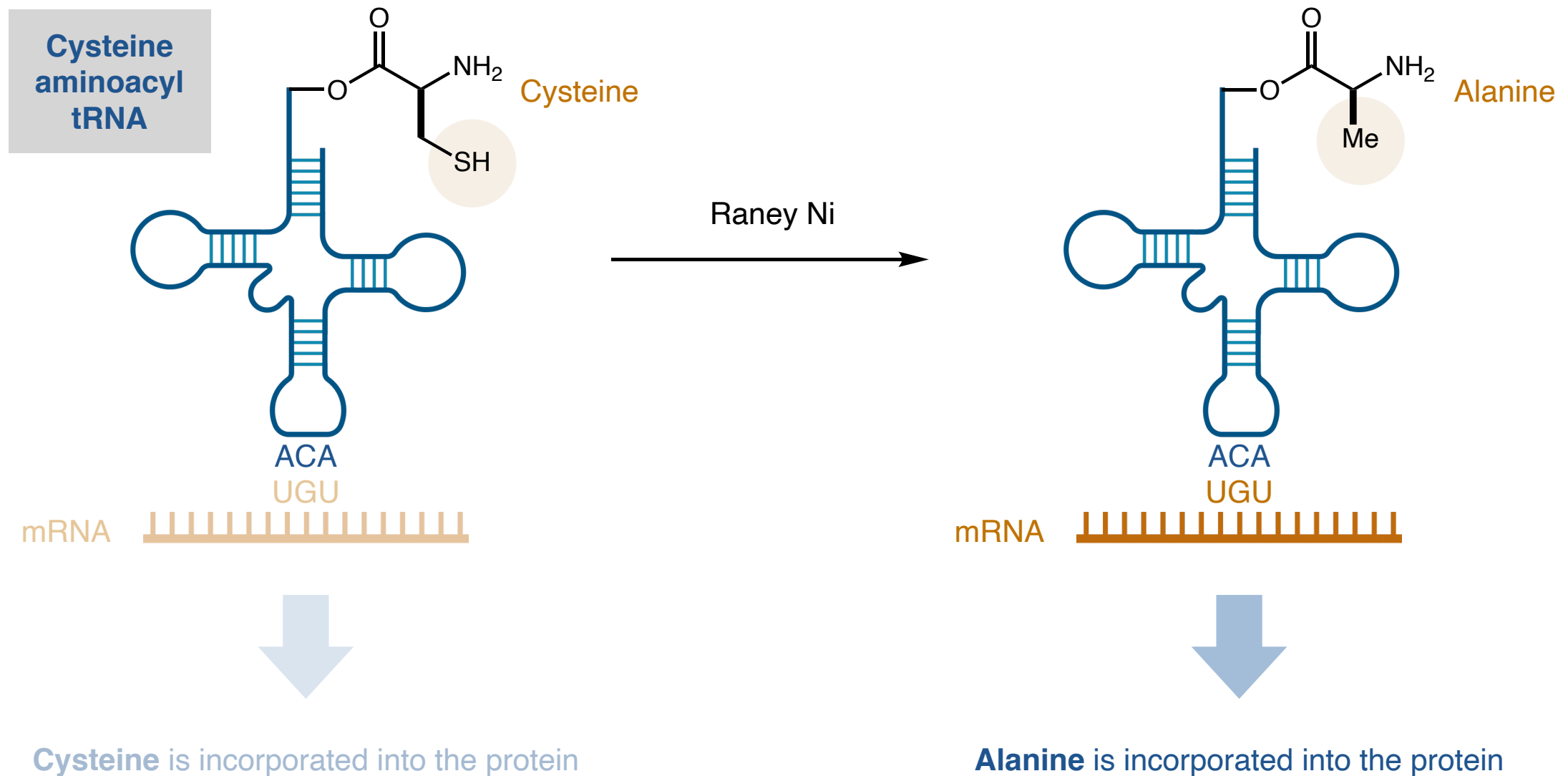
Production of Aminoacylated tRNAs



In most organisms, for each amino acid, there is a unique aminoacyl tRNA synthetase

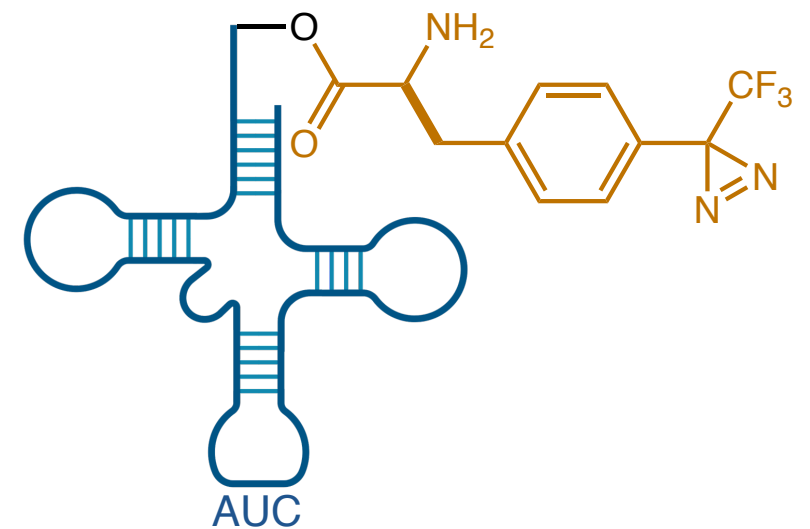
The Adaptor Hypothesis

“Amino acid position within a protein is determined by the binding of mRNA with a tRNA carrying the amino acid”

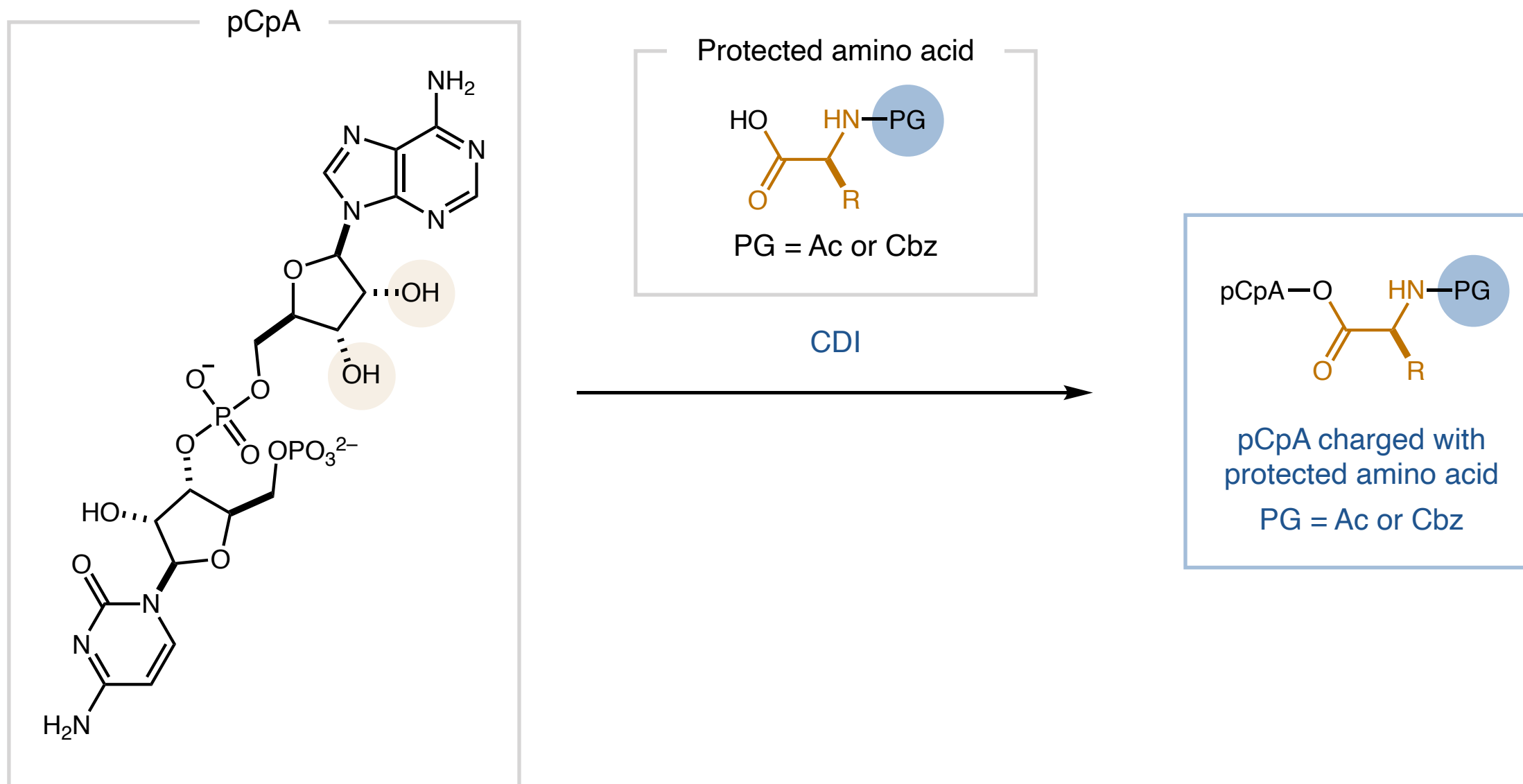


Expanding the Genetic Code

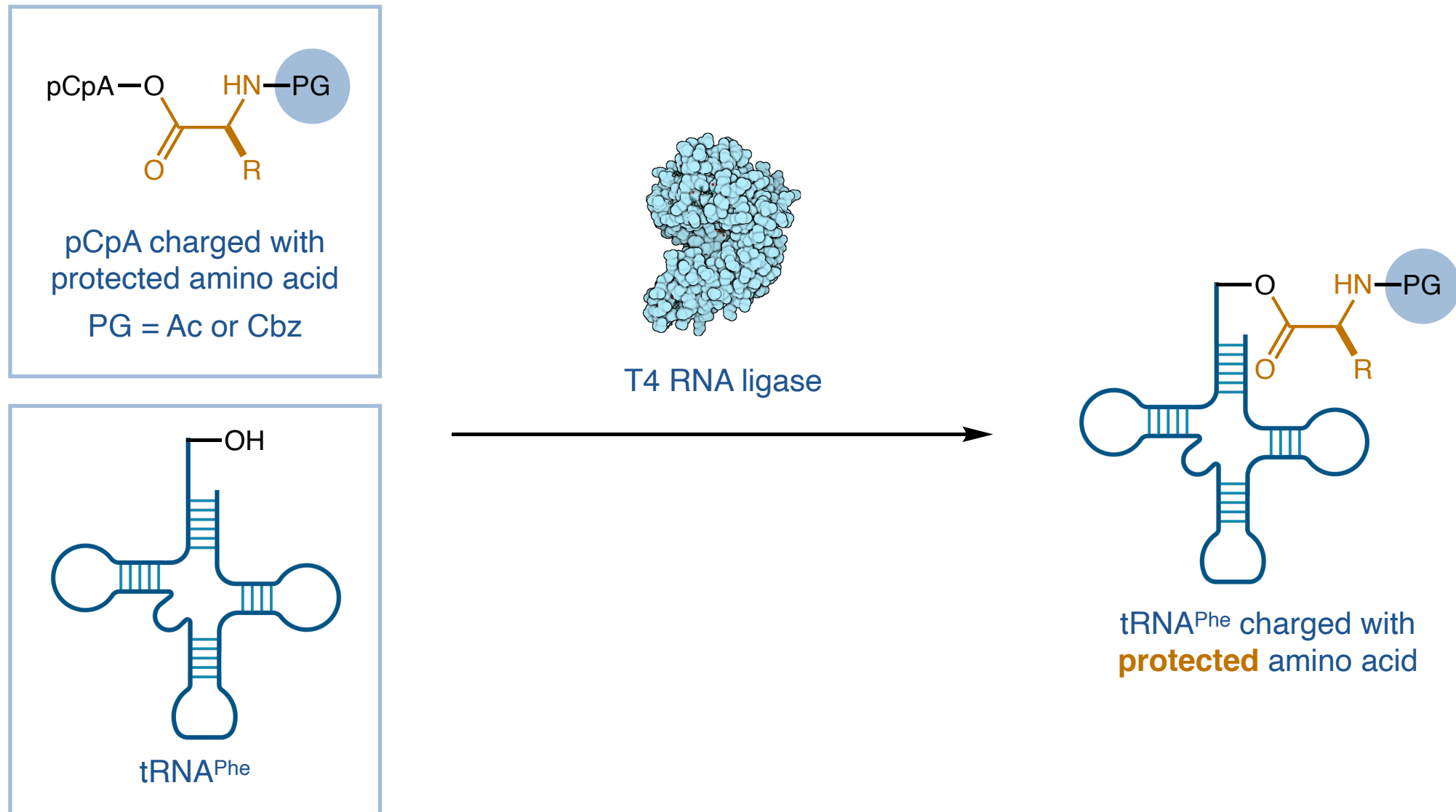
- The traditional genetic code
- Expanding the genetic code
 - In vitro
 - In eukaryotes, prokaryotes, and mammalian cells
- Orthogonal ribosomes
- Genetically recoded organisms and synonymous codon compression
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A General Method for the Synthesis of “Misacylated” tRNAs



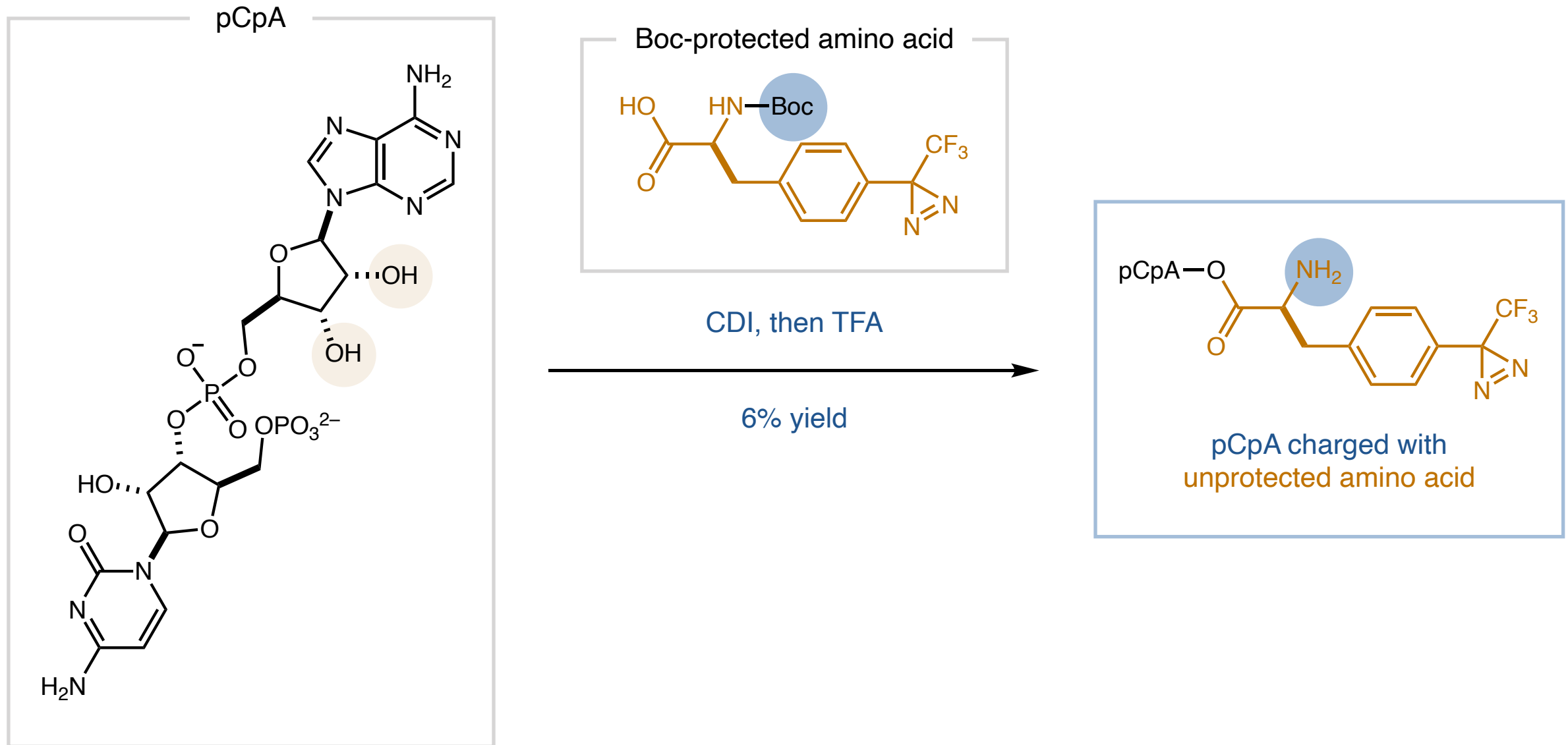
A General Method for the Synthesis of “Misacylated” tRNAs



tRNA^{Phe}s can be charged with protected amino acids of choice using T4 RNA ligase

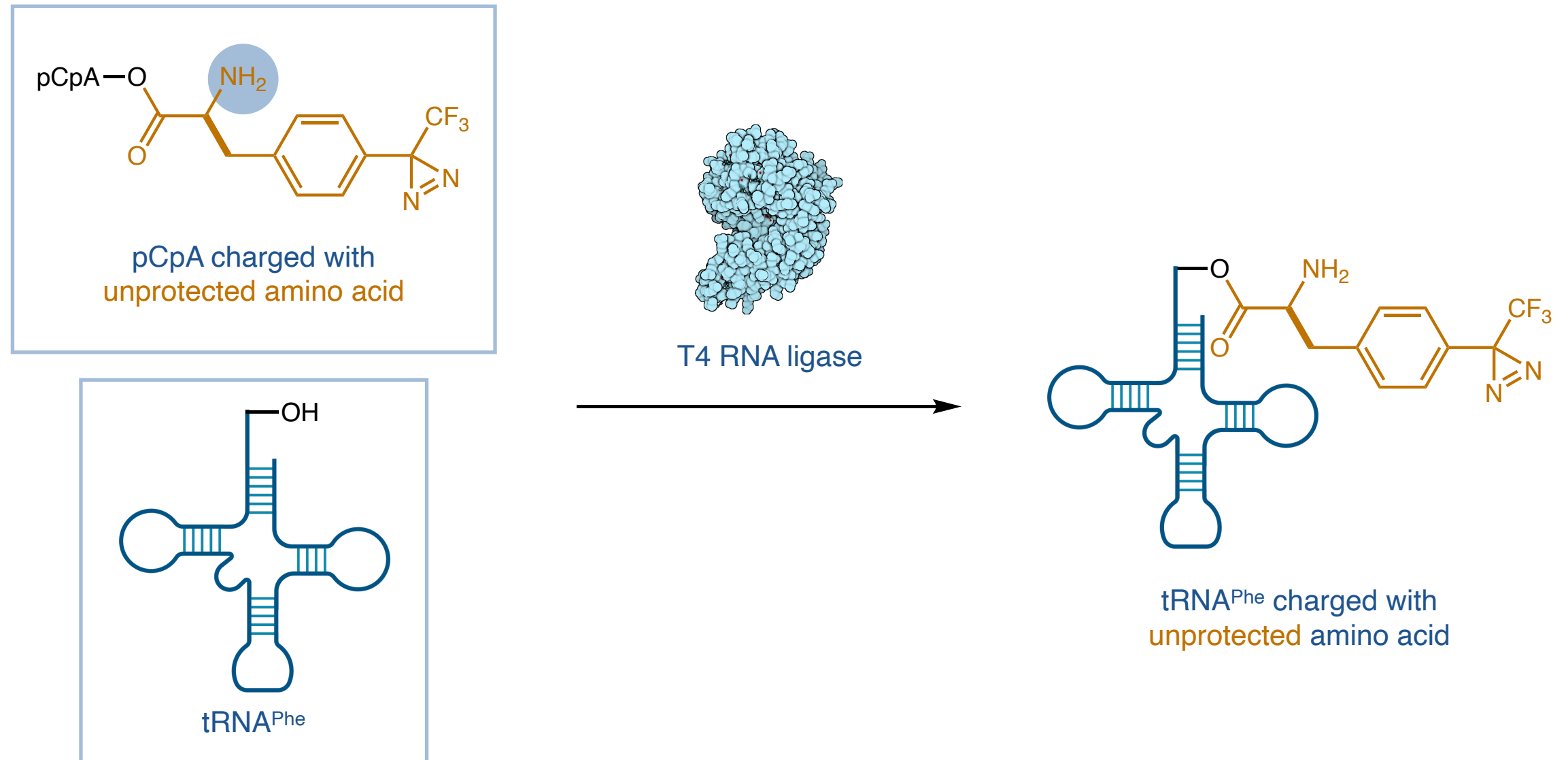
Problem: tRNA charged with protecting group cannot be accepted by the ribosome

Protein Synthesis with Unprotected Aminoacyl tRNAs



Boc protection and deprotection enables synthesis of pCpA charged with unprotected amino acid

Protein Synthesis with Unprotected Aminoacyl tRNAs



tRNA^{Phe} charged with **unprotected** noncanonical amino acid can be synthesized

Stop Codons

		Second Position				
		T	C	A	G	
First Position	T	TTT] Phe TTC] TTA] Leu TTG]	TCT] TCC] Ser TCA] TCG]	TAT] Tyr TAC] TAA STOP TAG STOP	TGT] Cys TGC] TGA STOP TGG Trp	T C A G
	C	CTT] CTC] Leu CTA] CTG]	CCT] CCC] Pro CCA] CCG]	CAT] His CAC] CAA] Gln CAG]	CGT] CGC] Arg CGA] CGG]	T C A G
	A	ATT] Ile ATC] ATA] ATG Met	ACT] ACC] Thr ACA] ACG]	AAT] Asn AAC] AAA] Lys AAG]	AGT] Ser AGC] AGA] Arg AGG]	T C A G
	G	GTT] Val GTC] GTA] GTG]	GCT] GCC] Ala GCA] GCG]	GAT] Asp GAC] GAA] Glu GAG]	GGT] GGC] Gly GGA] GGG]	T C A G

Stop Codons
“Stop translating protein”

Name	Codon	<i>E. coli</i>	Yeast	Human
Amber	UAG	0.3	0.5	0.5
Ochre	UAA	2.0	1.0	0.7
Opal	UGA	1.0	0.6	1.3
Frequency / thousand codons				

Of the three stop codons, the Amber stop codon is used the least in the genome

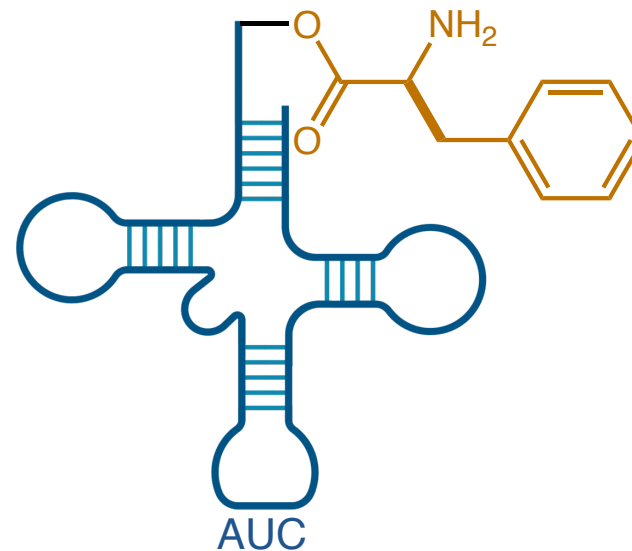
Codon frequency data: <https://www.genscript.com/tools/codon-frequency-table>

Bruce, A. G.; Atkins, J. F.; Wills, N.; Uhlenbeck, O.; Gesteland, R. F. *Proc. Natl. Acad. Sci. U. S. A.* **1982**, 79, 7127.

Amber Suppression with a Amber Suppressor tRNA Charged with Phe

Amber suppression: Amber codon (UAG) has been reassigned from encoding “stop” to encoding an amino acid

Amber Suppressor
Aminoacyl tRNA
charged with **phenylalanine**



RNA sequence	UUU	AAC	AAC	CGG	GCG	UAG	GCG	AAC	CGG	UAA
Protein sequence	Phe	Asn	Asn	Arg	Ser	Stop	Ser	Asn	Arg	Stop

Traditional rules:
5 amino acid
peptide

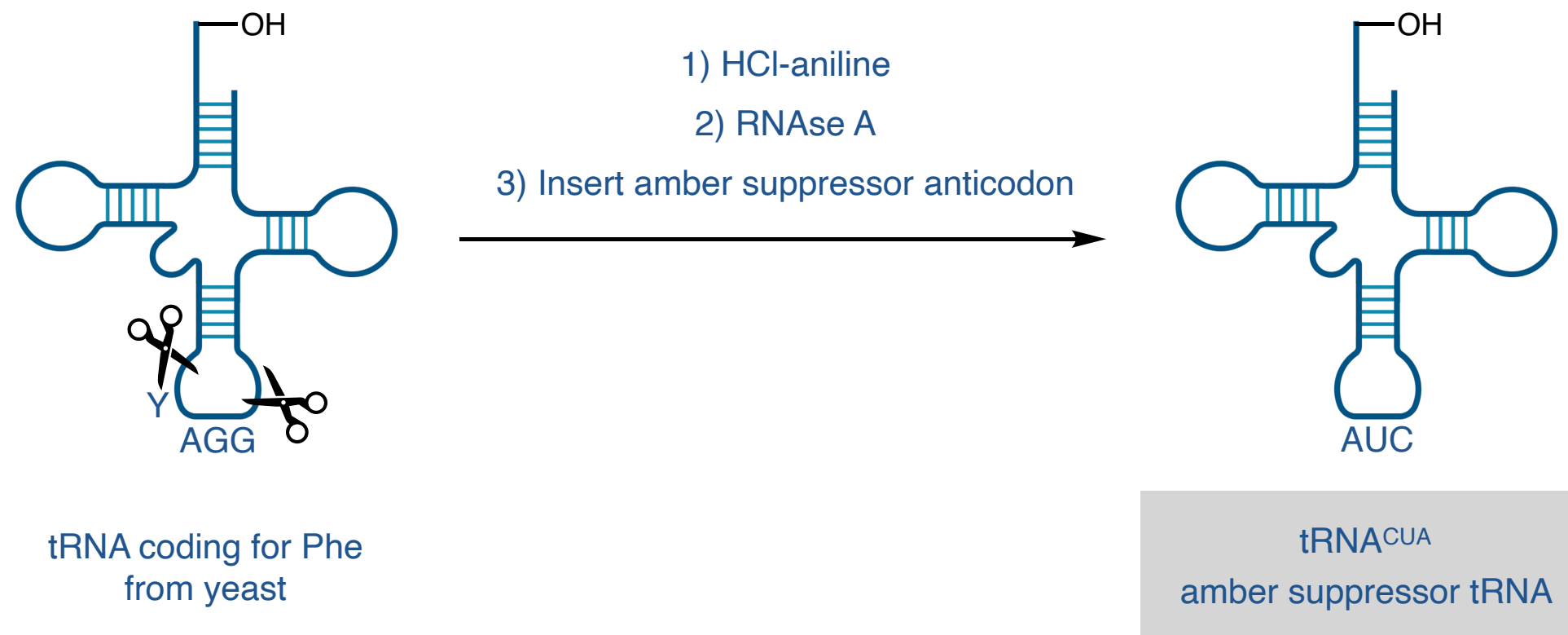
Amber
Suppression

Protein sequence with Amber Suppression	Phe	Asn	Asn	Arg	Ser	Phe	Ser	Asn	Arg	Stop
--	-----	-----	-----	-----	-----	-----	-----	-----	-----	------

Amber suppression:
9 amino acid
peptide

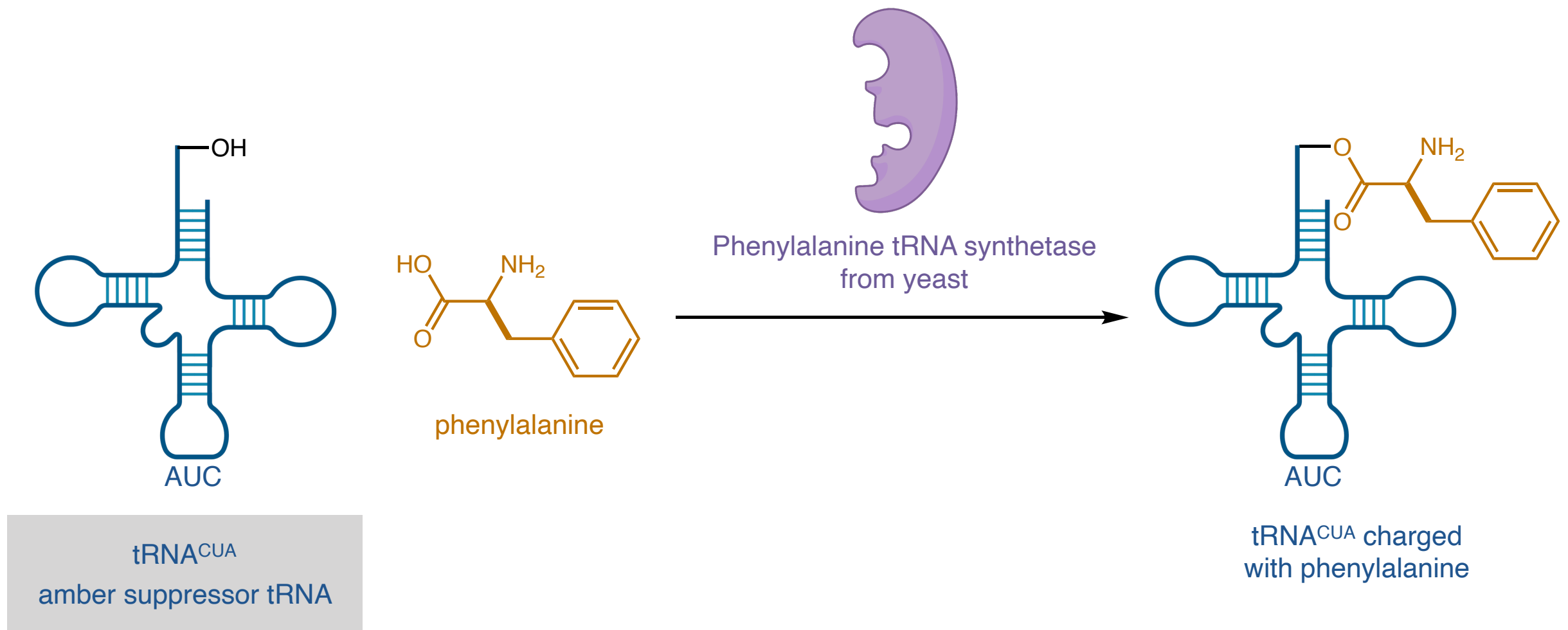
Amber Suppression with a Amber Suppressor tRNA Charged with Phe

Step 1: Preparation of tRNA^{CUA} (amber suppressor tRNA) via anticodon loop replacement



Amber Suppression with a Amber Suppressor tRNA Charged with Phe

Step 2: Preparation of tRNA^{CUA} charged with phenylalanine

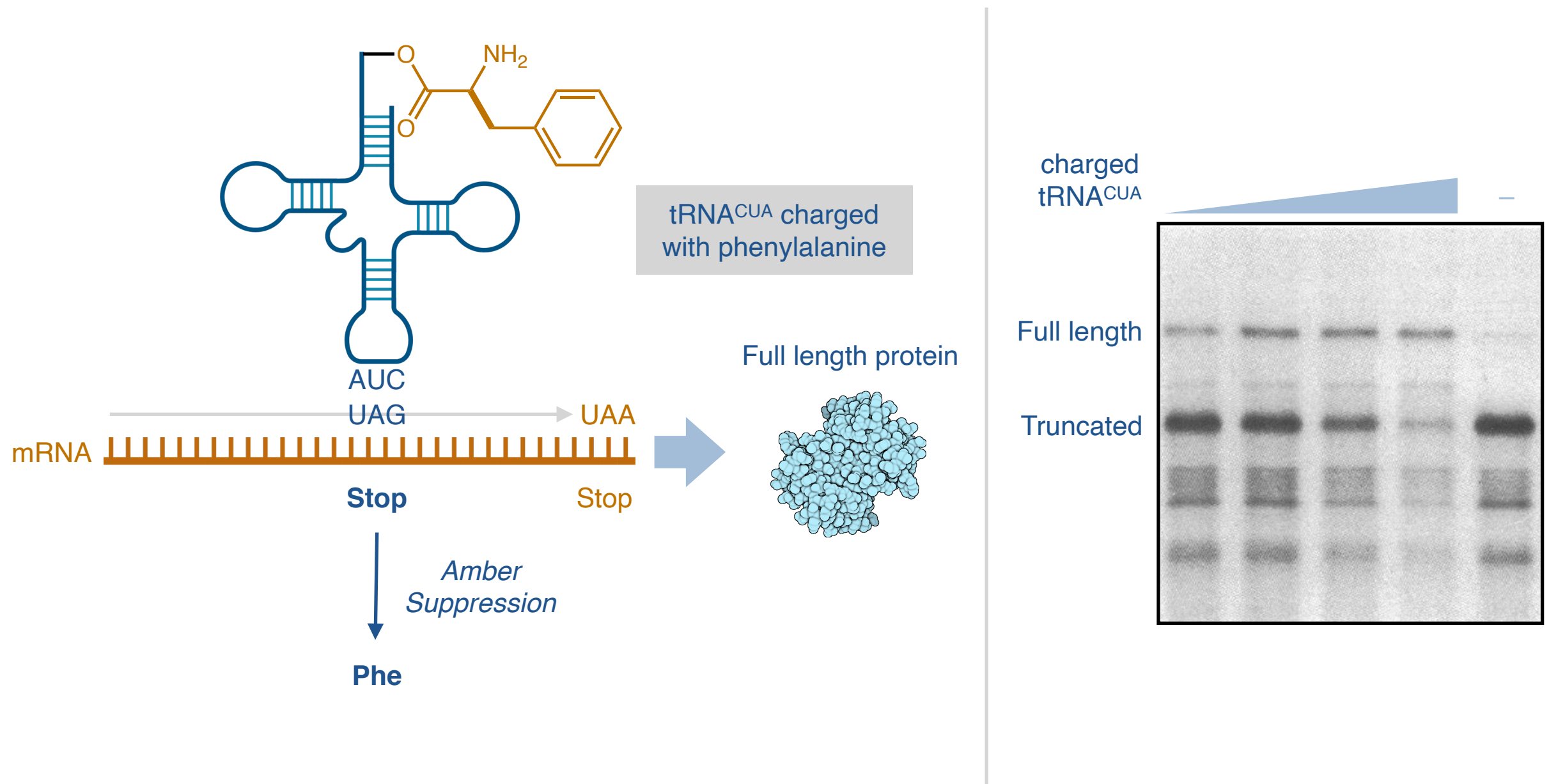


Phenylalanine tRNA synthetase accepts tRNA^{CUA}

Amber Suppression with a Amber Suppressor tRNA Charged with Phe



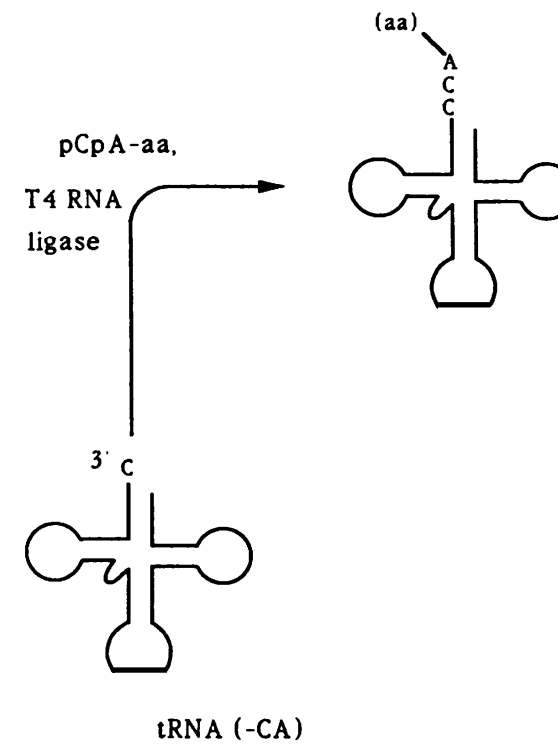
Amber Suppression with a Amber Suppressor tRNA Charged with Phe



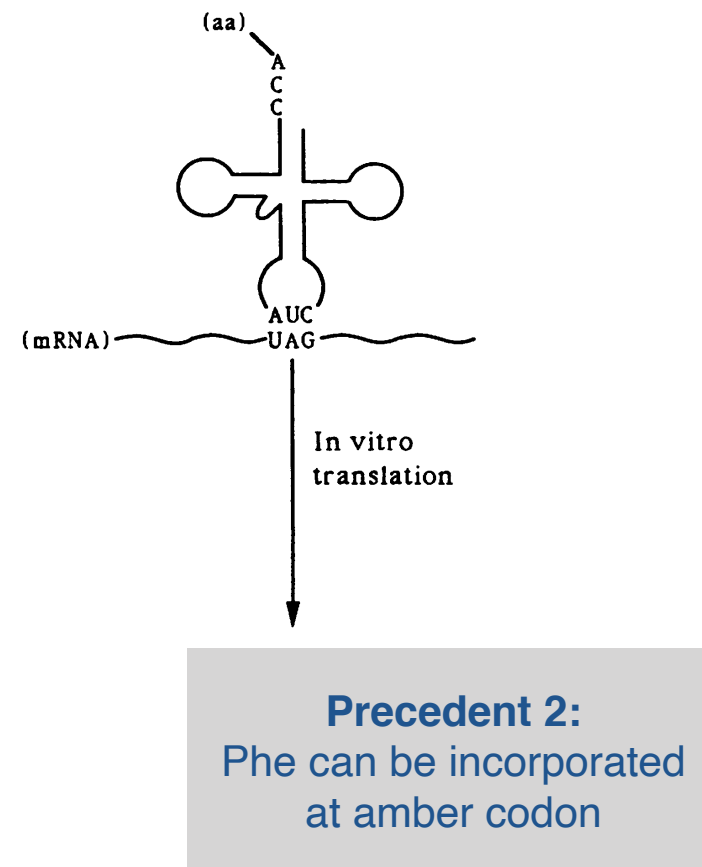
Full length protein expression is dependent upon presence of tRNA charged with phenylalanine

The Precedent for the Breakthrough

Precedent 1:
tRNAs can be charged
with any amino acid
using T4 ligase and pCpA-aa



The Precedent for the Breakthrough

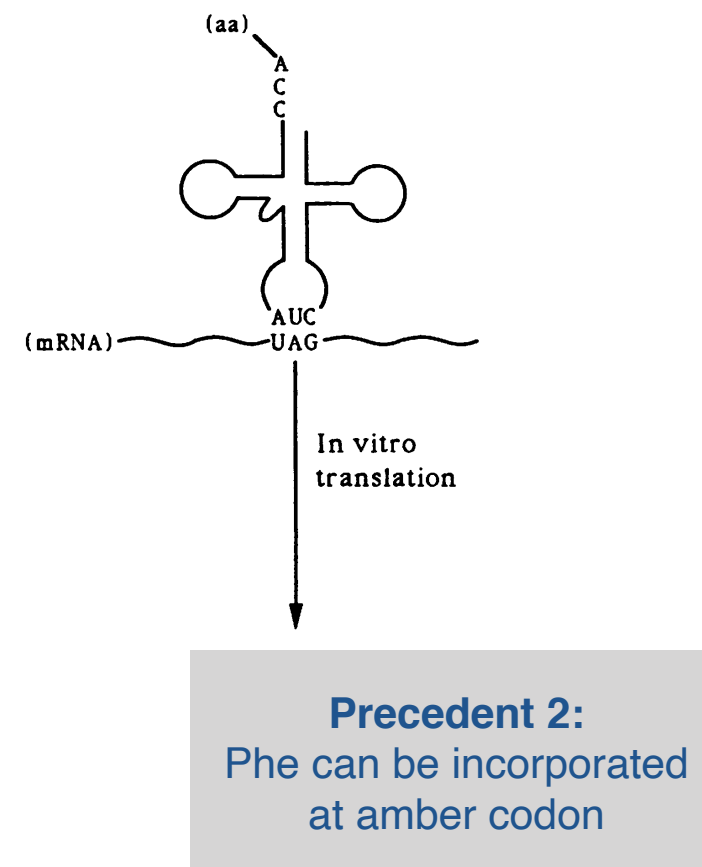


The Breakthrough: Amber Suppression to Incorporate Noncanonical Amino Acids



Peter Schultz

Current Institution: Scripps Research



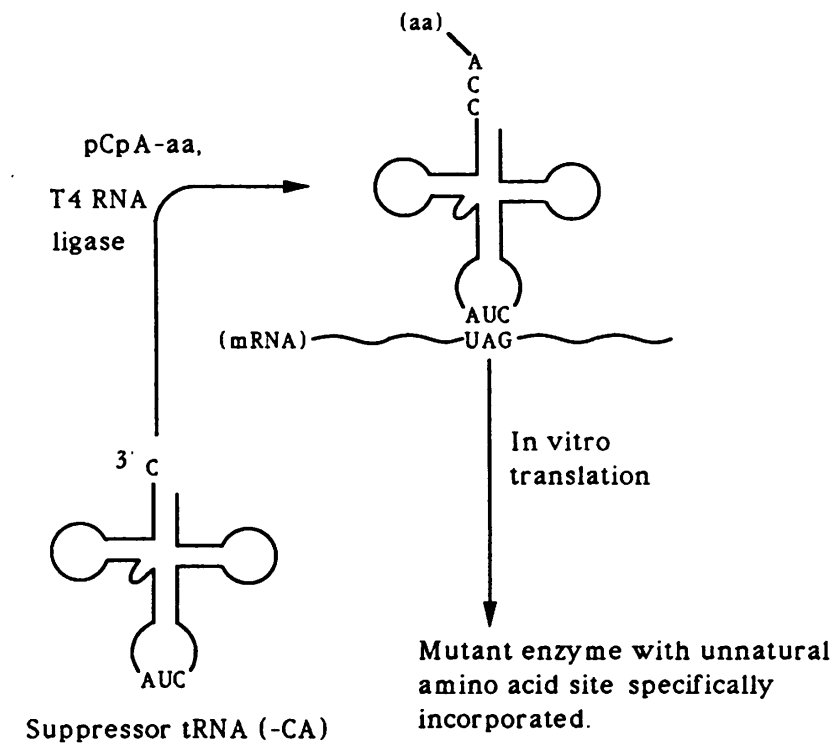
“aa” can be an unnatural amino acid

The Breakthrough: Amber Suppression to Incorporate Noncanonical Amino Acids



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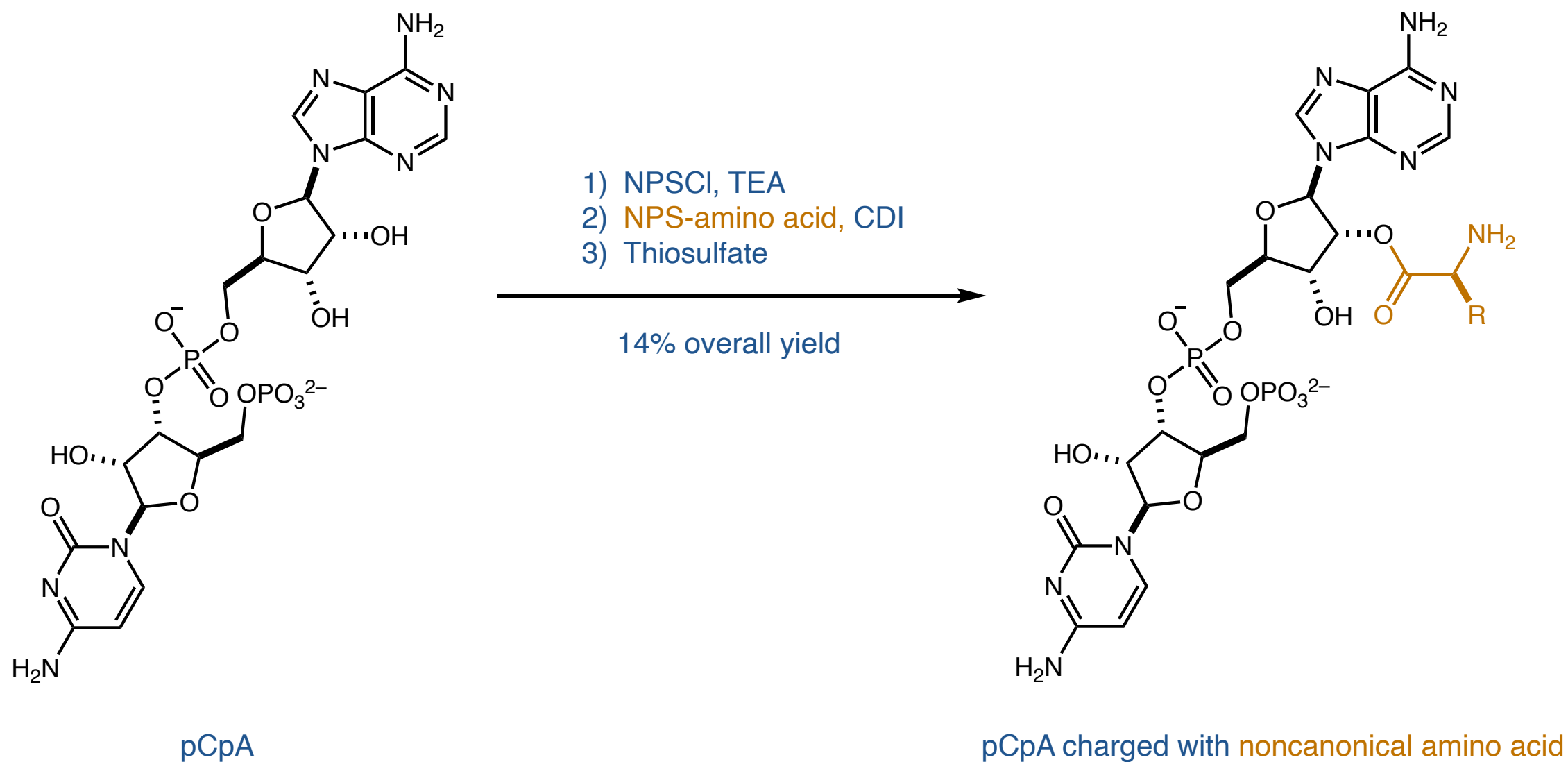
“aa” can be an unnatural amino acid

Can noncanonical amino acids be incorporated into proteins using this method?

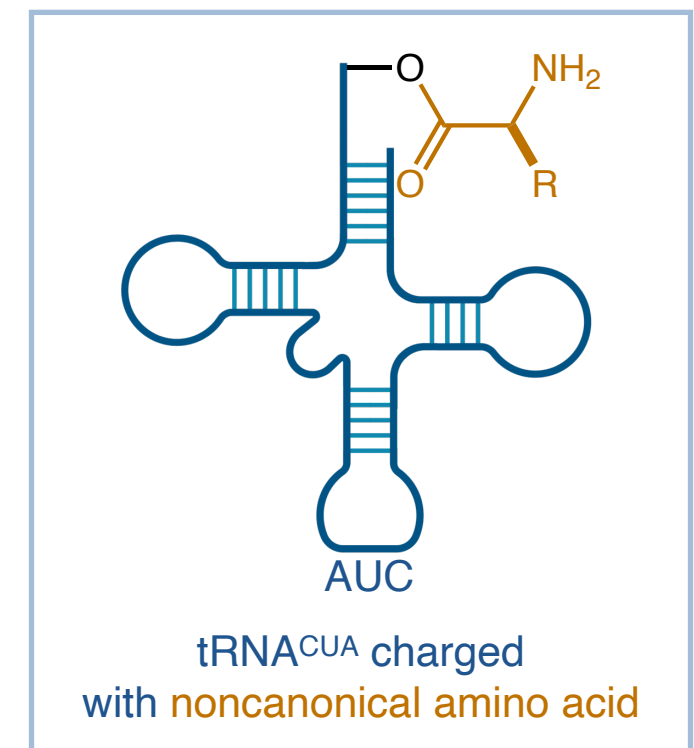
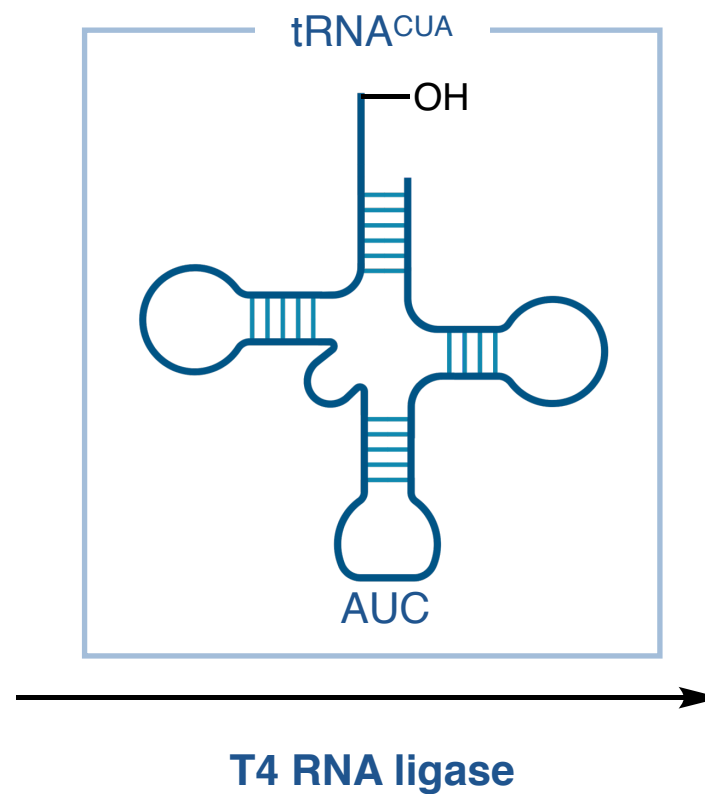
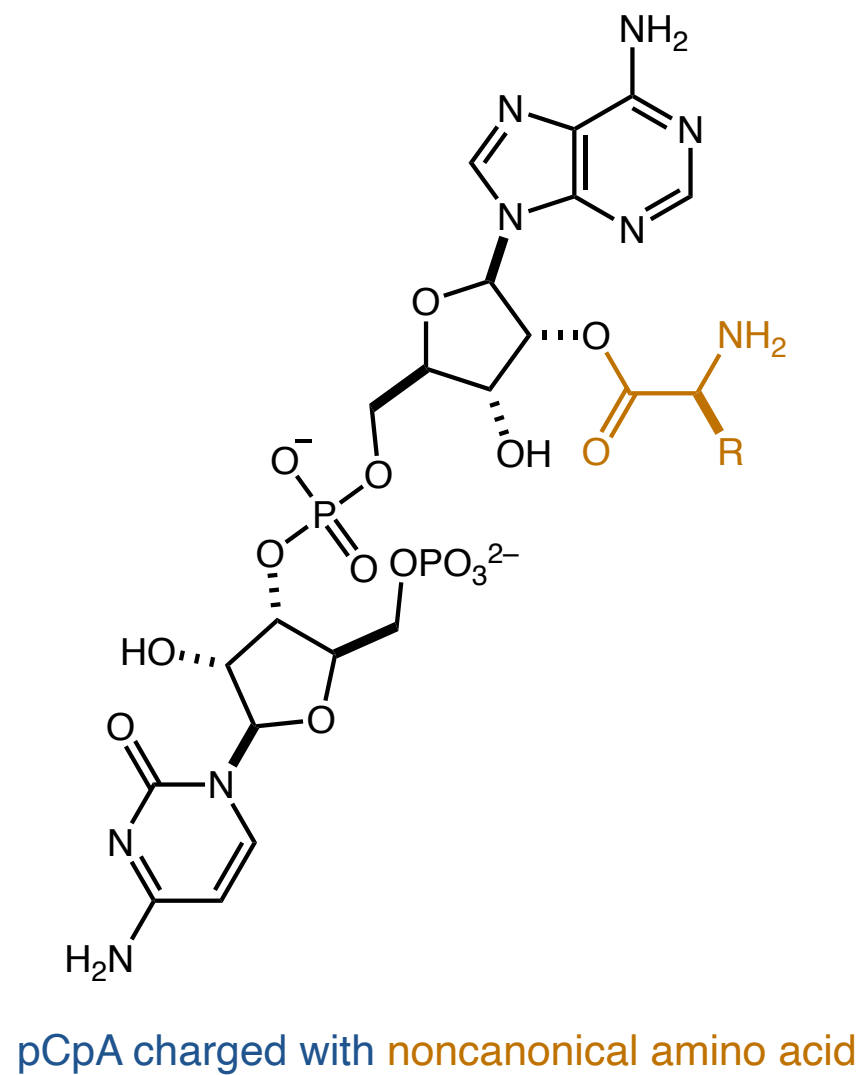
Noren, C. J.; Anthony-Cahill, S. J.; Griffith, M. C.; Schutz, P. G. *Science* **1989**, 244, 182.

The Breakthrough: Amber Suppression to Incorporate Noncanonical Amino Acids

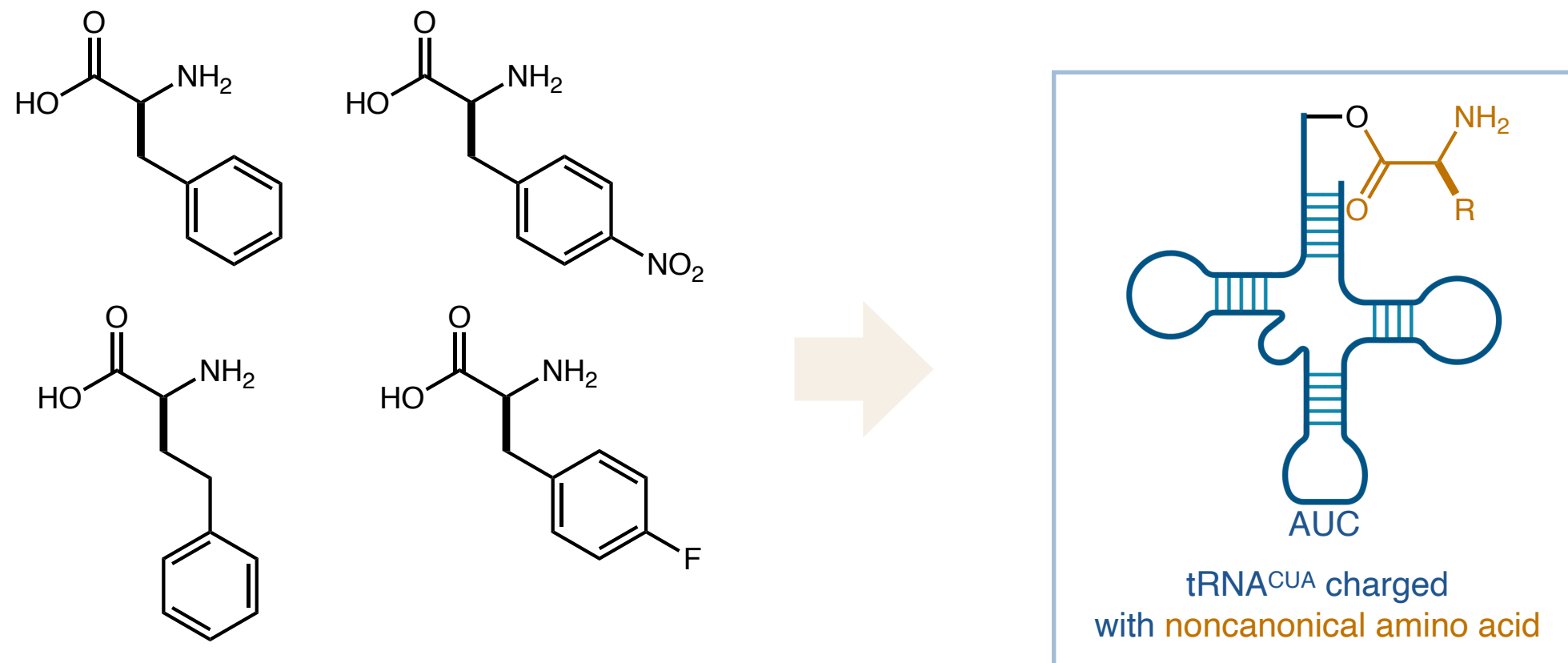
Preparation of pCpA charged with noncanonical amino acid



The Breakthrough: Amber Suppression to Incorporate Noncanonical Amino Acids

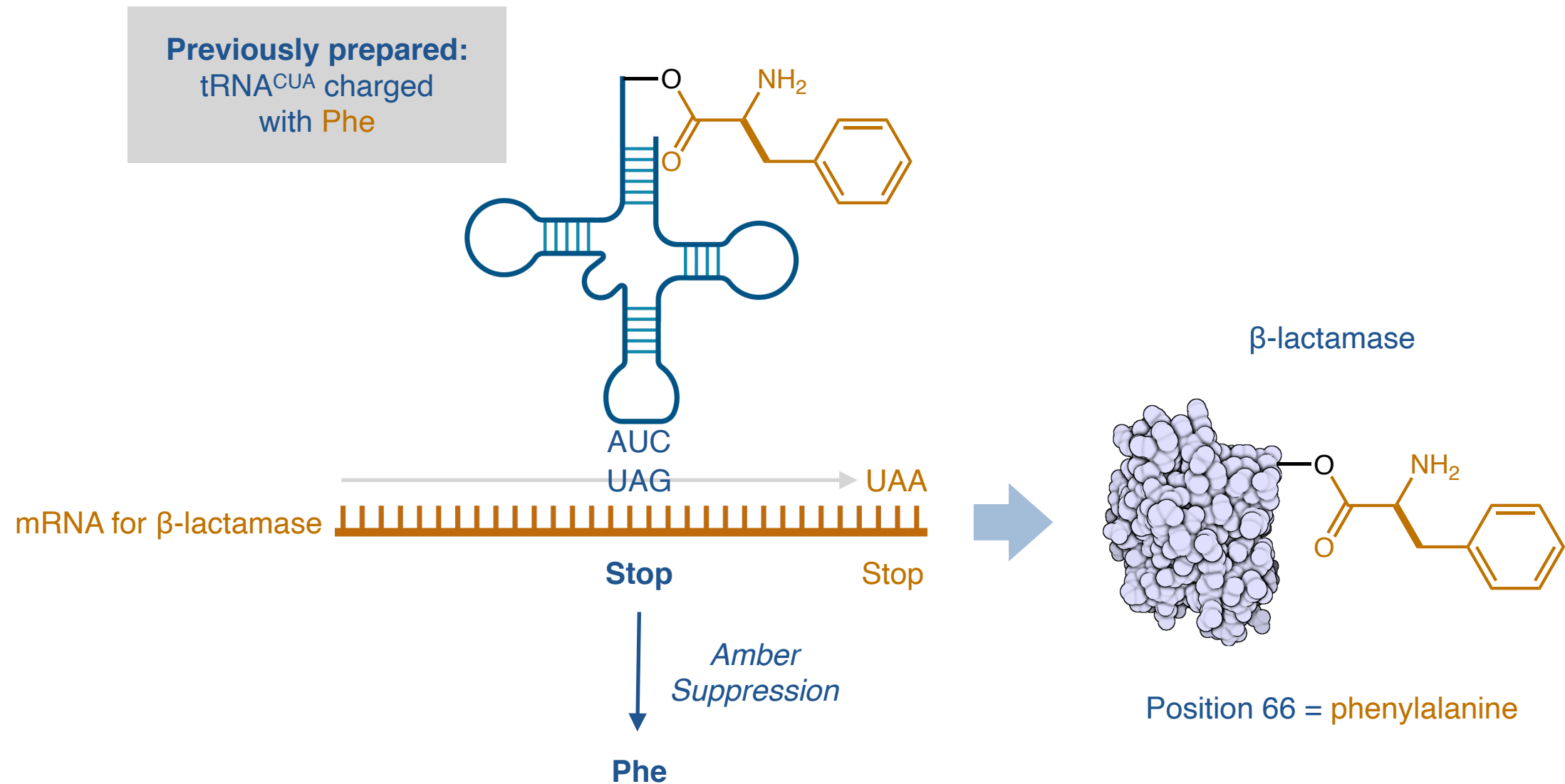


The Breakthrough: Amber Suppression to Incorporate Noncanonical Amino Acids



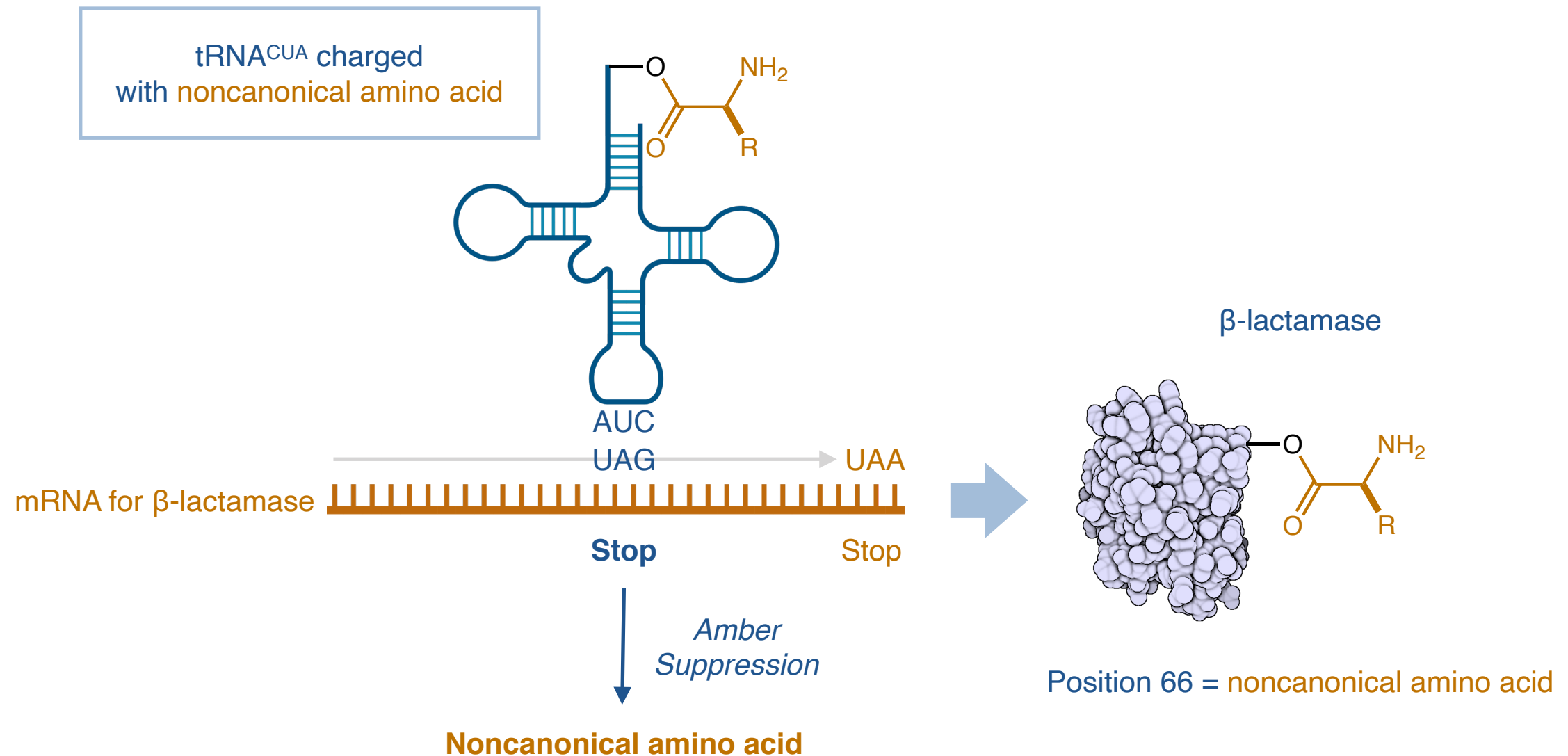
Method can be used to prepare tRNA^{CUA} with a variety of noncanonical amino acids

The Breakthrough: Amber Suppression to Incorporate Noncanonical Amino Acids



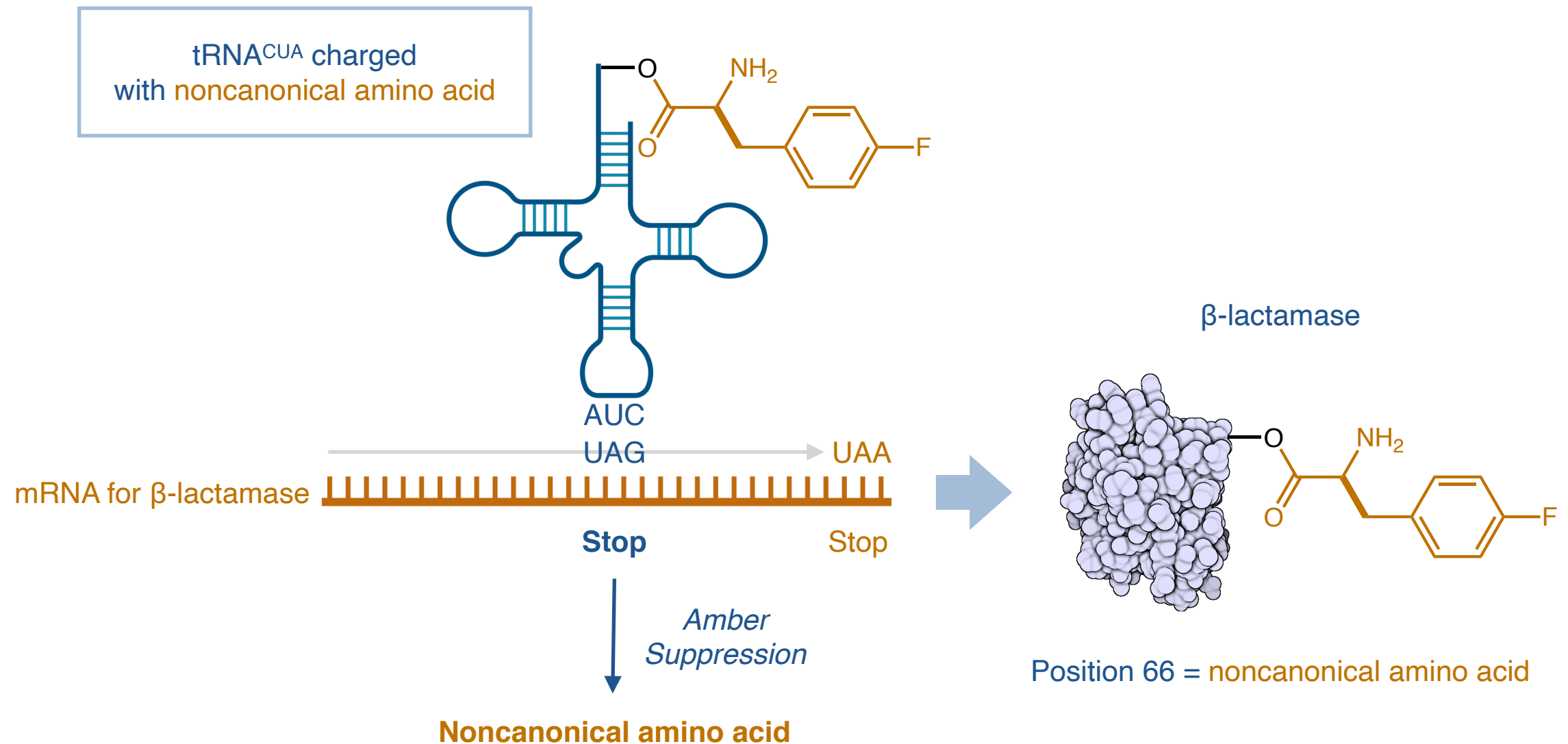
Native β -lactamase can be expressed in *E. coli* lysate using amber suppression

The Breakthrough: Amber Suppression to Incorporate Noncanonical Amino Acids



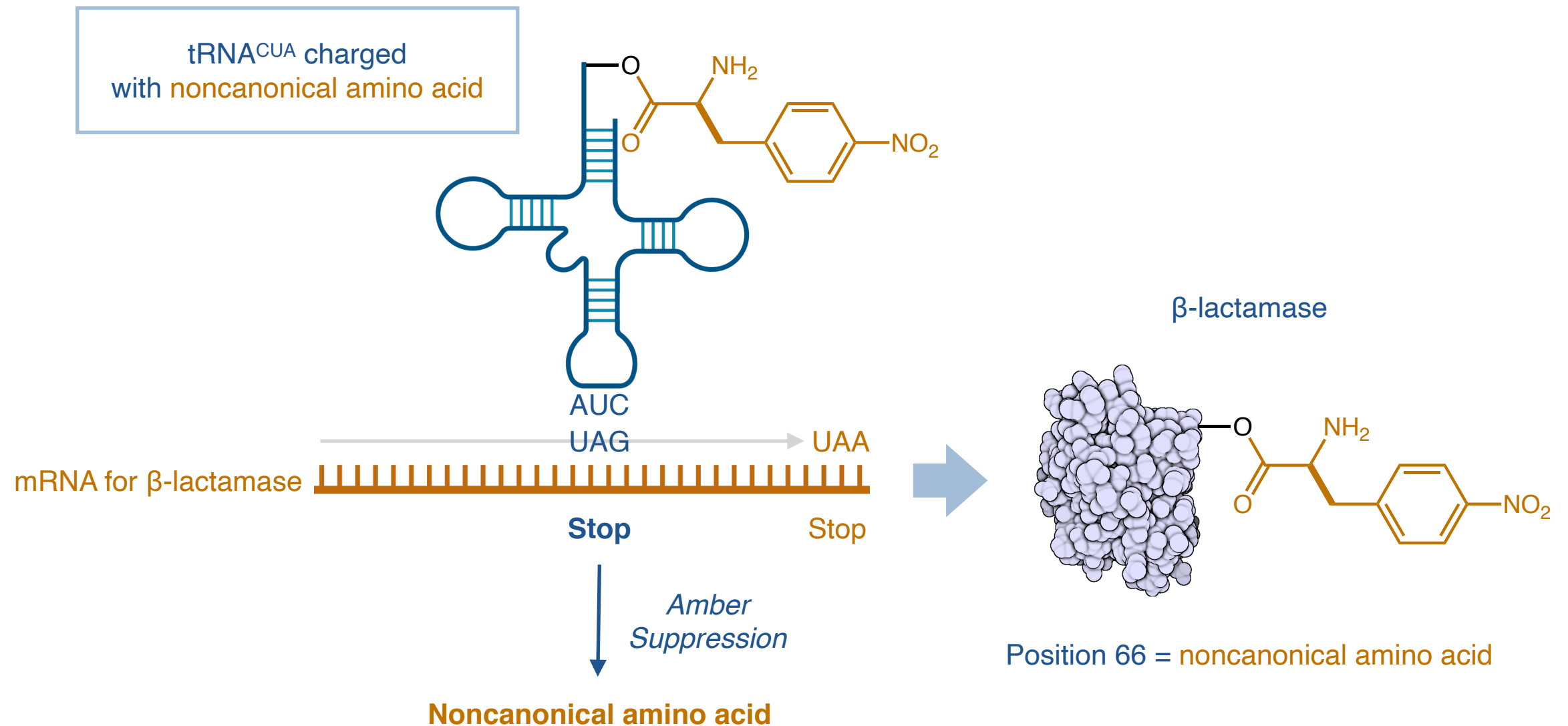
tRNA^{CUA} charged with noncanonical amino acid incorporates the noncanonical amino acid at position 66 in the protein

The Breakthrough: Amber Suppression to Incorporate Noncanonical Amino Acids



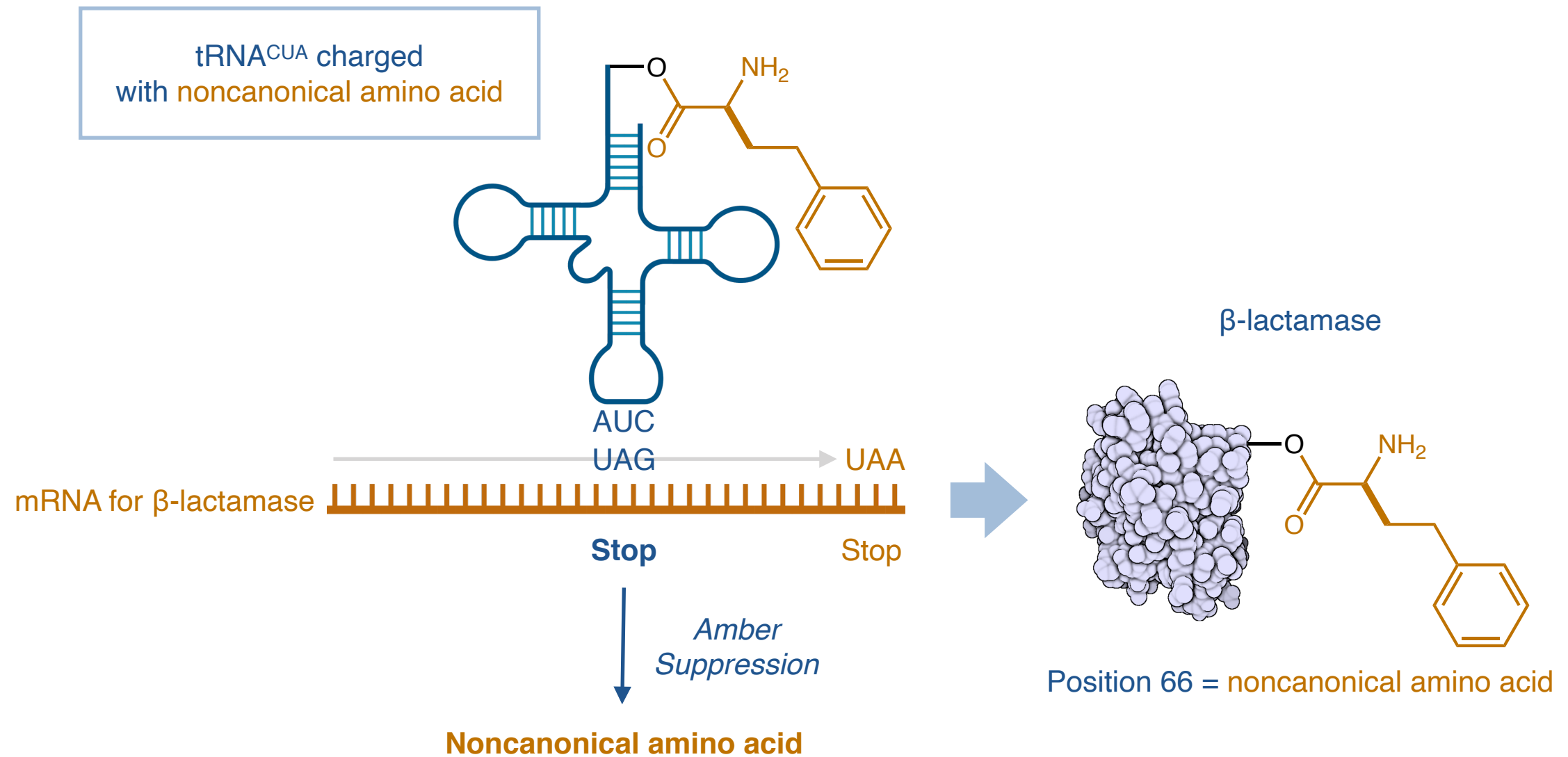
tRNA^{CUA} charged with noncanonical amino acid incorporates the noncanonical amino acid at position 66 in the protein

The Breakthrough: Amber Suppression to Incorporate Noncanonical Amino Acids



tRNA^{CUA} charged with noncanonical amino acid incorporates the noncanonical amino acid at position 66 in the protein

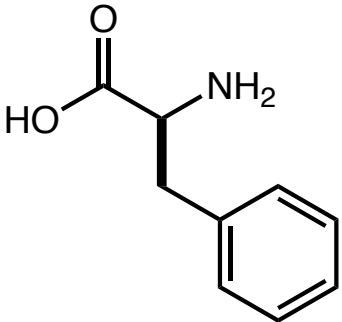
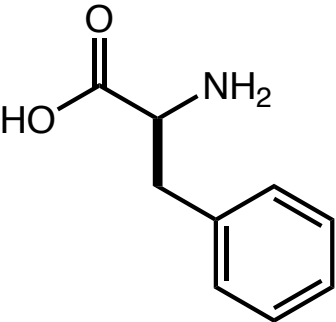
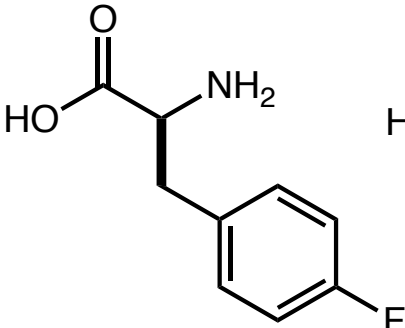
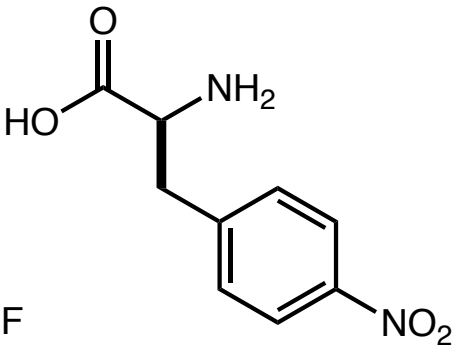
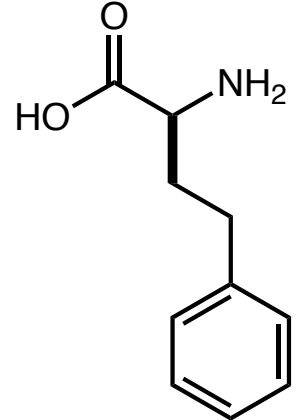
The Breakthrough: Amber Suppression to Incorporate Noncanonical Amino Acids



tRNA^{CUA} charged with noncanonical amino acid incorporates the noncanonical amino acid at position 66 in the protein

The Breakthrough: Amber Suppression to Incorporate Noncanonical Amino Acids

Properties of β -lactamase mutants with noncanonical amino acids

wild type β -lactamase		β -lactamase prepared using tRNA ^{CUA} with Phe or noncanonical amino acid			
Amino acid at position 66 of β -lactamase					
K_m (substrate binding)	55 ± 5	59 ± 6	59 ± 2	57 ± 4	72 ± 14
k_{cat} (turnover #)	880 ± 10	870	1120 ± 290	370 ± 70	150 ± 60

para-fluorophenylalanine increases enzyme turnover number

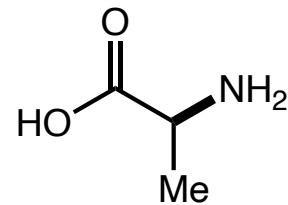
Expanding the Repertoire of Noncanonical Amino Acids

Expression efficiency (vs. wild type expression)

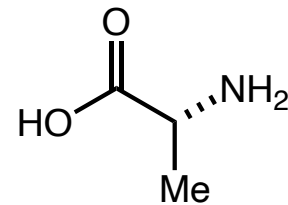
T4 Lysozyme



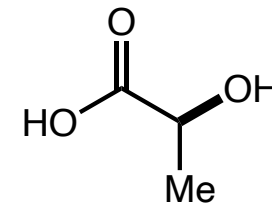
Position 82 =
noncanonical amino acid



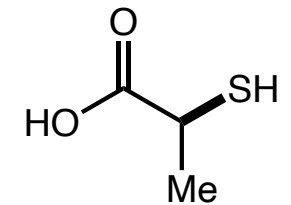
wild type



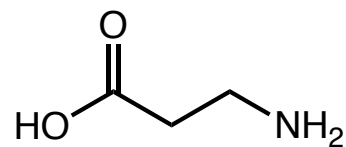
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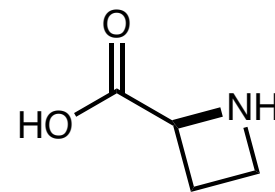
30%



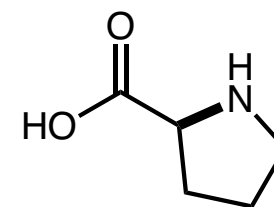
incorporated, but
efficiency not reported



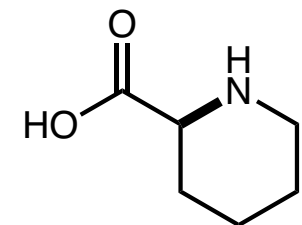
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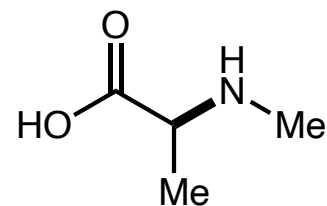
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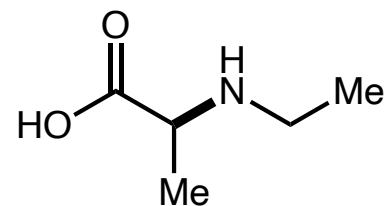
46%



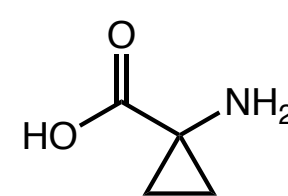
43%



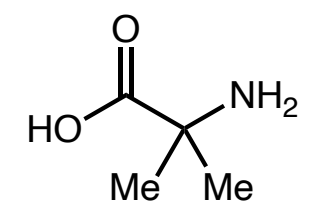
24%



< 5%



28%



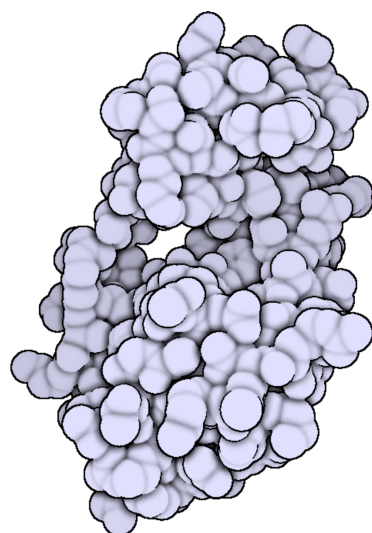
23%

A diverse range of non canonical amino acids can be incorporated via amber suppression

Expanding the Repertoire of Noncanonical Amino Acids

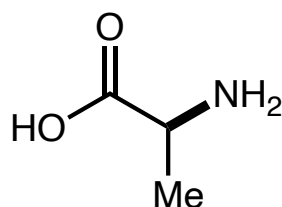
Thermodynamic stability (T_m)

T4 Lysozyme



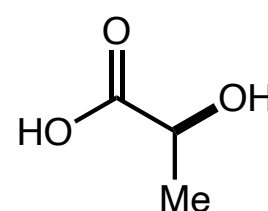
Position 82 =
noncanonical amino acid

Wild type

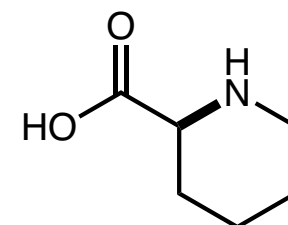


43.4 ± 0.25 °C

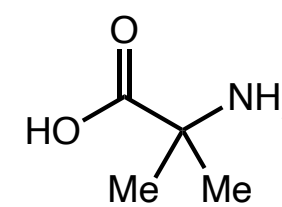
Noncanonical amino acids



39.7 ± 0.25 °C



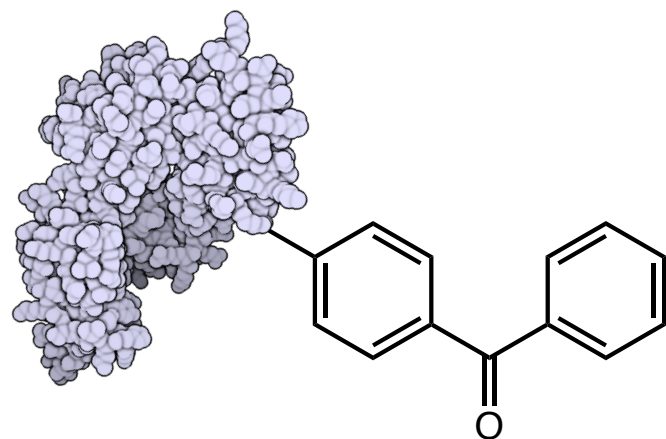
41.3 ± 0.25 °C



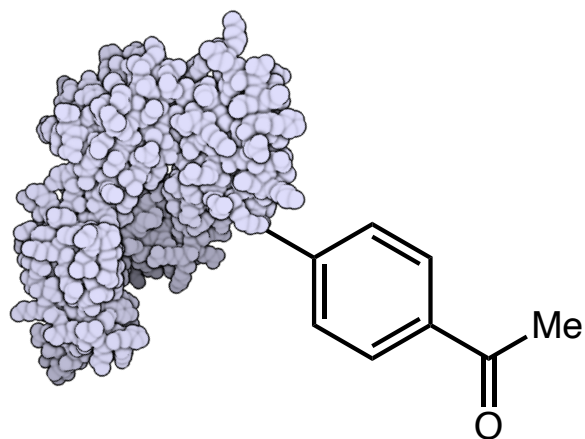
44.6 ± 0.25 °C

Changes in amino acid substitution at Ala82 affect thermal stability of the protein

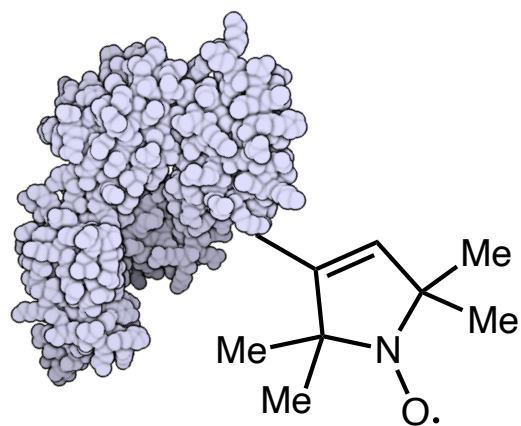
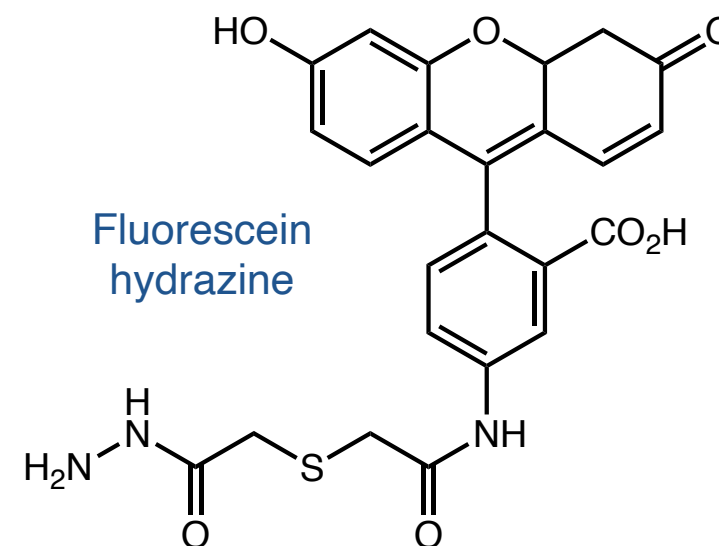
Expanding the Repertoire of Noncanonical Amino Acids



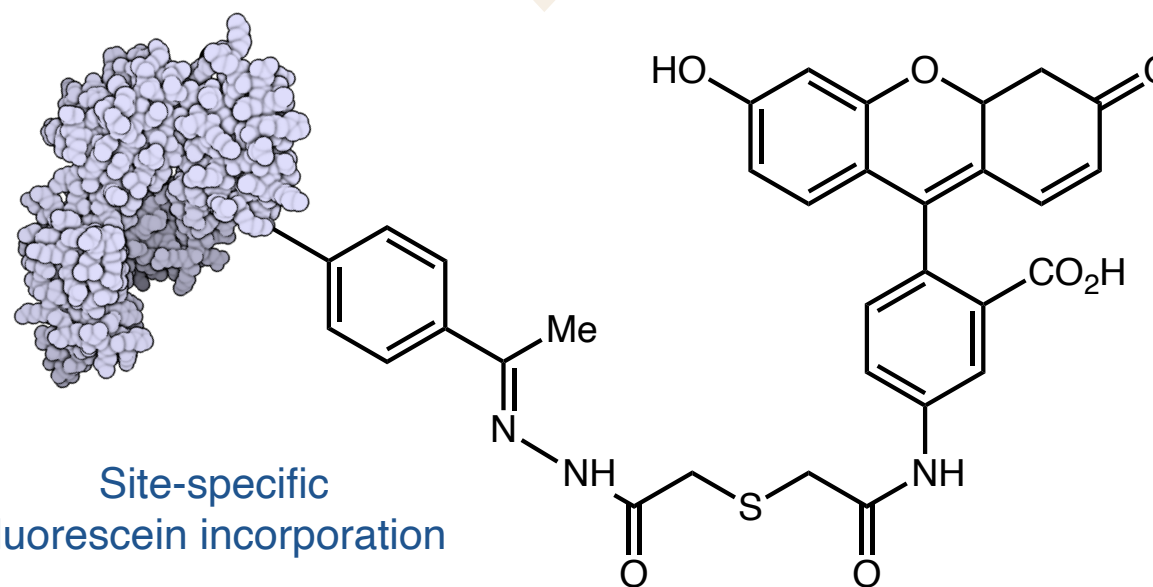
Photoaffinity label



Ketone handle



EPR probe

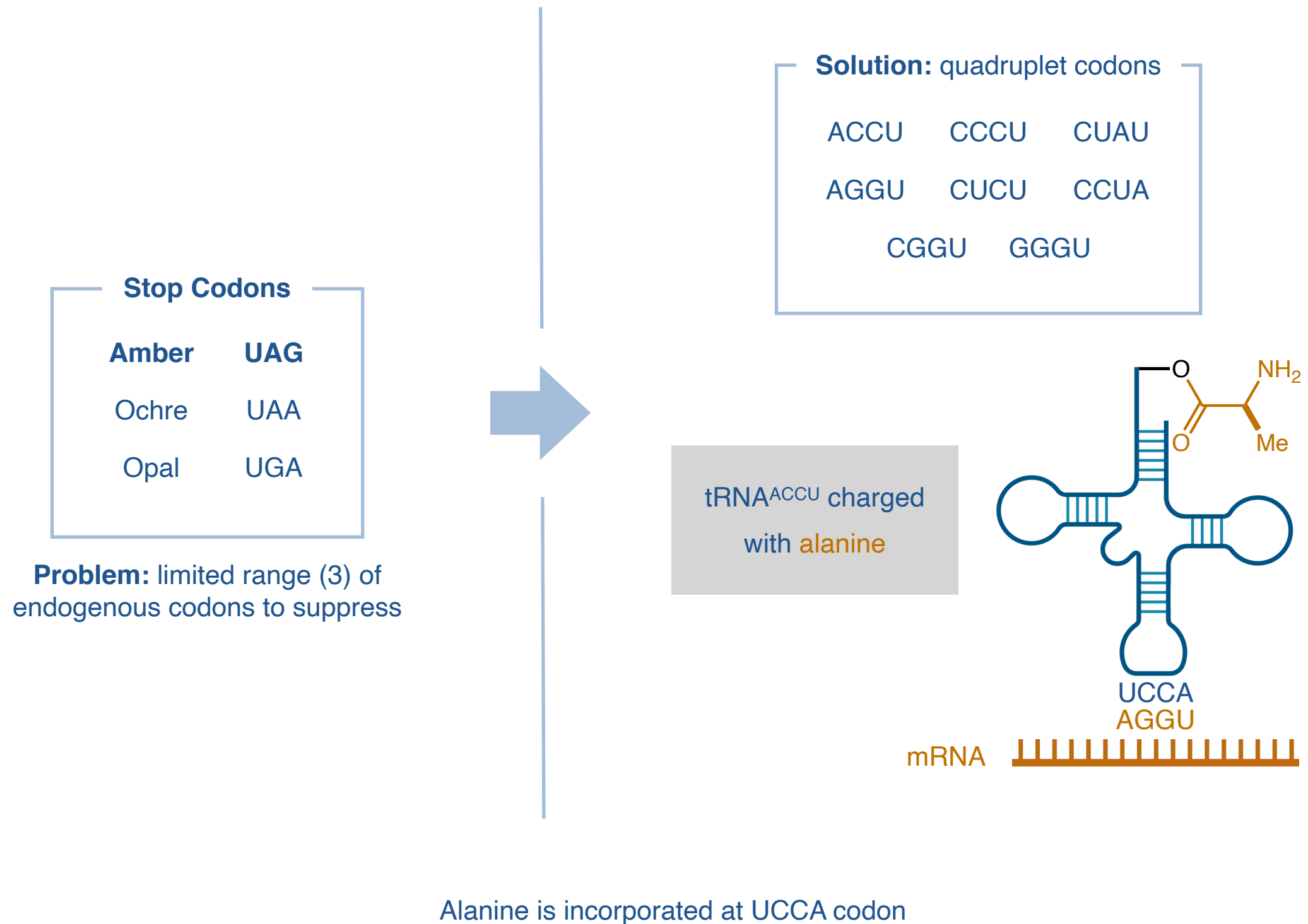


Site-specific
fluorescein incorporation

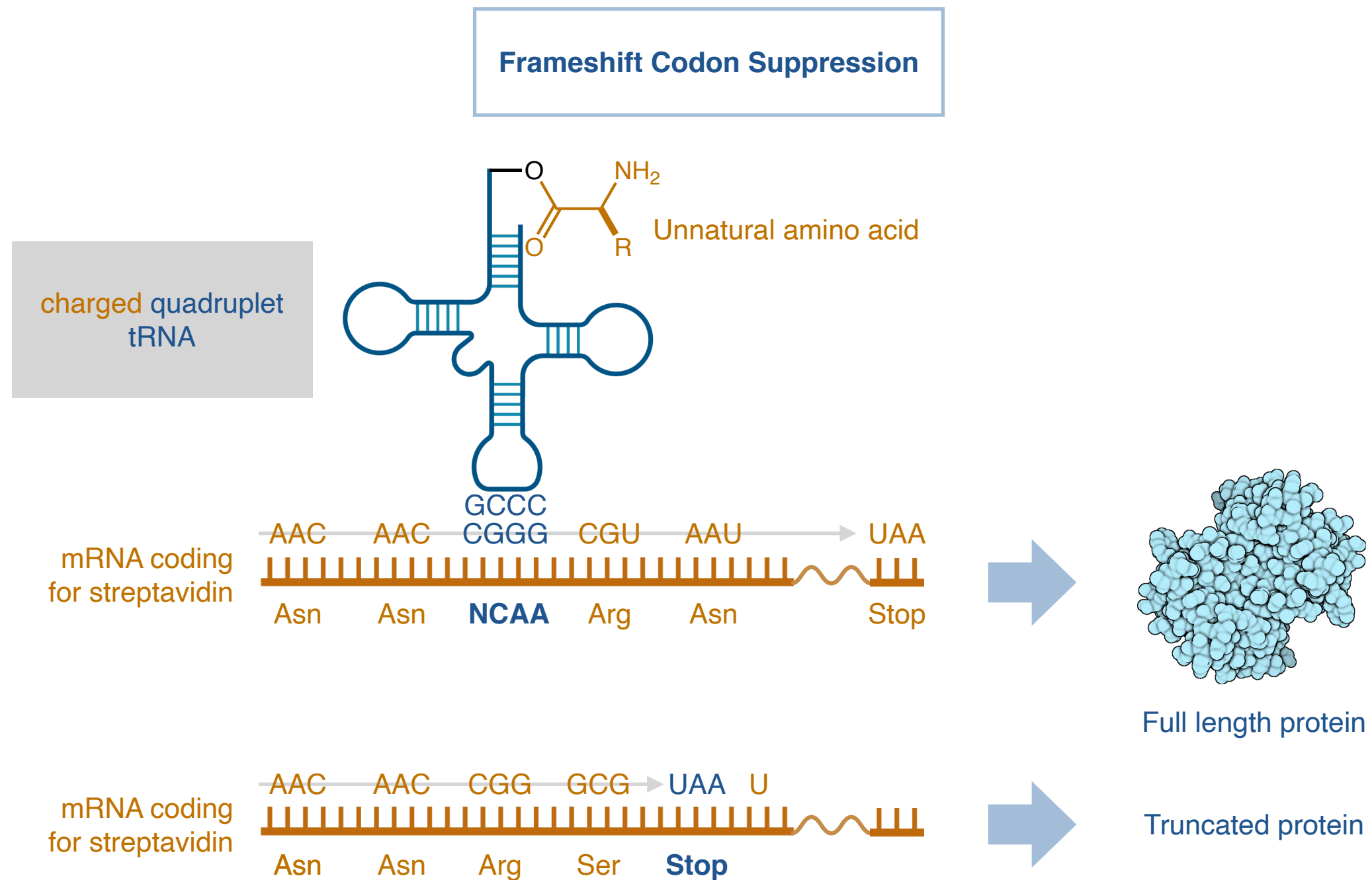
Cornish, V. W.; Hahn, K.; Schultz, P. G. *J. Am. Chem. Soc.* **1996**, *118*, 8150.

Cornish, V. W. et al. *Proc. Natl. Acad. Sci. U. S. A.* **1994**, *91*, 2910.

Alternate Codons for UAA Incorporation: Quadruplet Codons



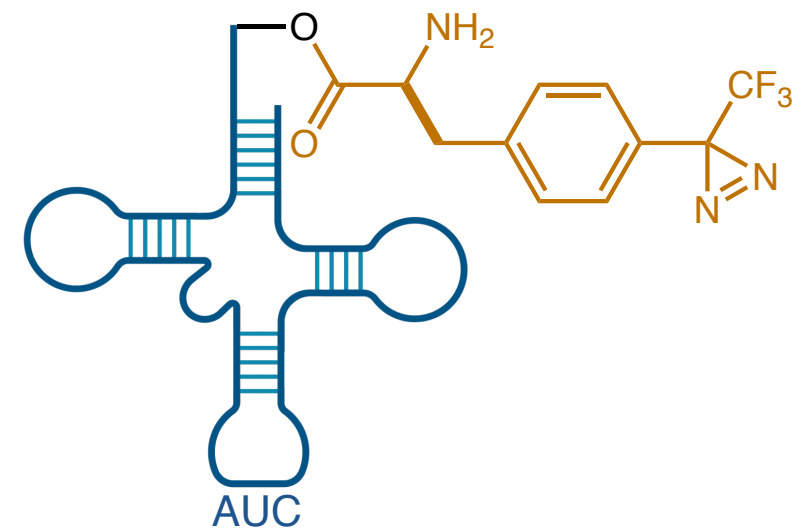
Alternate Codons for UAA Incorporation: Quadruplet Codons



When the frameshift does not happen, a termination codon (UAA) appears, forming the truncated protein

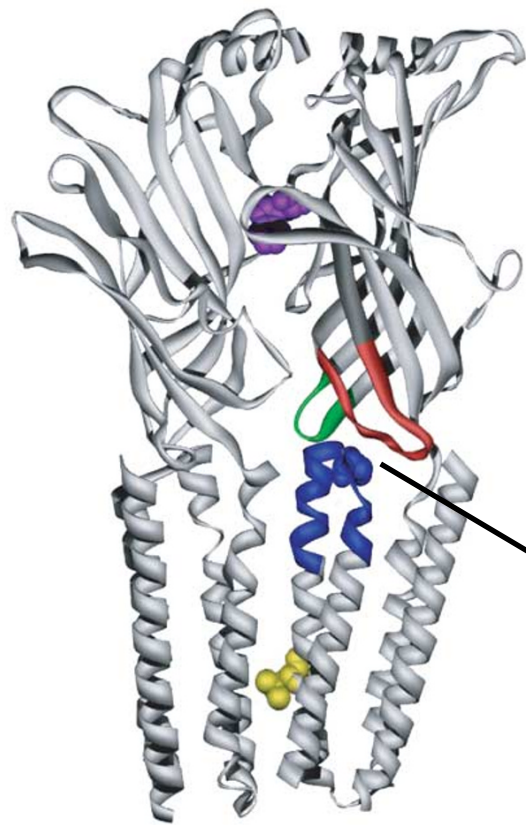
Expanding the Genetic Code

- The traditional genetic code
- Expanding the genetic code
 - In vitro
 - In eukaryotes, prokaryotes, and mammalian cells
- Orthogonal ribosomes
- Genetically recoded organisms and synonymous codon compression
- Outlook

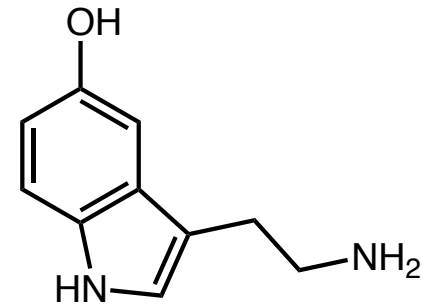


Incorporation of UAAs in Eukaryotic Systems

**5-hydroxytryptamine
type 3 receptor (5-HT₃)**



serotonin binding leads to
ion channel opening



5-hydroxytryptamine (serotonin)

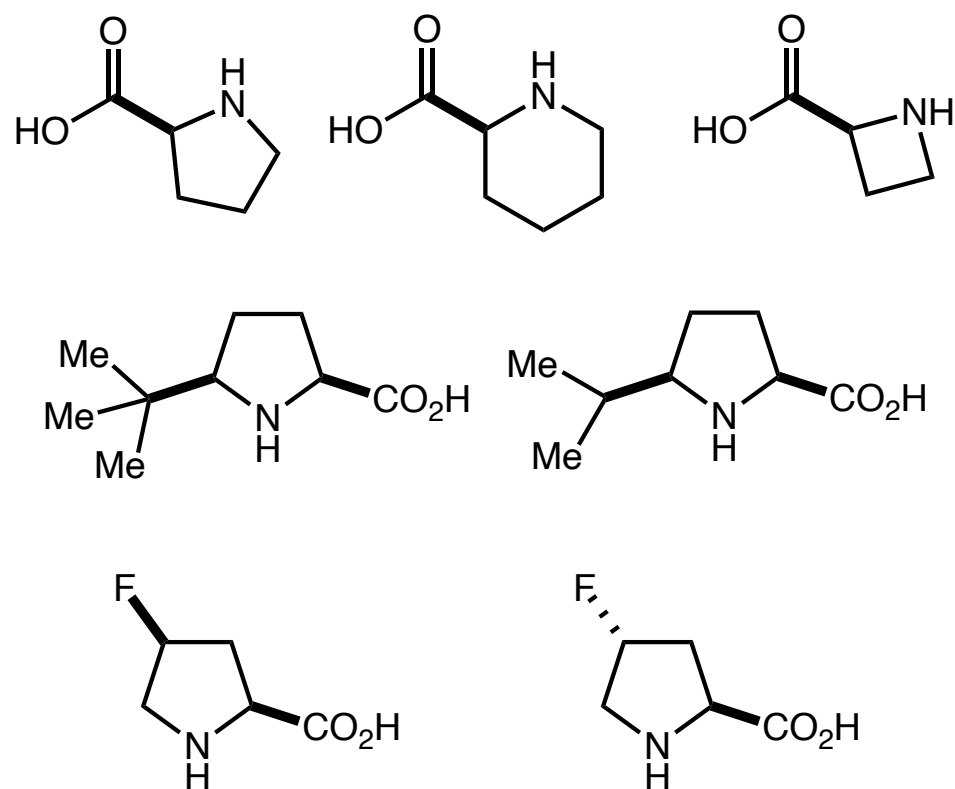
Proline 8

Hypothesis: Proline 8 plays an important role
linking serotonin binding to channel opening
through proline cis-trans isomerization

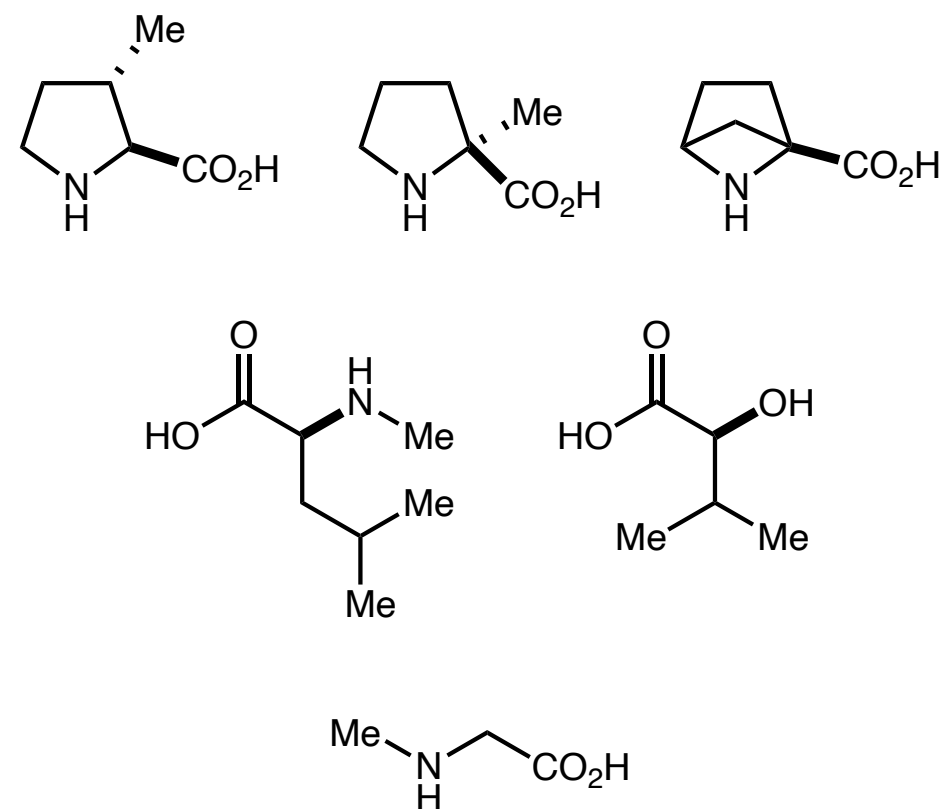
Question: How does cis-trans isomerization of proline 8 influence ion channel opening?

Incorporation of UAAs in Eukaryotic Systems

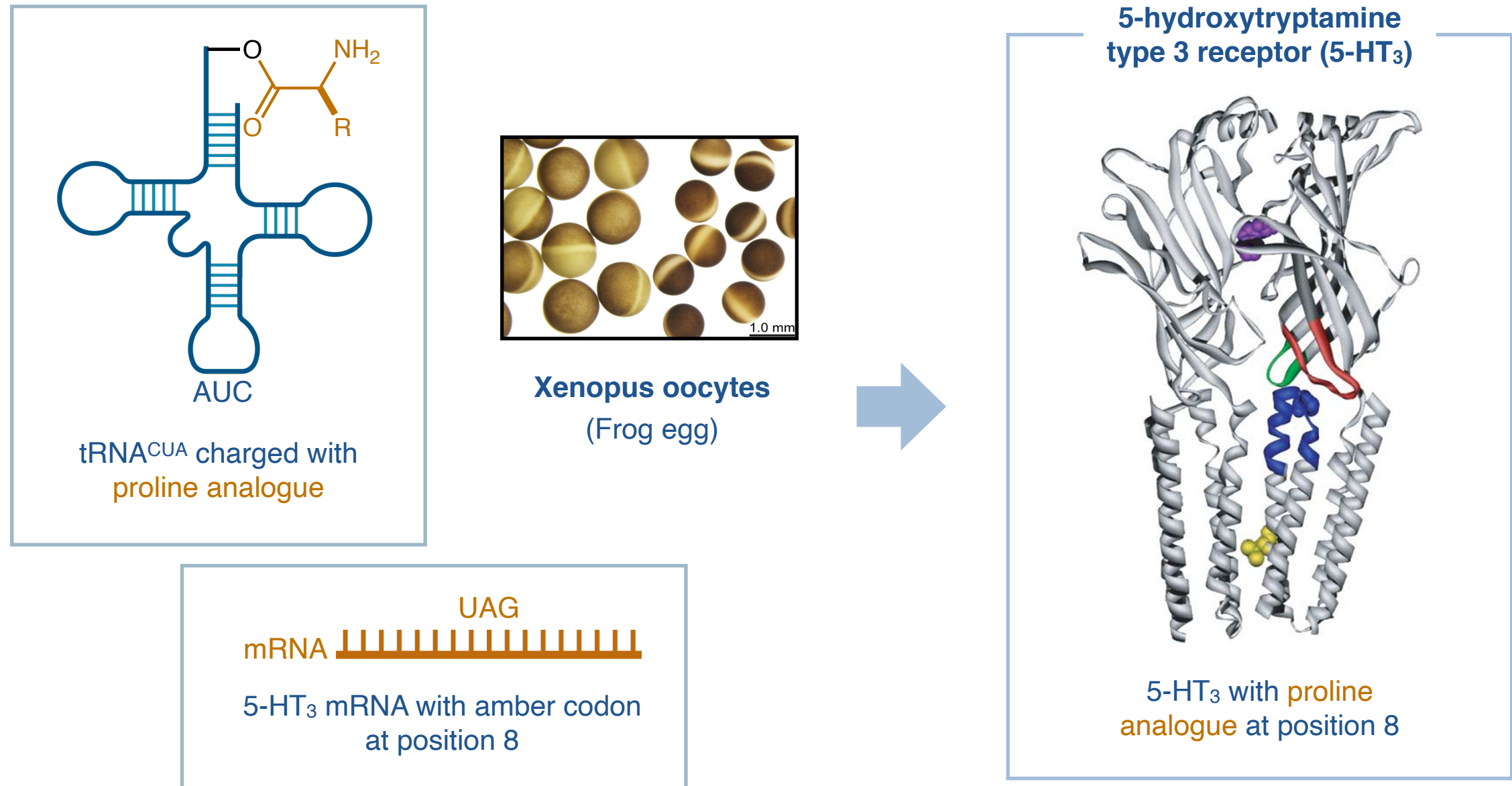
Proline analogues favoring the cis conformer



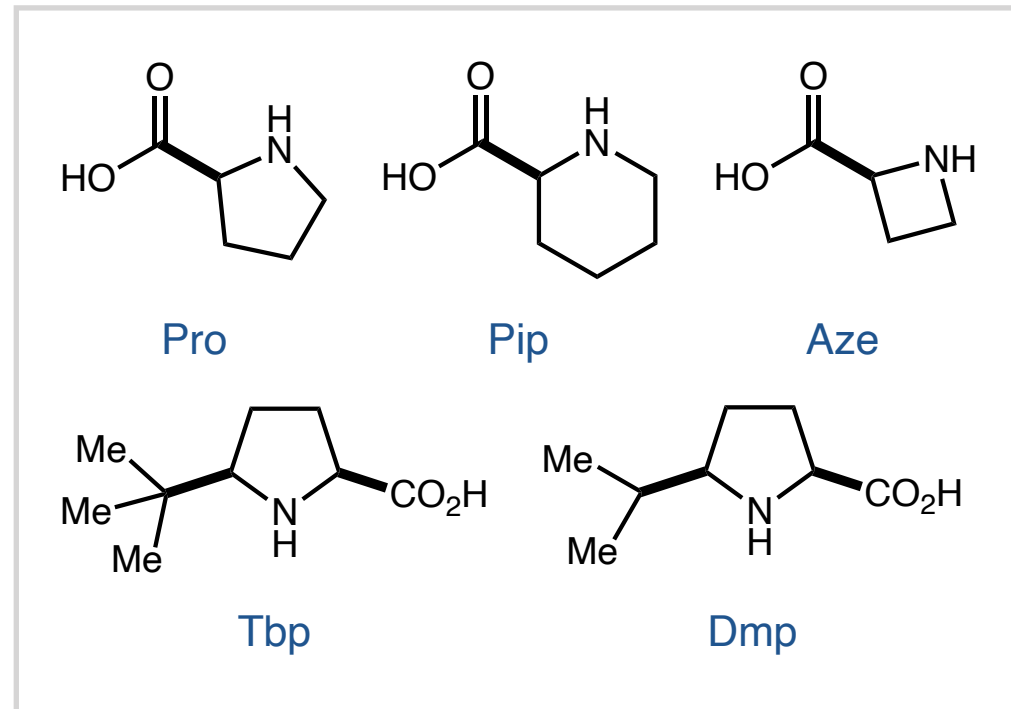
Proline analogues favoring the trans conformer



Incorporation of UAAs in Eukaryotic Systems



Incorporation of UAAs in Eukaryotic Systems

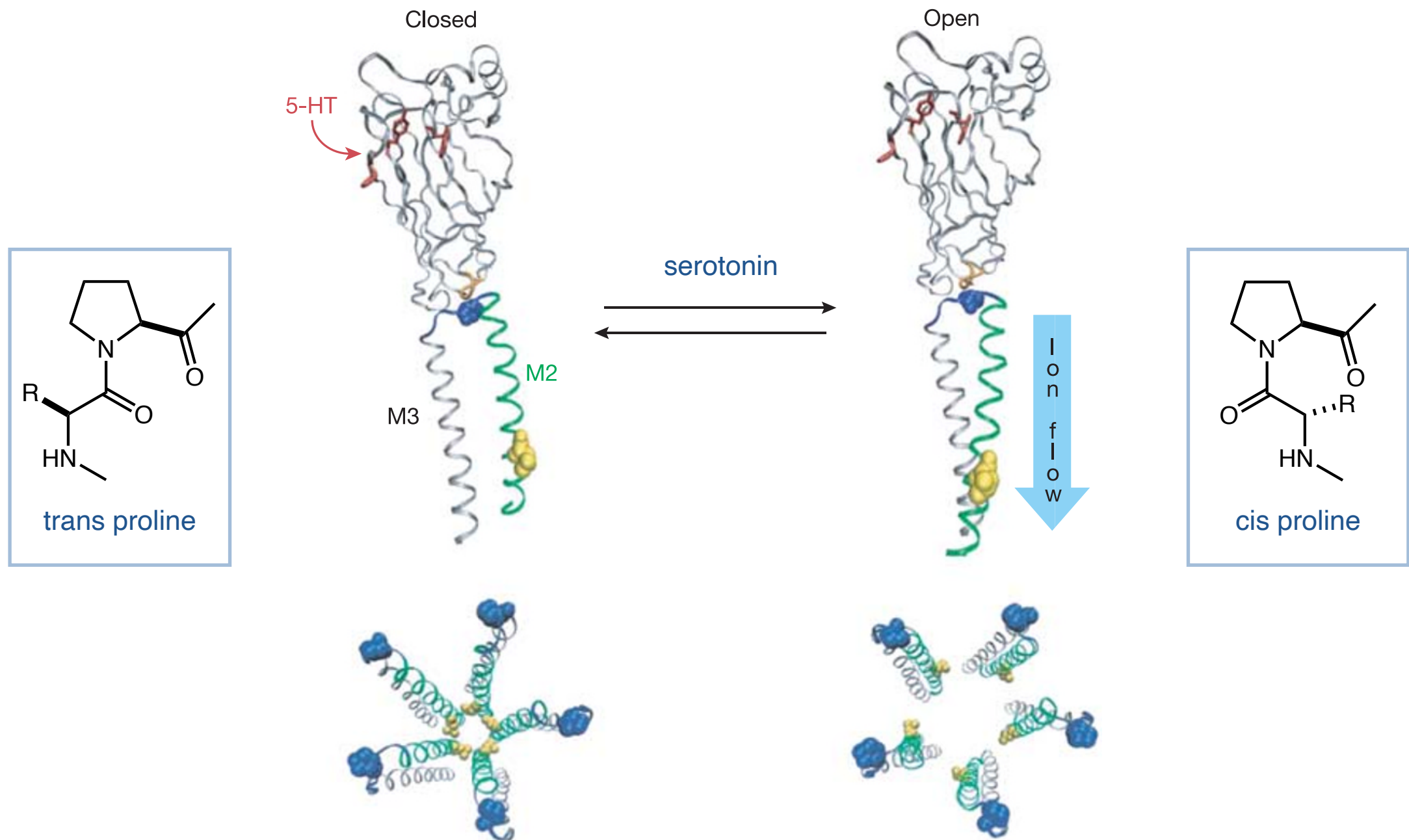


Residue	Per cent <i>cis</i> *	EC ₅₀ (μ M) [†]
Pro	5	1.29 \pm 0.07
Pip	12	0.75 \pm 0.06
Aze	18	0.42 \pm 0.03
Tbp	55	0.030 \pm 0.024
Dmp	71	0.021 \pm 0.009

Percent *cis* of proline isomer and EC₅₀ for serotonin dependent ion channel opening are correlated

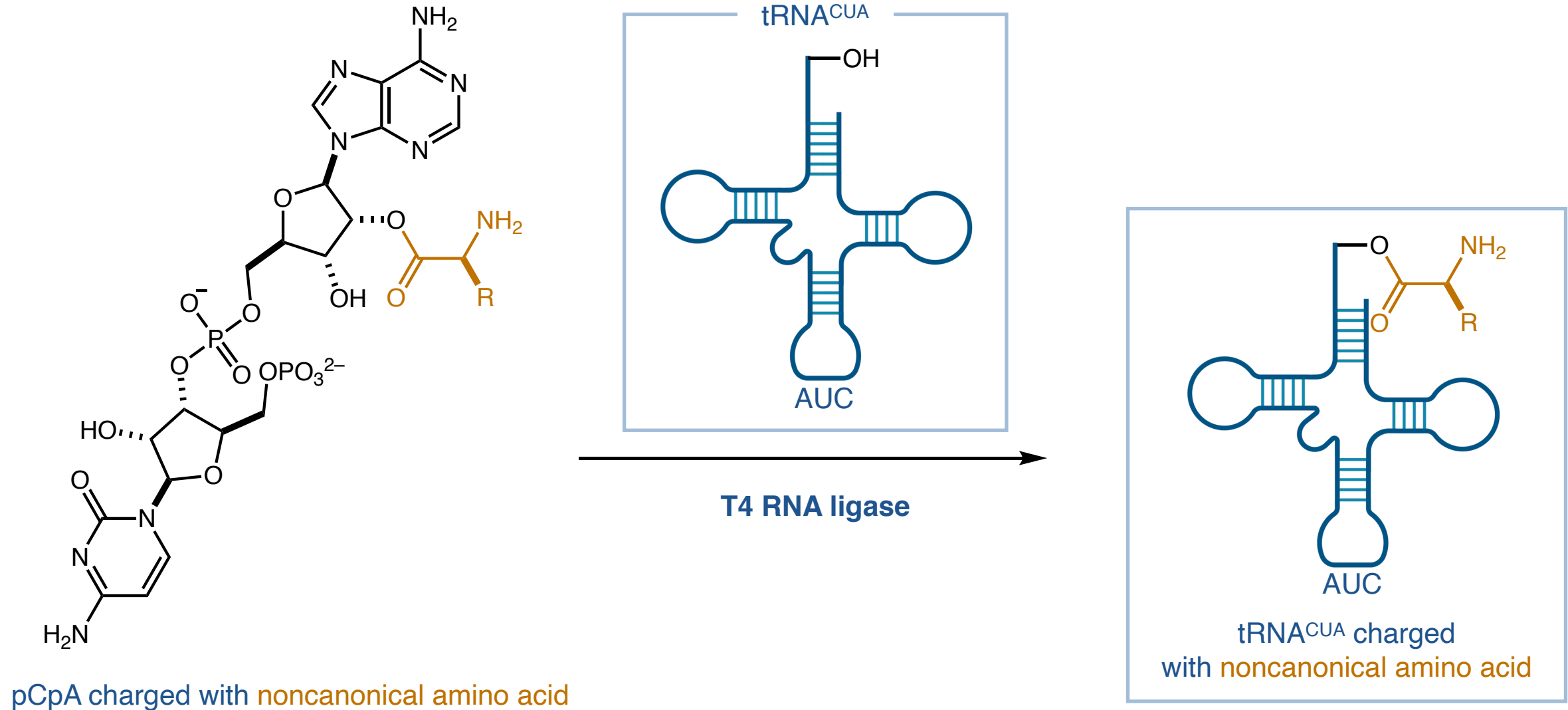
Proline analogues favoring the *cis* isomer produce an ion channel highly dependent on serotonin binding

Incorporation of UAAs in Eukaryotic Systems



Results suggest cis-trans isomerization of proline 8 interconverts the open and closed states of the ion channel

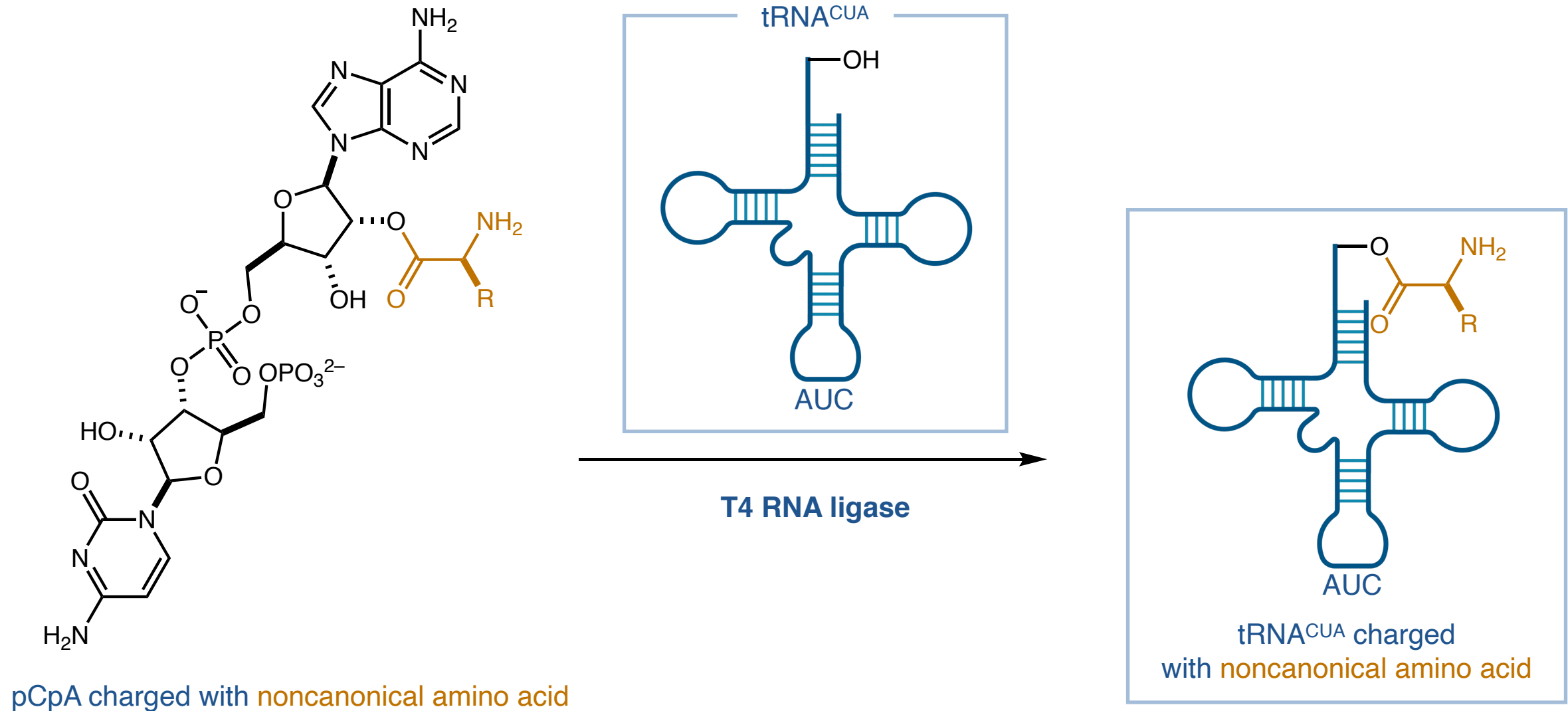
Noncanonical Amino Acid Incorporation in Live Cells



All works mentioned thus far prepared tRNA^{CUA} charged with non canonical amino acid via T4 RNA ligase

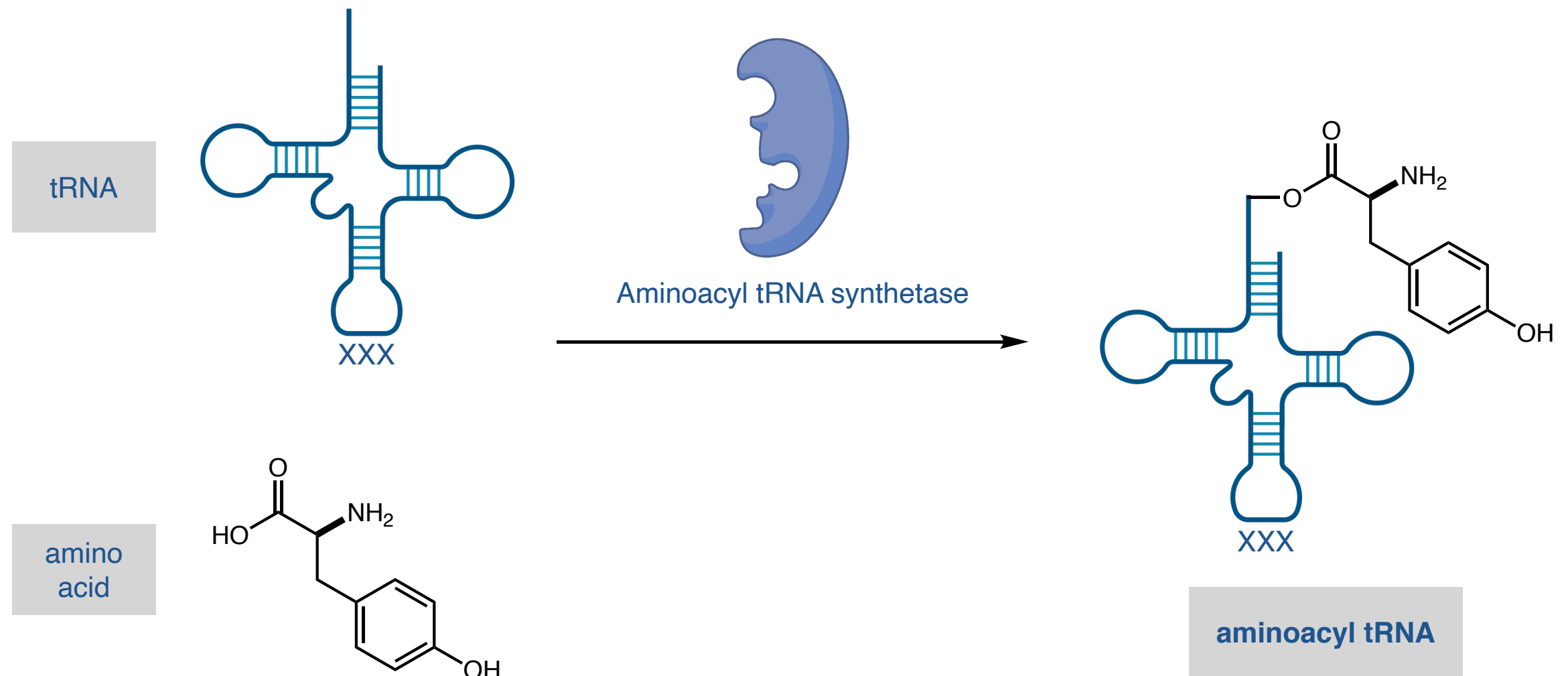
Question: Can the tRNA^{CUA} charged with the non canonical amino acid be generated directly in cells?

Noncanonical Amino Acid Incorporation in Live Cells



Solution: Express enzymatic machinery to generate aminoacylated tRNA directly in *E. coli*

Noncanonical Amino Acid Incorporation in Live Cells

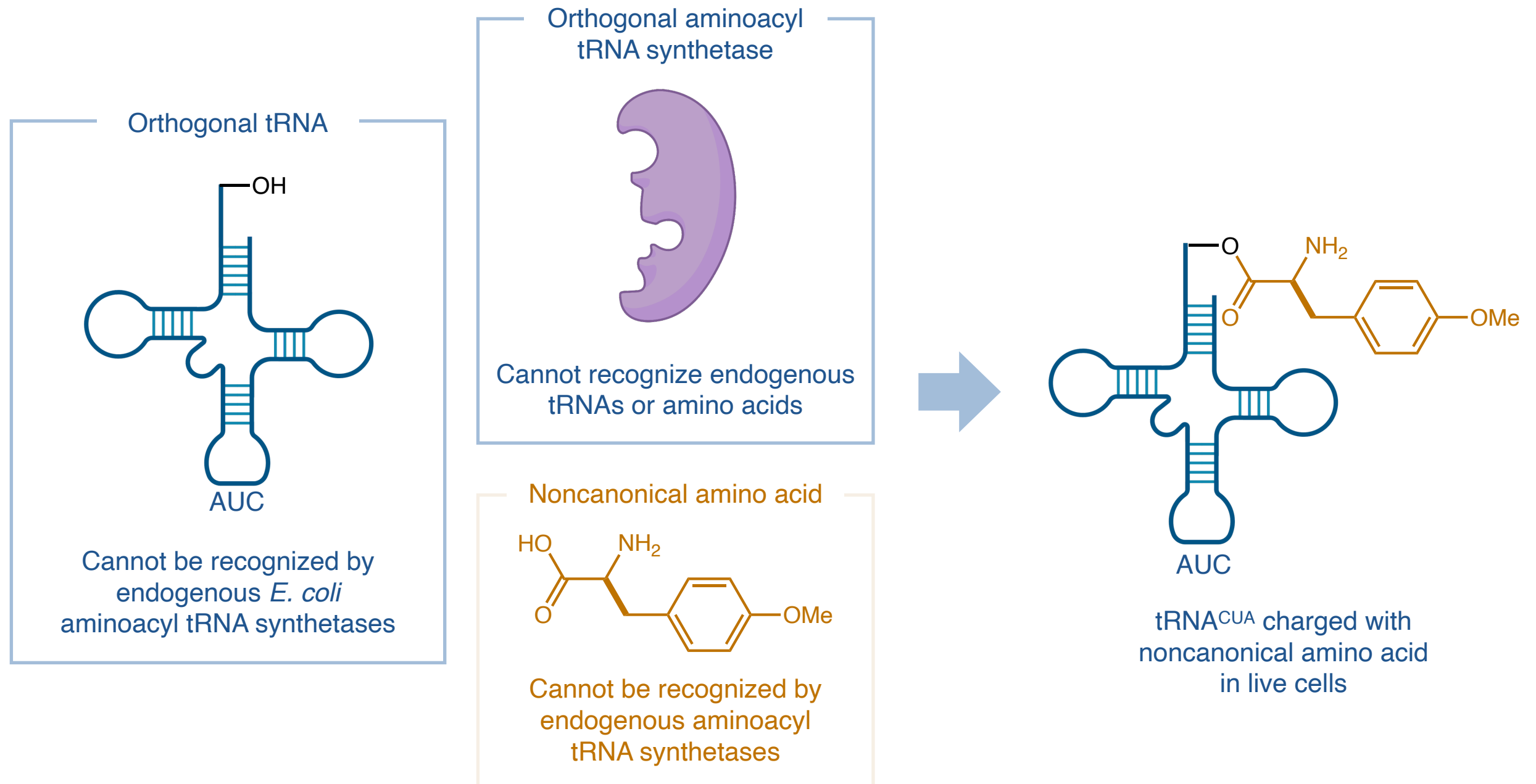


The aminoacyl tRNA synthetase is responsible for “charging” the tRNA with amino acid to form an aminoacyl tRNA

For the 20 canonical amino acids, there are at least 20 different aminoacyl tRNAs charged by 20 different aminoacyl tRNA synthetases

Noncanonical Amino Acid Incorporation in Live Cells

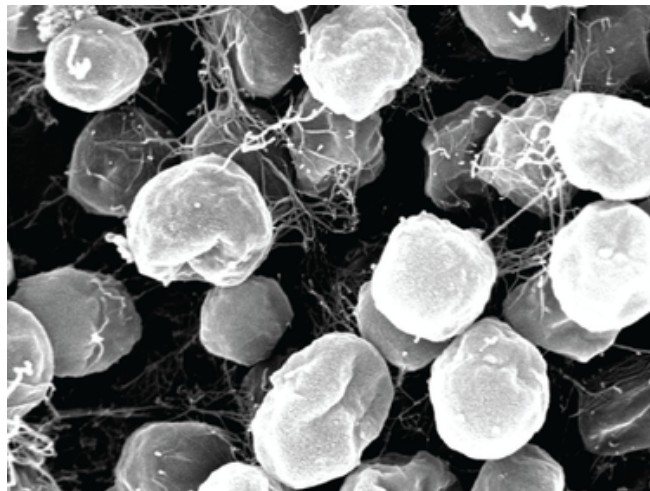
The quest for an orthogonal tRNA / aminoacyl tRNA synthetase pair to be used in *E. coli*



Noncanonical Amino Acid Incorporation in Live Cells

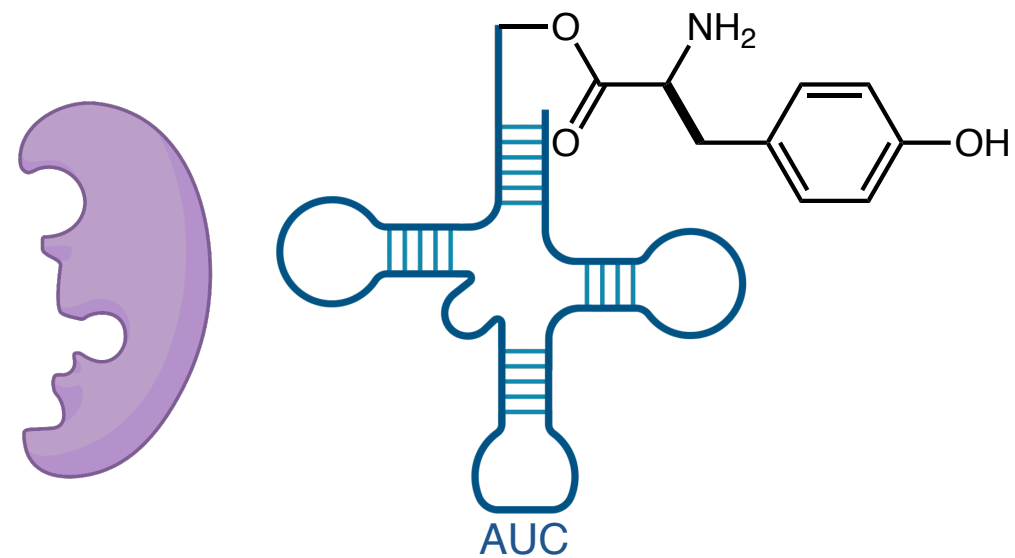
The quest for an orthogonal tRNA / aminoacyl tRNA synthetase pair to be used in *E. coli*

Methanococcus jannaschii



Hyperthermophilic organism belonging to the kingdom Archaea

*The tyrosyl tRNA / aminoacyl tRNA synthetase pair from *M. jannaschii**

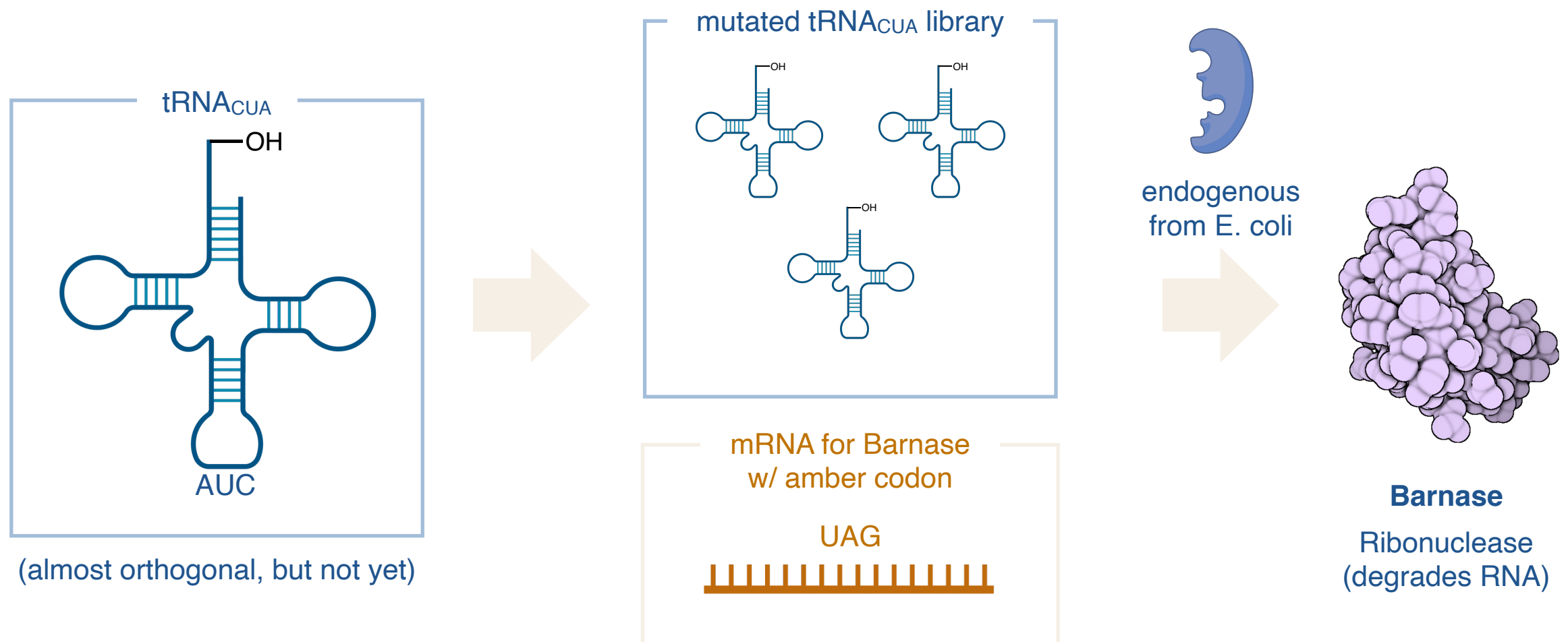


- tRNA synthetase not recognize *E. coli* tRNAs
- Previously shown to charge tRNA^{CUA} with Tyr
- Can perform amber suppression in *E. coli*

Can the tyrosyl tRNA / aminoacyl tRNA synthetase pair from *Methanococcus* be evolved to be orthogonal?

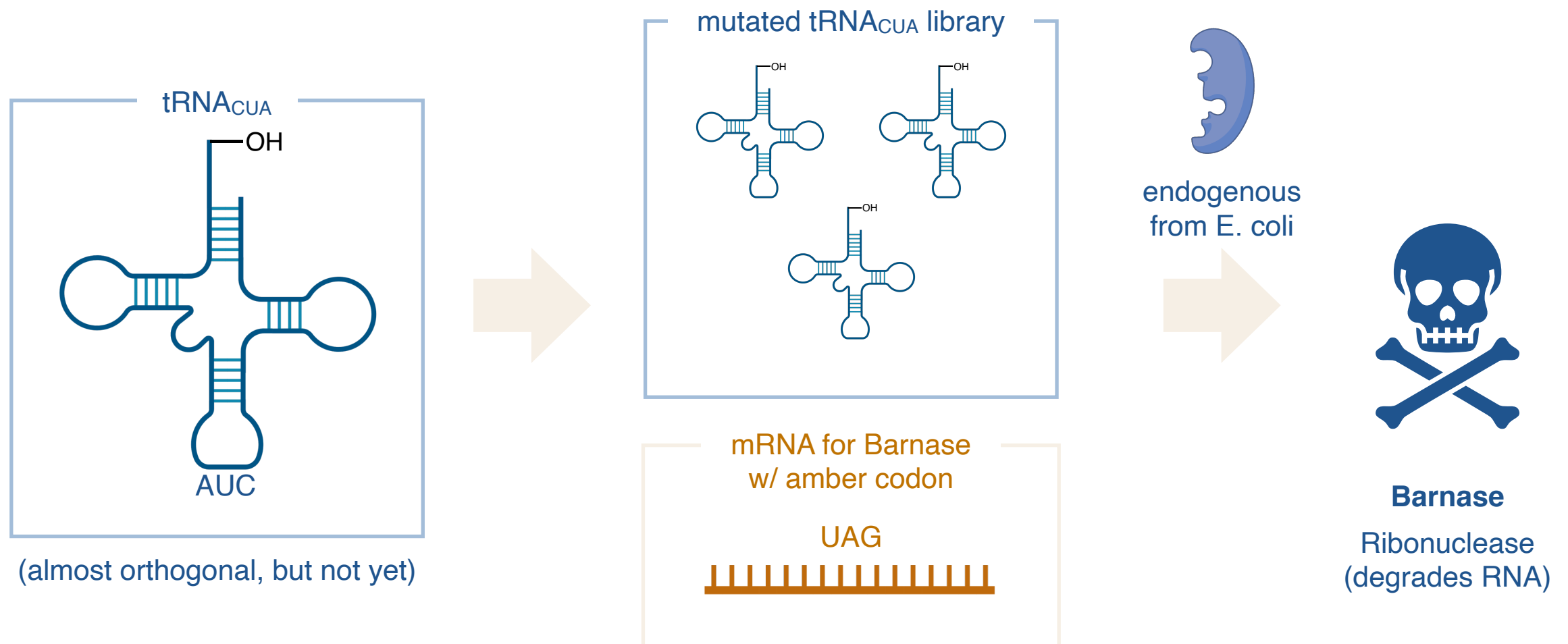
Noncanonical Amino Acid Incorporation in Live Cells

Problem: orthogonal tRNA is still recognized by E. Coli aminoacyl tRNA synthetases



Noncanonical Amino Acid Incorporation in Live Cells

Problem: orthogonal tRNA is still recognized by E. Coli aminoacyl tRNA synthetases



Negative selection: If endogenous aminoacyl tRNA synthetase charges $tRNA_{CUA}$, barnase is produced, leading to cell death

Result: Orthogonal $tRNA^{CUA}$ that cannot be recognized by E. coli aminoacyl tRNA synthetases

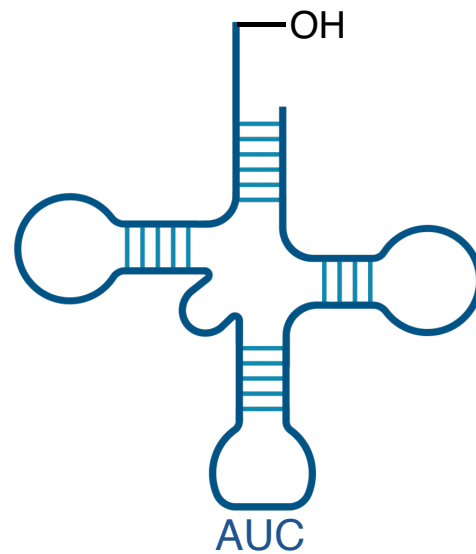
Noncanonical Amino Acid Incorporation in Live Cells

Goal: Evolve an orthogonal aminoacyl tRNA synthetase

aminoacyl tRNA
synthetase
from *M. jannaschii*

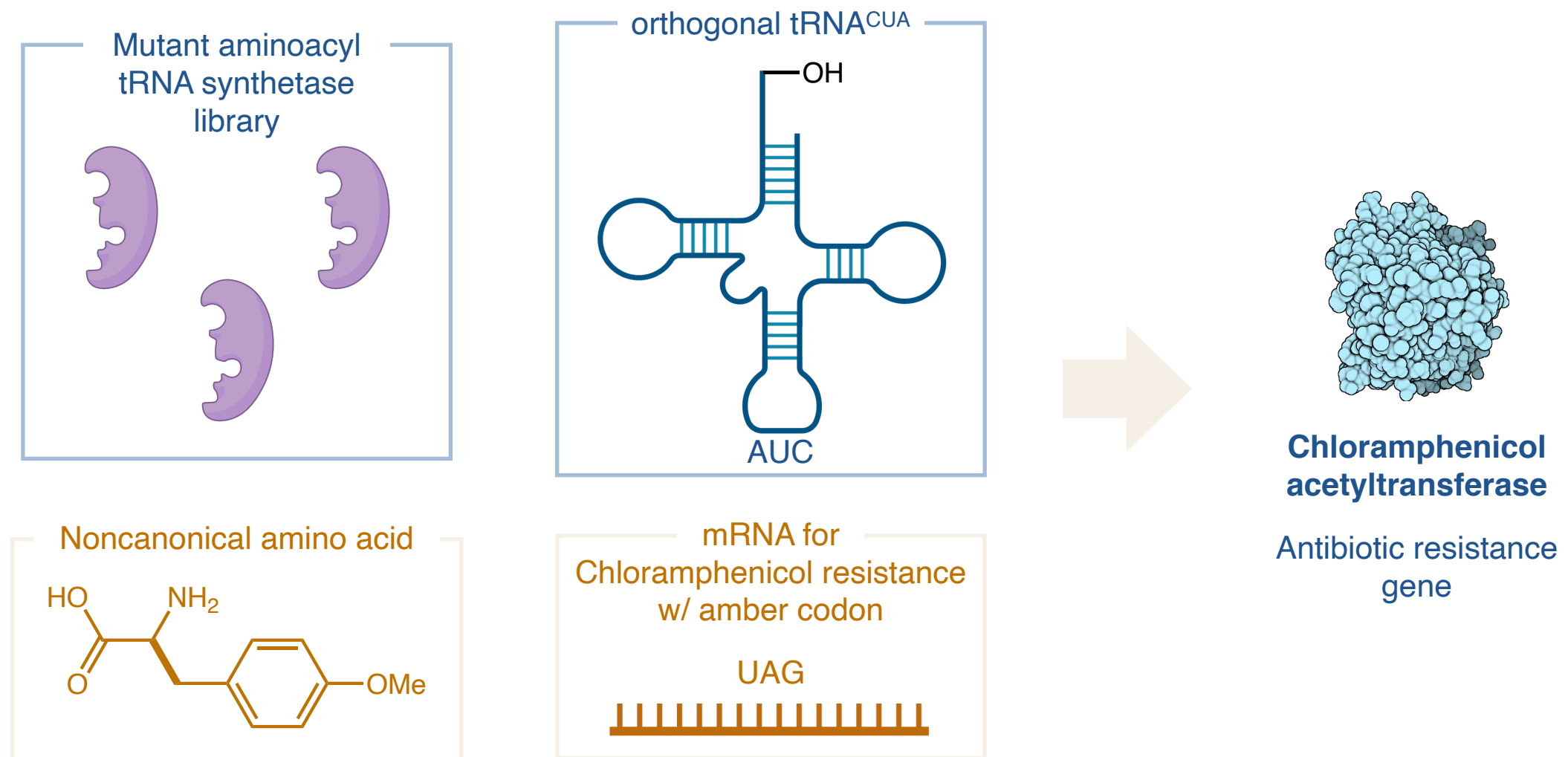


orthogonal tRNA^{CUA}



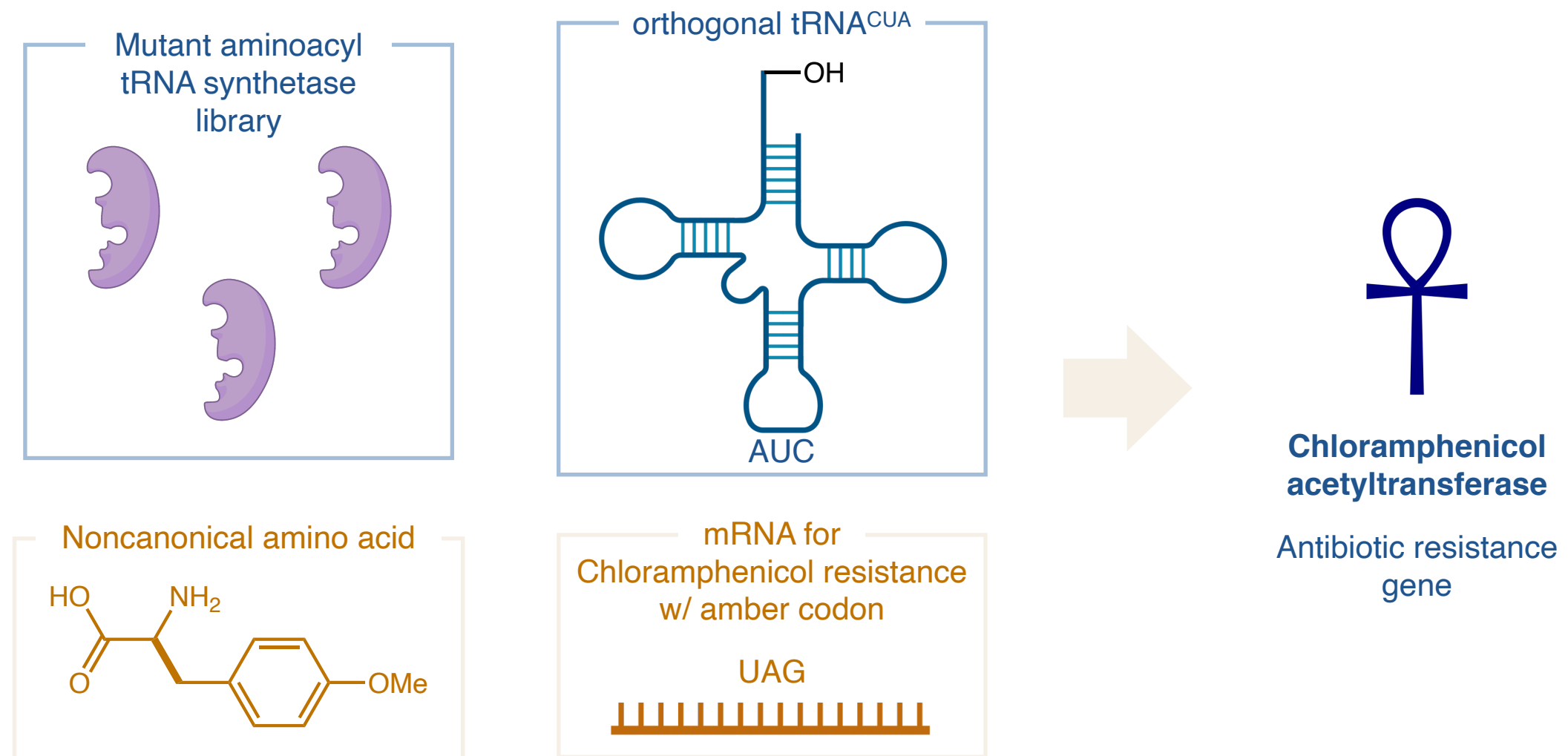
Noncanonical Amino Acid Incorporation in Live Cells

Goal: Evolve an orthogonal aminoacyl tRNA synthetase



Noncanonical Amino Acid Incorporation in Live Cells

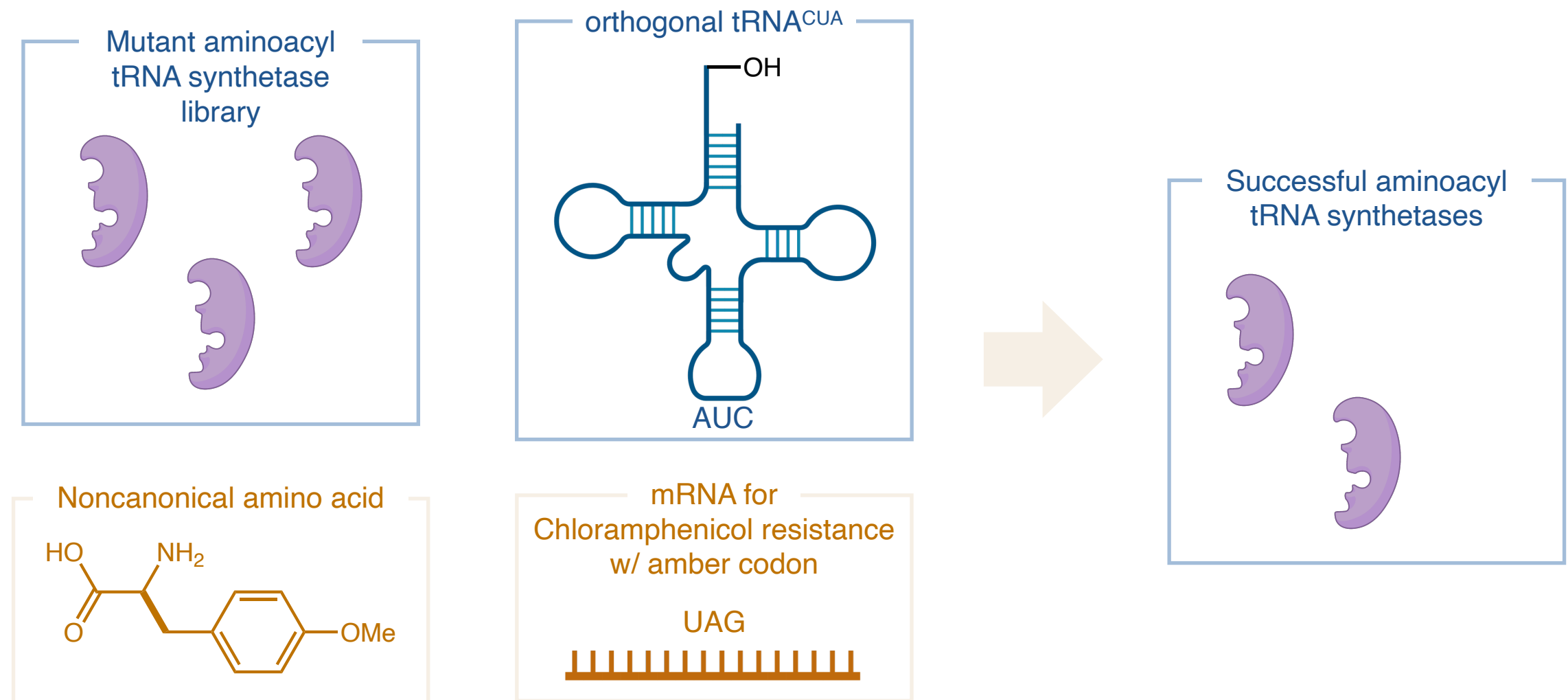
Goal: Evolve an orthogonal aminoacyl tRNA synthetase



Positive selection: If the mutant aminoacyl tRNA synthetase can charge tRNA^{CUA} with any amino acid, the cells are antibiotic resistant

Noncanonical Amino Acid Incorporation in Live Cells

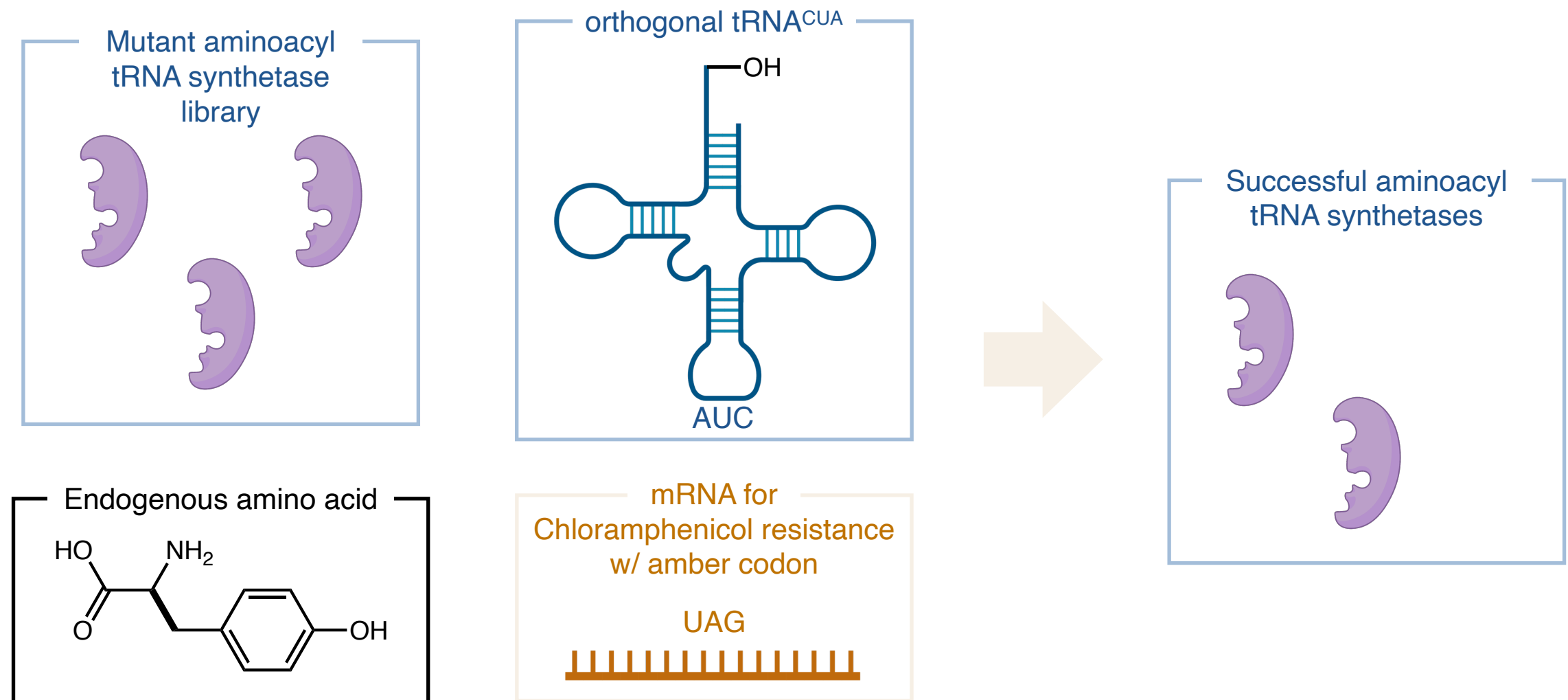
Goal: Evolve an orthogonal aminoacyl tRNA synthetase



Positive selection: If the mutant aminoacyl tRNA synthetase can charge tRNA^{CUA} with any amino acid, the cells are antibiotic resistant

Noncanonical Amino Acid Incorporation in Live Cells

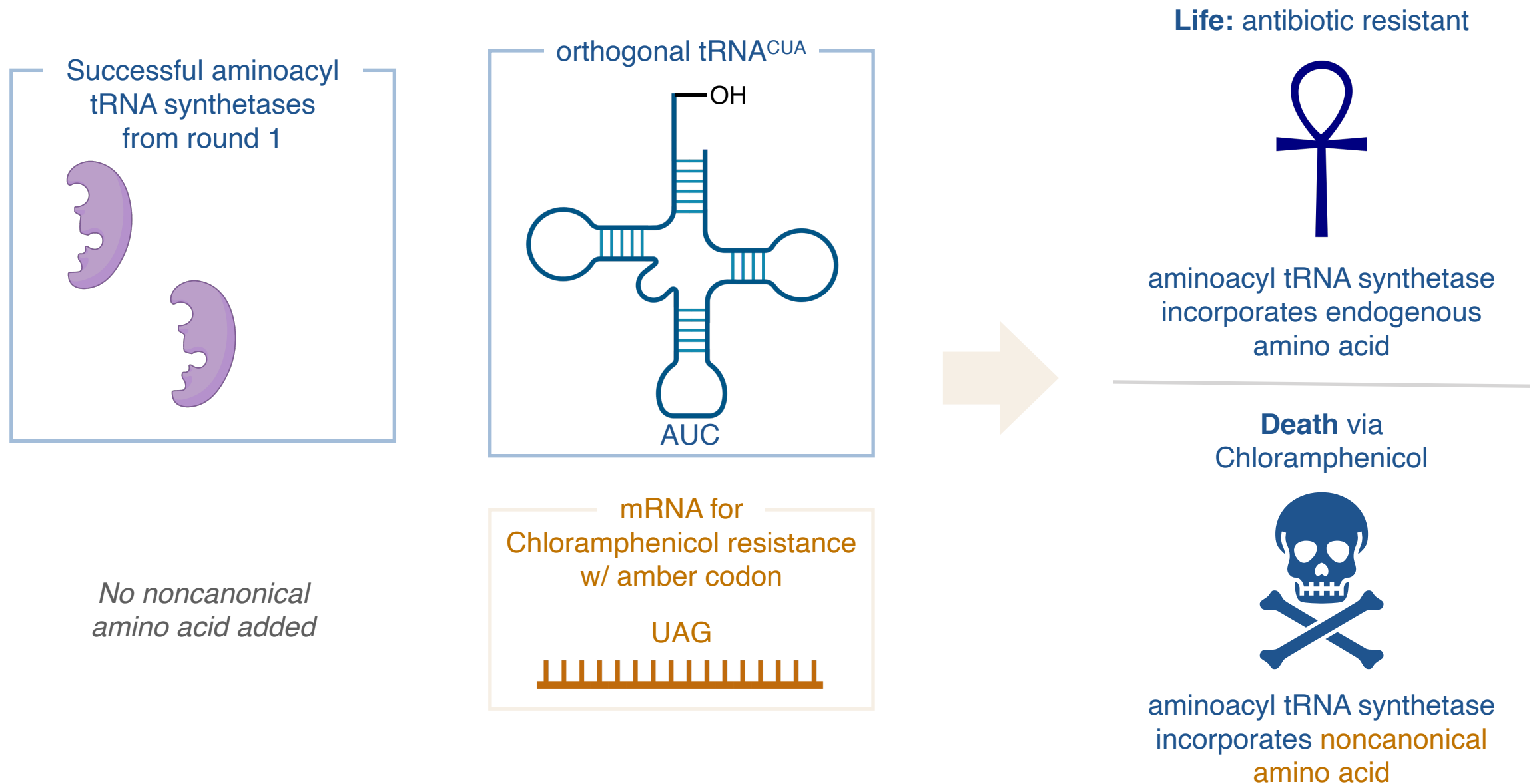
Goal: Evolve an orthogonal aminoacyl tRNA synthetase



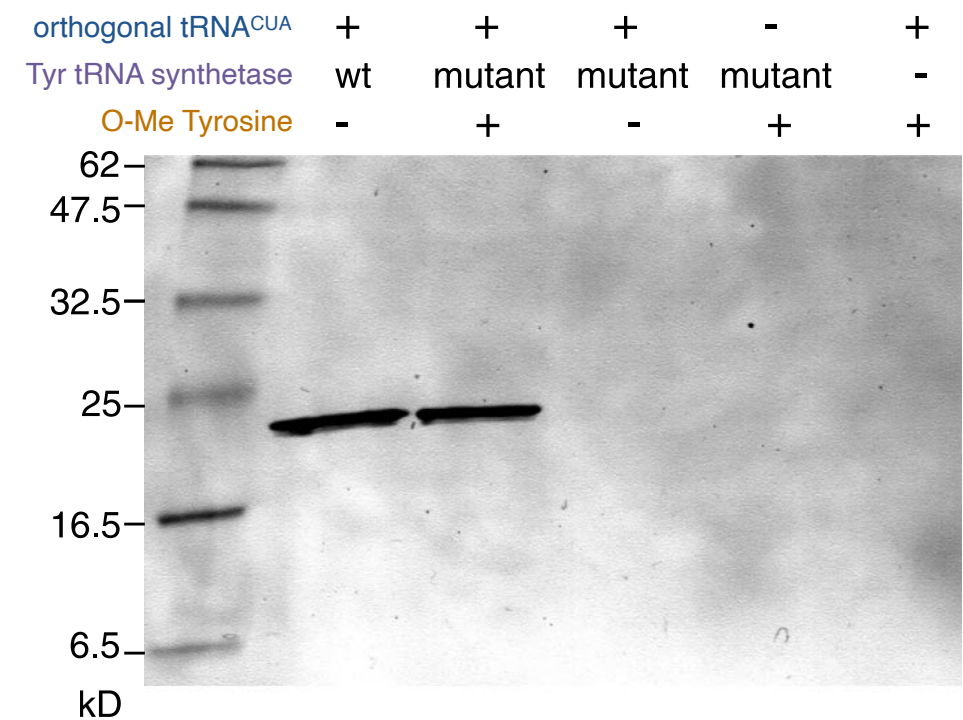
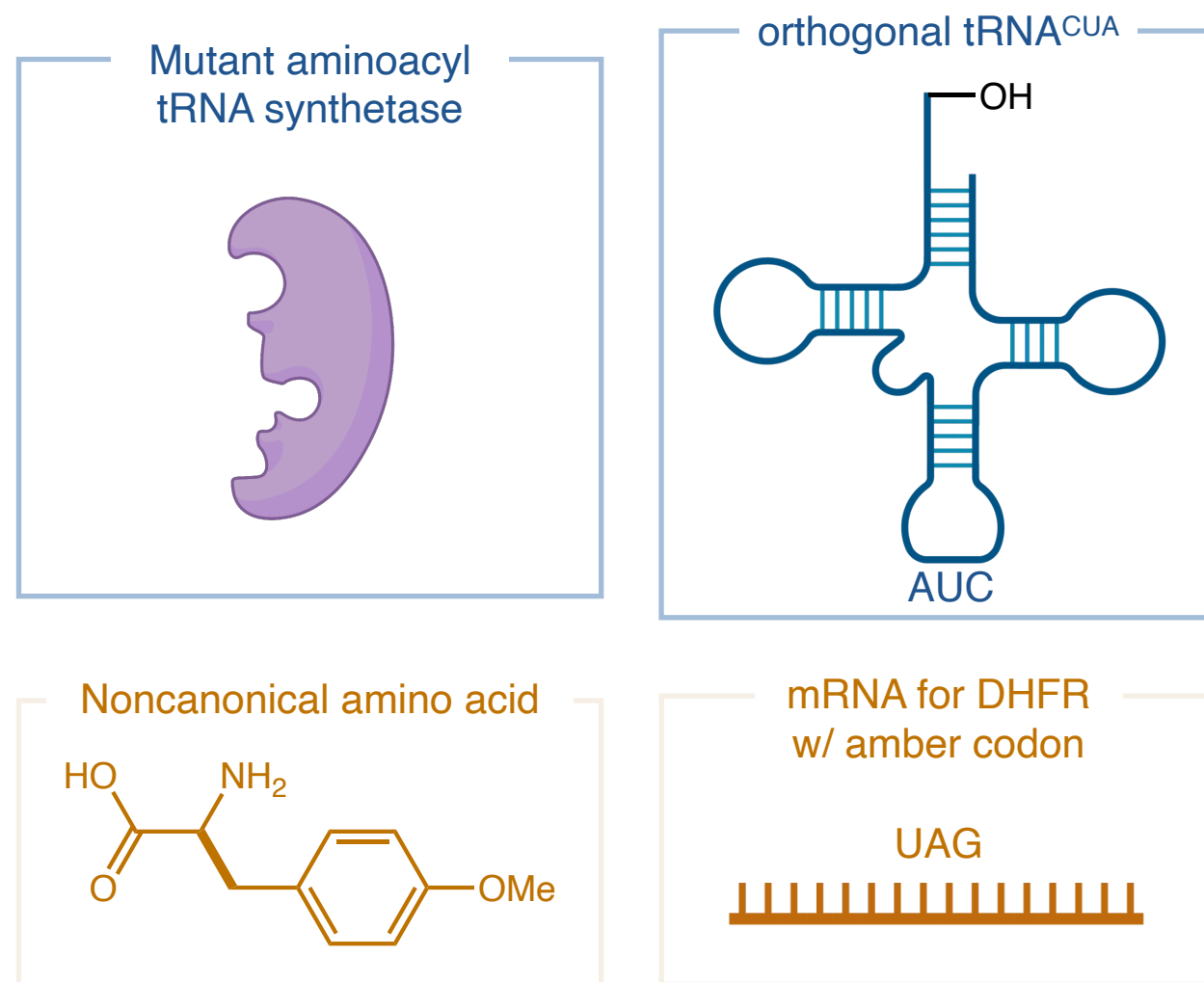
Problem: The mutant aminoacyl tRNA synthetase can charge tRNA^{CUA} with an endogenous amino acid and still survive

Noncanonical Amino Acid Incorporation in Live Cells

Goal: Evolve an orthogonal aminoacyl tRNA synthetase



Noncanonical Amino Acid Incorporation in Live Cells



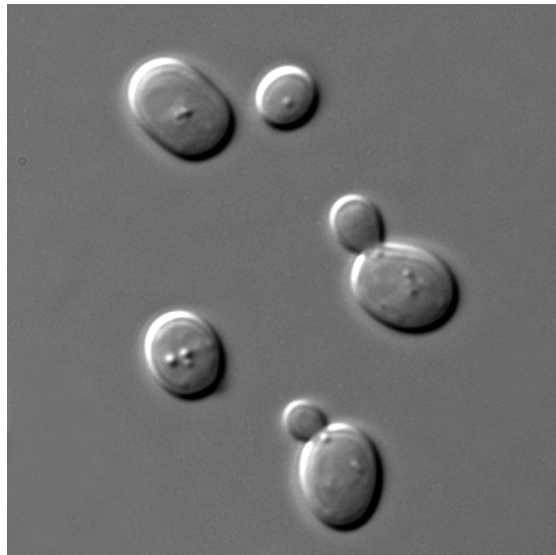
Orthogonal tRNA synthetase / tRNA pair incorporates O-Me tyrosine into DHFR

All components required for expression of DHFR with noncanonical amino acid

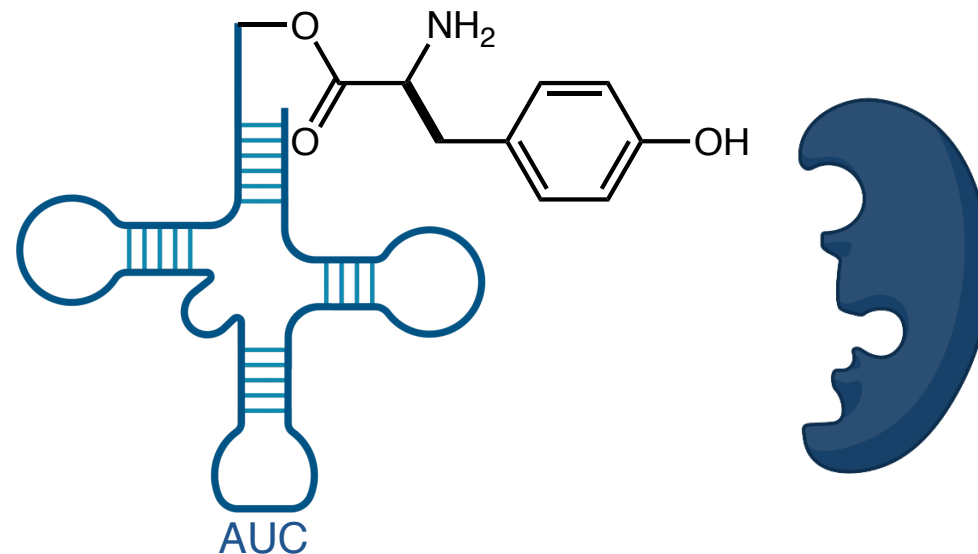
Noncanonical Amino Acid Incorporation in Yeast

Goal: Evolve an orthogonal aminoacyl tRNA synthetase for use in yeast

Yeast

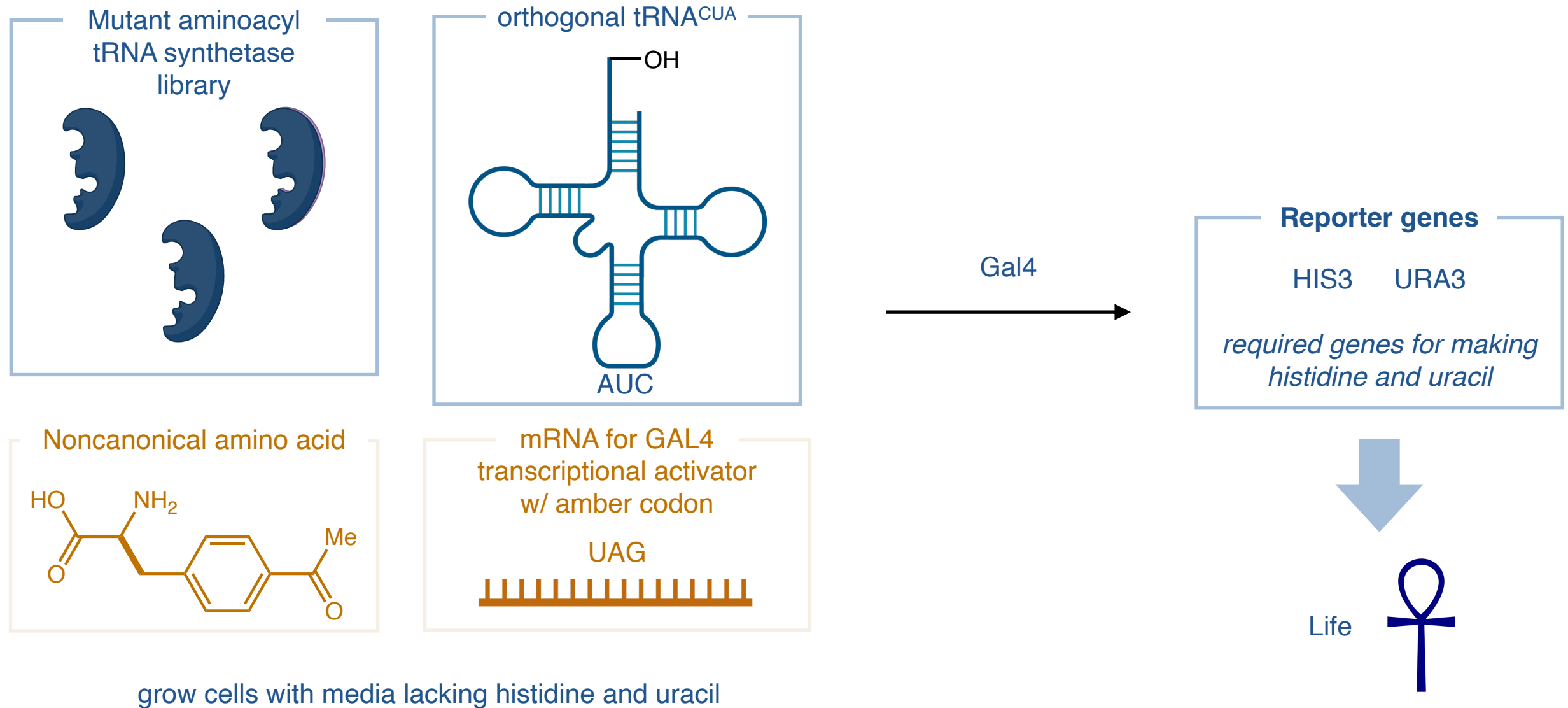


The tyrosyl tRNA / aminoacyl tRNA synthetase pair from *E. coli*



Noncanonical Amino Acid Incorporation in Yeast

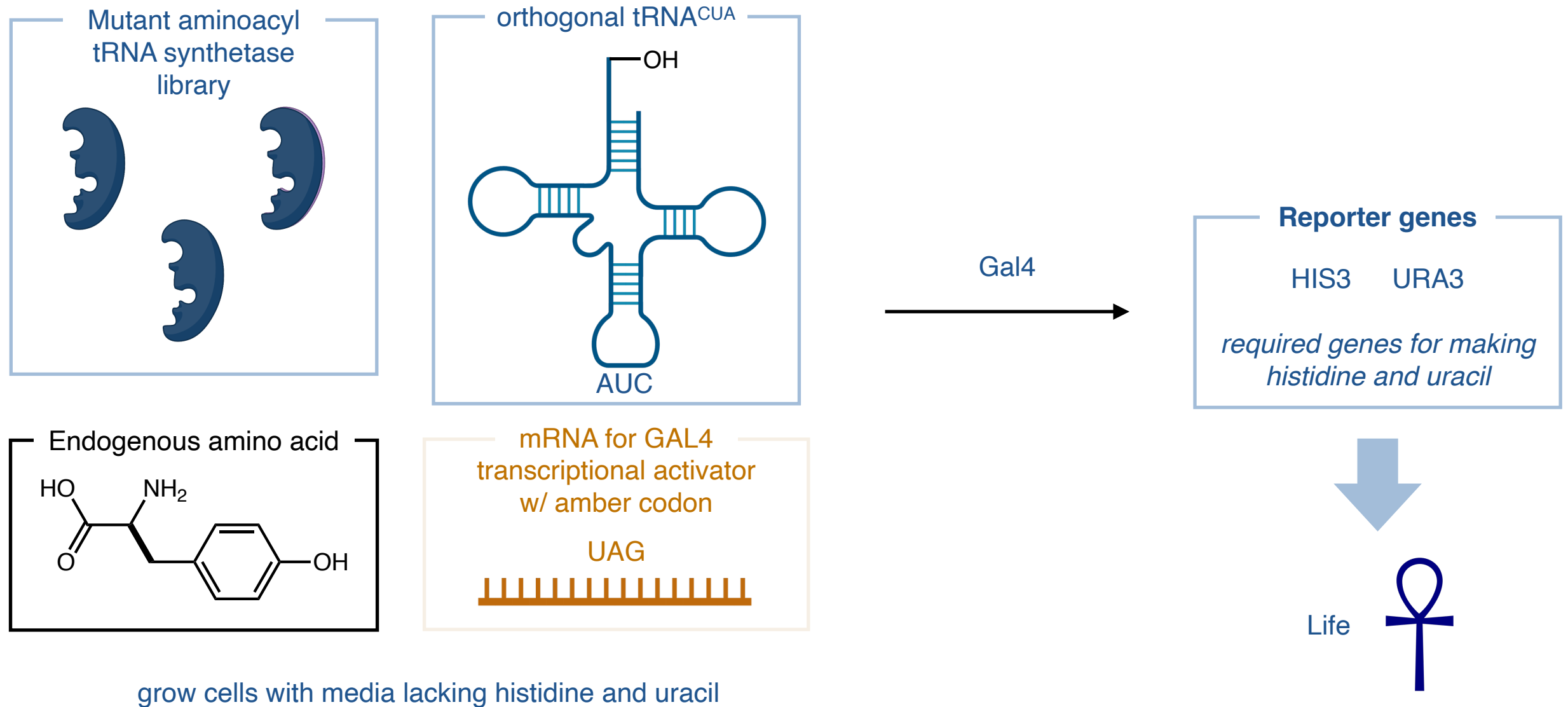
Goal: Evolve an orthogonal aminoacyl tRNA synthetase for use in yeast



Positive selection: If the mutant aminoacyl tRNA synthetase can charge tRNA^{CUA} with any amino acid, the cells produce histidine and uracil and live

Noncanonical Amino Acid Incorporation in Yeast

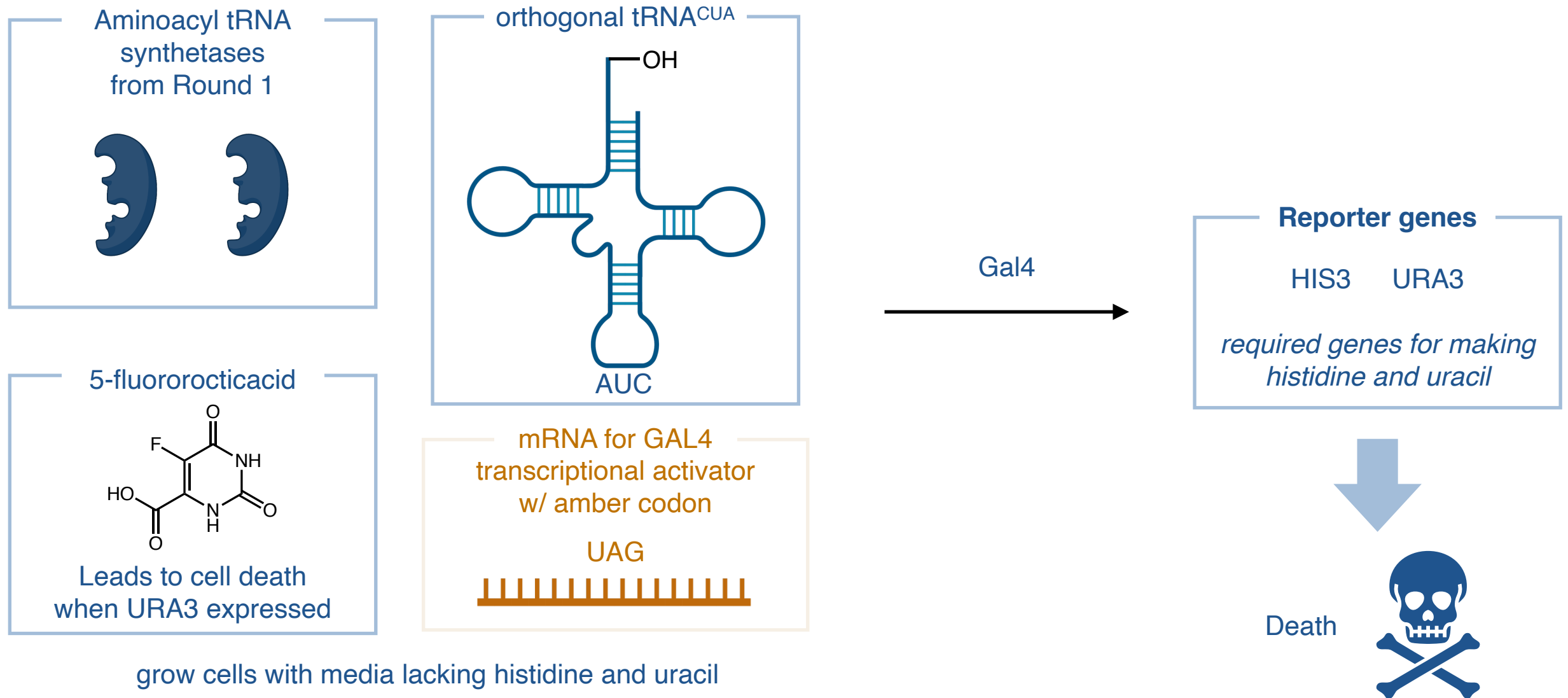
Goal: Evolve an orthogonal aminoacyl tRNA synthetase for use in yeast



Positive selection: If the mutant aminoacyl tRNA synthetase can charge tRNA^{CUA} with any amino acid, the cells produce histidine and uracil and live

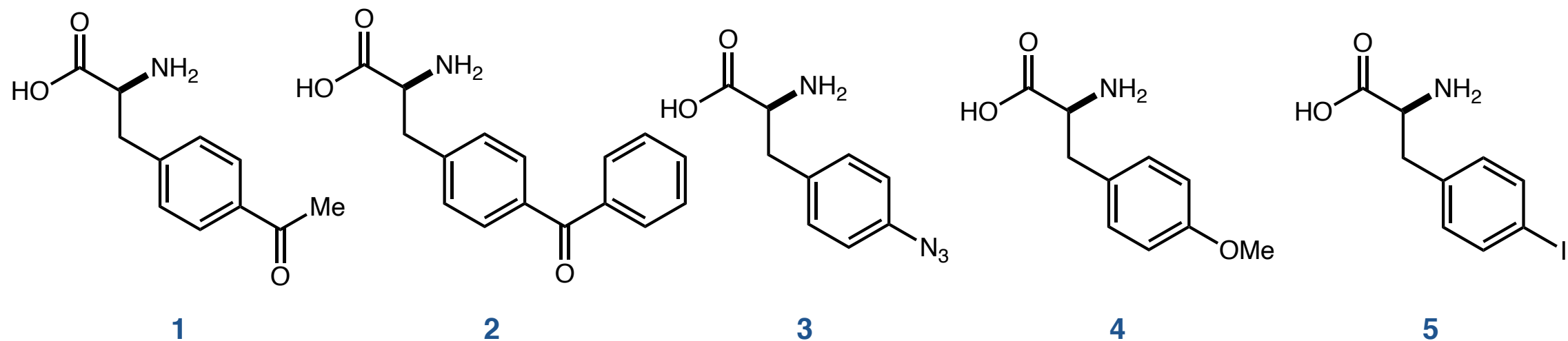
Noncanonical Amino Acid Incorporation in Yeast

Goal: Evolve an orthogonal aminoacyl tRNA synthetase for use in yeast

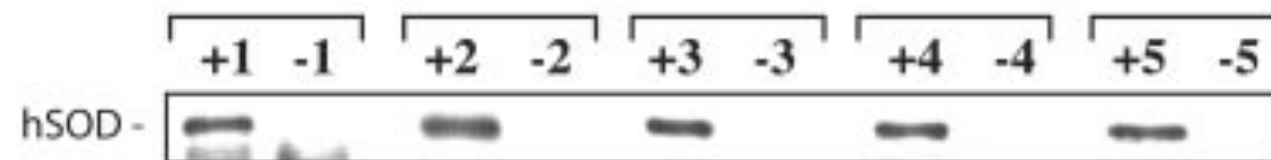


Negative selection: If the mutant aminoacyl tRNA synthetase can charge tRNA^{CUA} with an endogenous amino acid, URA3 will be expressed, and the cell will die via 5-fluoroorotic acid

Noncanonical Amino Acid Incorporation in Yeast



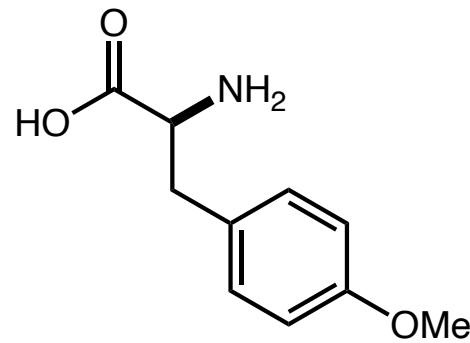
Unique aminoacyl tRNA synthetase evolved for each noncanonical amino acid



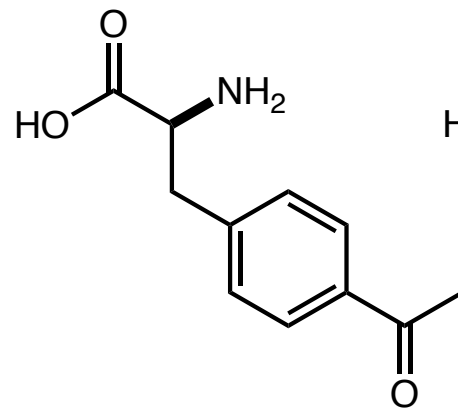
Noncanonical amino acids are successfully incorporated into human superoxide dismutase (hSOD) in yeast

Noncanonical Amino Acid Incorporation in Mammalian Cells

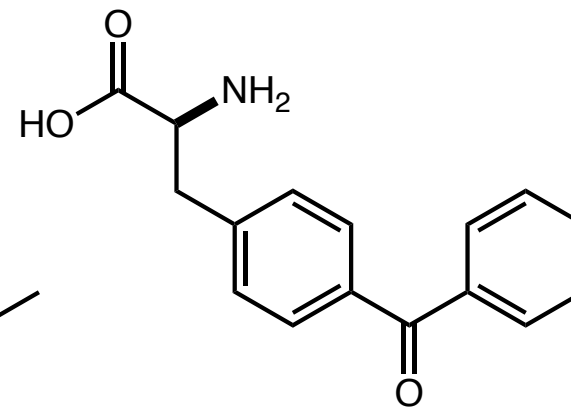
Noncanonical amino acid incorporation in CHO and 293T cells



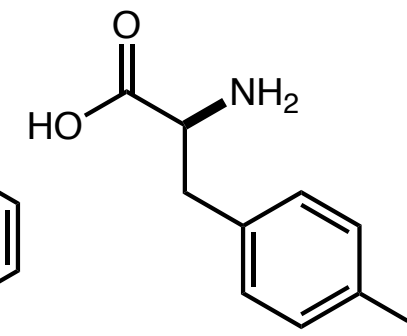
pMpa



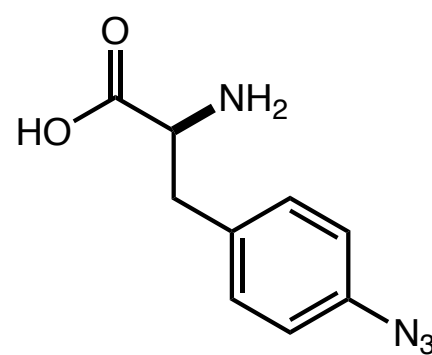
pApa



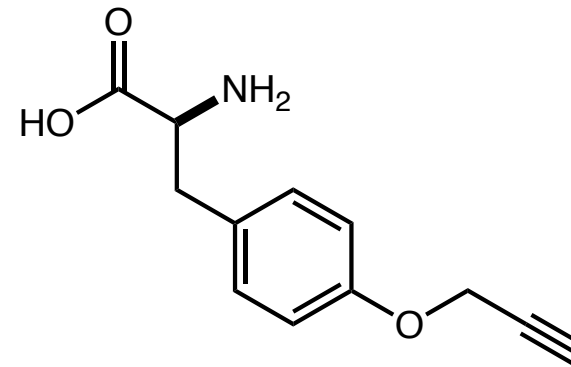
pBpa



plpa



pAzpa

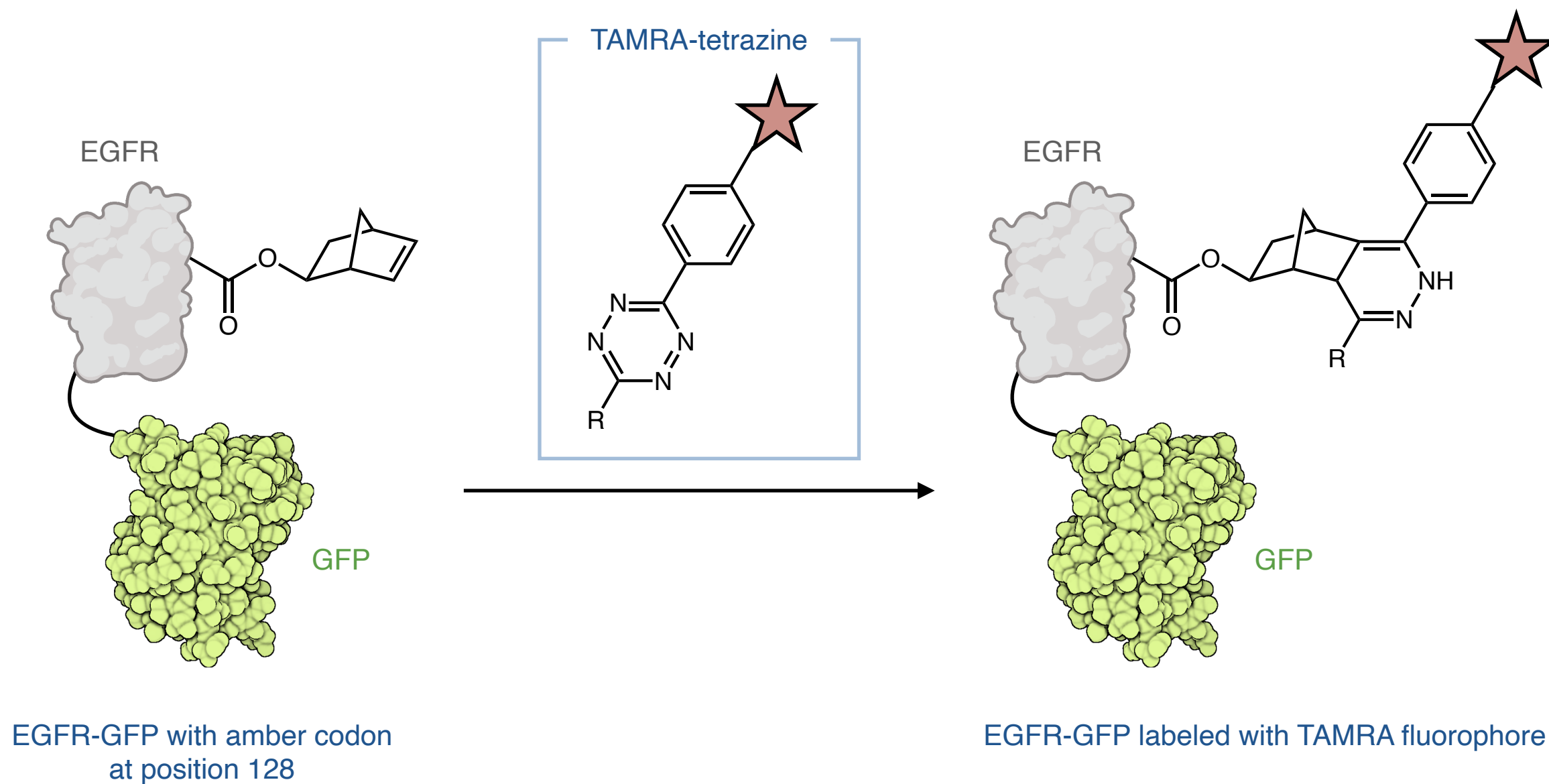


pPpa

A unique aminoacyl tRNA synthetase was evolved for each amino acid

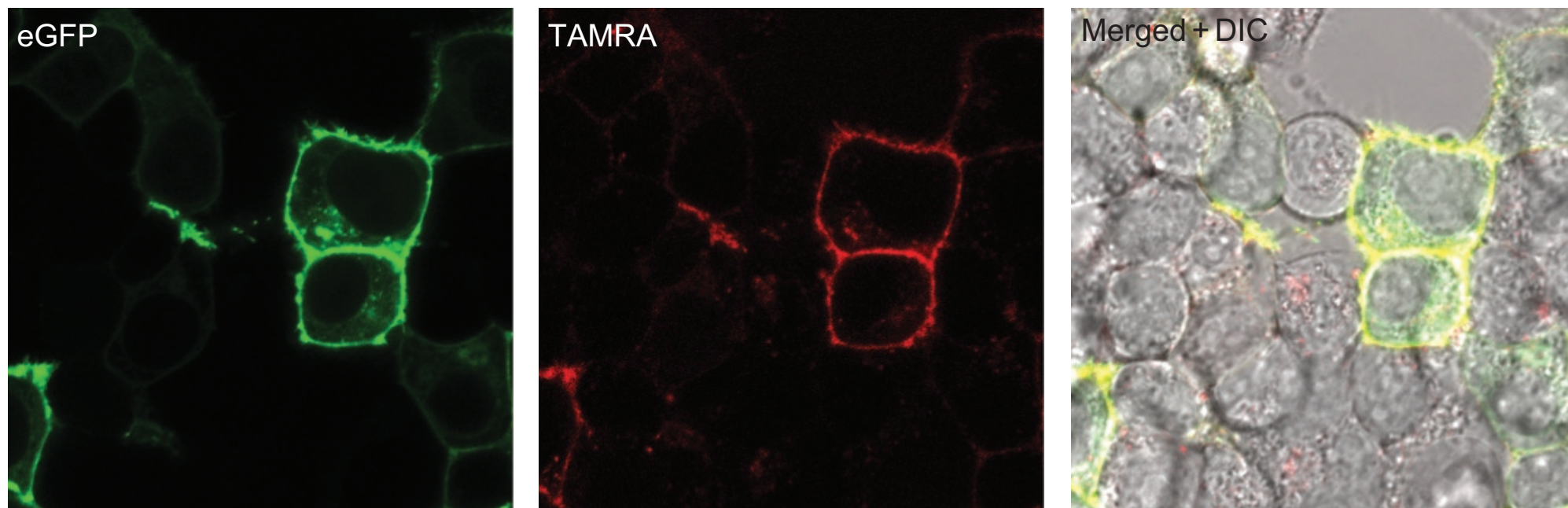
Noncanonical Amino Acid Incorporation in Mammalian Cells for Imaging

Imaging cell surface proteins via bioorthogonal click chemistry



Noncanonical Amino Acid Incorporation in Mammalian Cells for Imaging

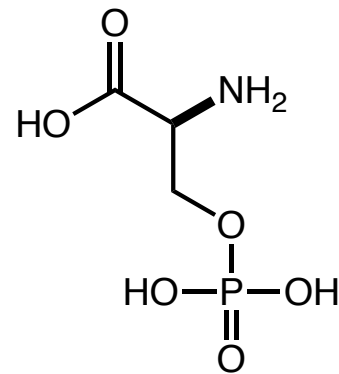
Imaging cell surface proteins via bioorthogonal click chemistry



eGFP and TAMRA signal colocalize

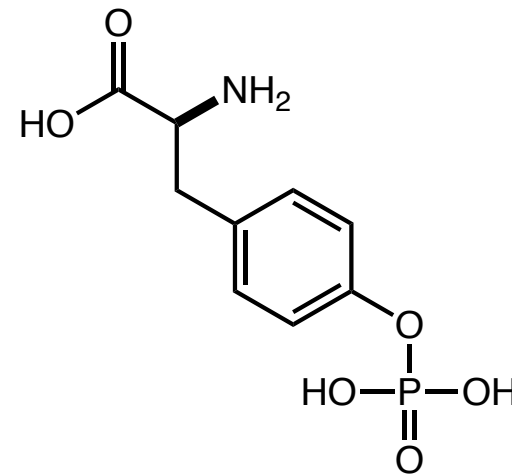
Genetic Encoding of Traceless Post-Translational Modifications

Phosphorylation of a protein can lead to activation, deactivation, degradation, or membrane transport



Phosphoserine

Science 2011



Phosphotyrosine

Nat. Chem. Biol. 2017

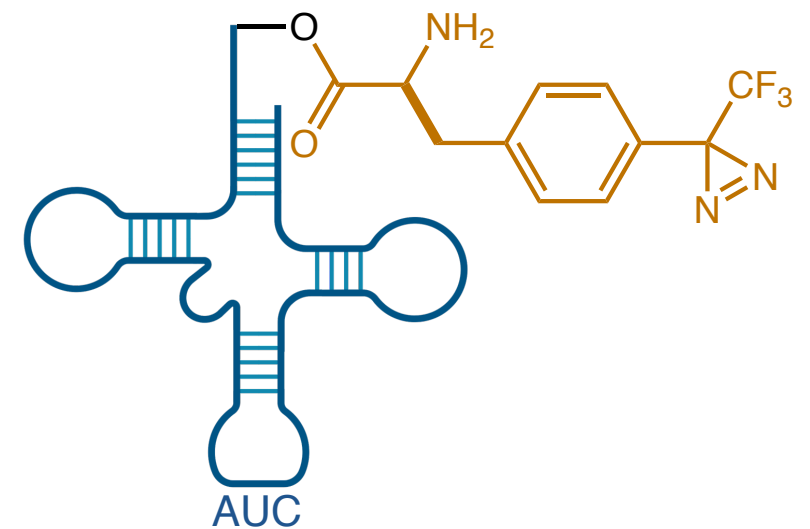
Phosphorylated serine and tyrosine can be installed at specific positions via noncanonical amino acid incorporation

Hoppmann, C. et al. *Nat. Chem. Biol.* **2017**, 13, 842.

Park, H-S. et al. *Science* **2011**, 333, 1151.

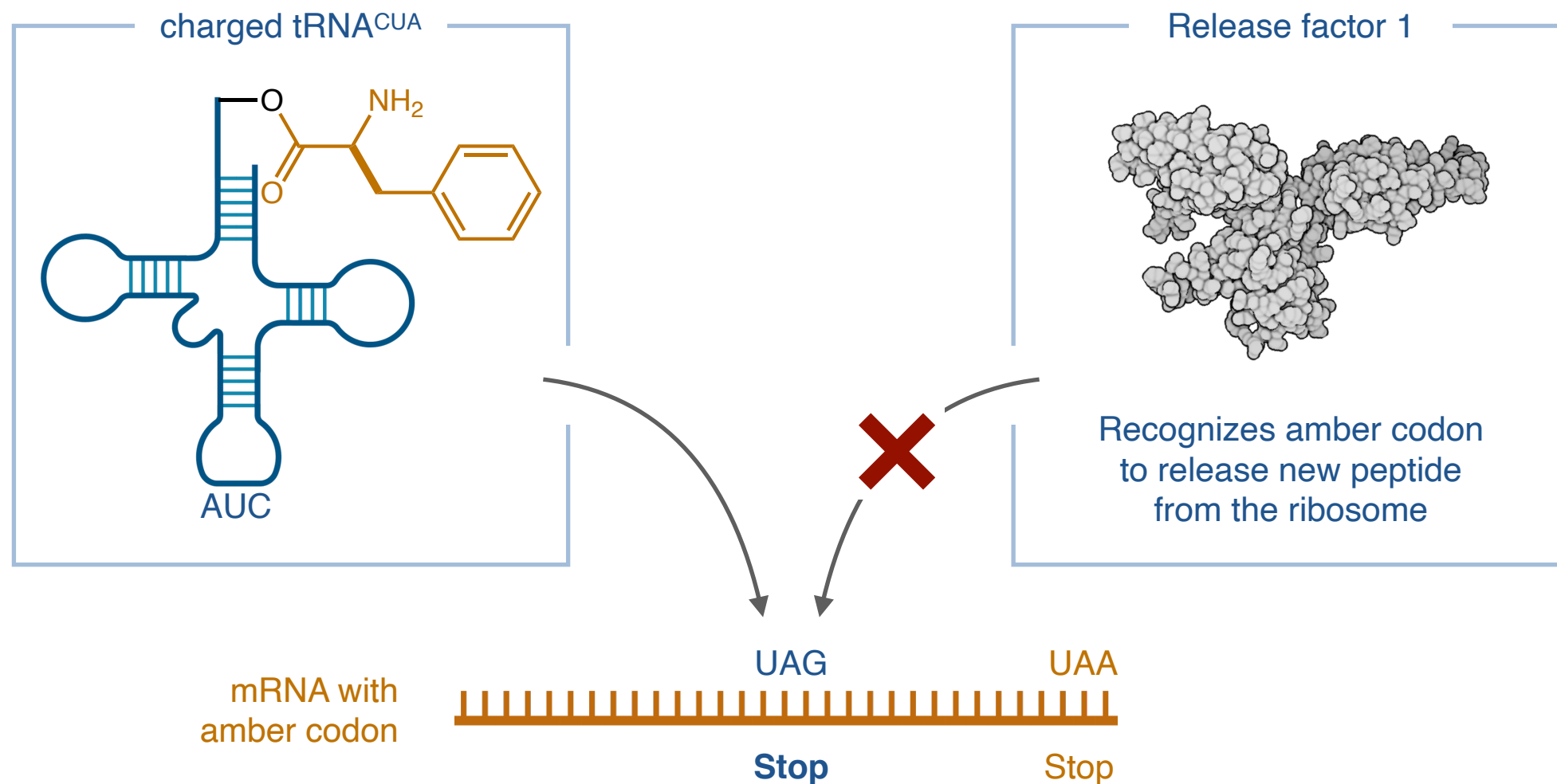
Expanding the Genetic Code

- The traditional genetic code
- Expanding the genetic code
 - In vitro
 - In eukaryotes, prokaryotes, and mammalian cells
- Orthogonal ribosomes
- Genetically recoded organisms and synonymous codon compression
- Outlook



Orthogonal Ribosomes

Problem: Release factors compete with tRNA^{CUA}, diminishing amber suppression efficiency



Decreased interaction of release factor 1 would lead to increased efficiency of amber suppression

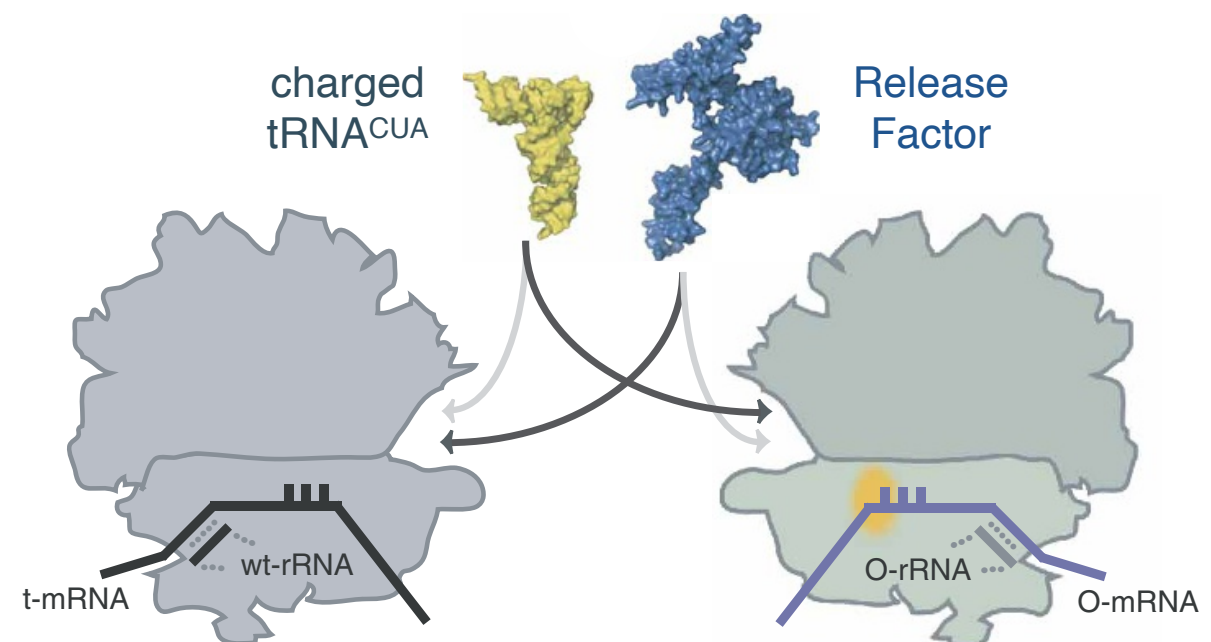
Orthogonal Ribosomes

Problem: Release factors compete with tRNA^{CUA}, diminishing amber suppression efficiency



Jason W. Chin

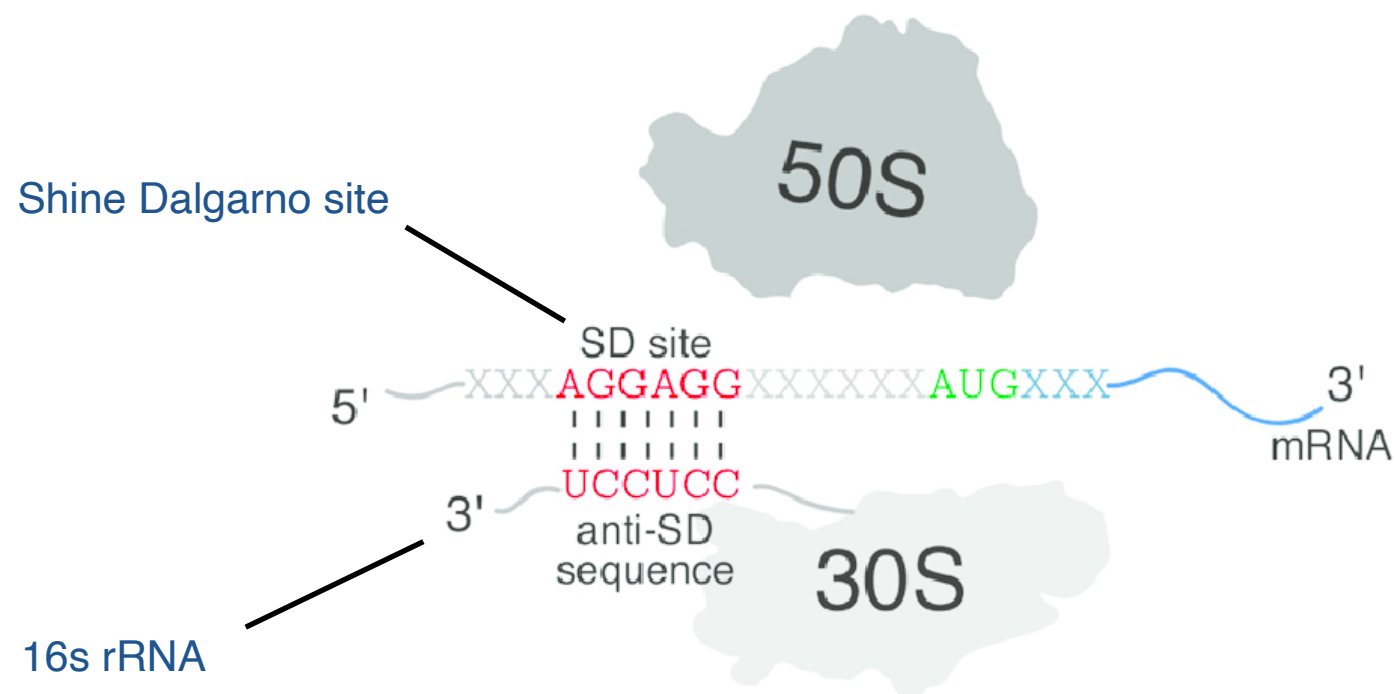
Current Institution:
MRC Laboratory of Molecular Biology



Can an orthogonal ribosome be engineered to specifically translate an orthogonal mRNA and increase amber suppression?

Orthogonal Ribosomes

16S rRNA of 30S ribosome recognizes the Shine-Dalgarno (SD) site upstream of the start codon



Solution an orthogonal ribosome: Alternate Shine-Dalgarno site and anti-SD sequence

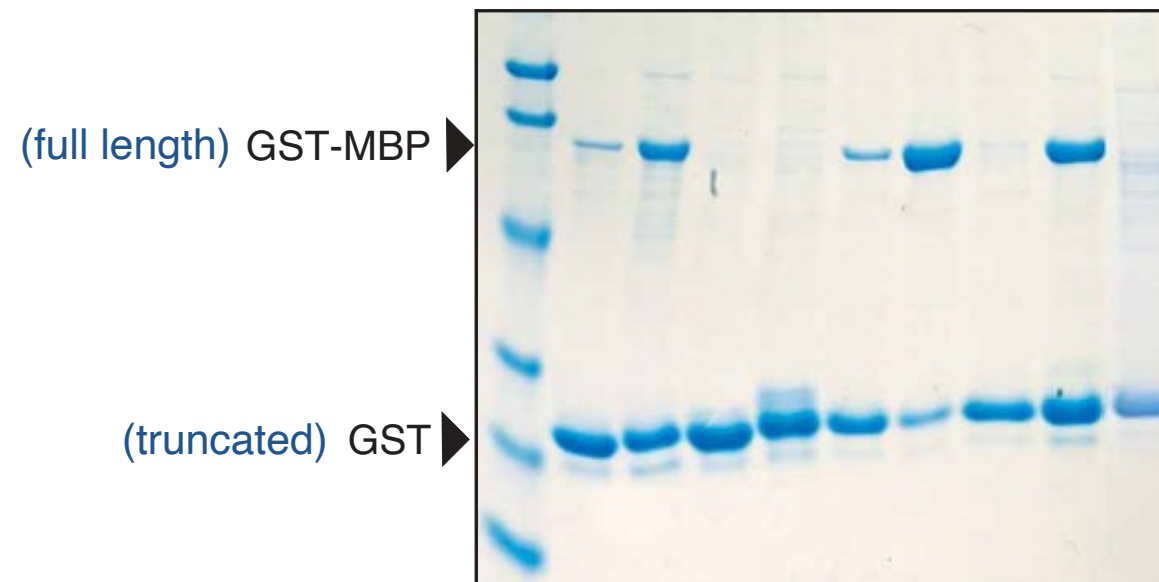
Image source: Researchgate

Rackham, O.; Chin, J. W. *Nat. Chem. Biol.* **2005**, *1*, 159.

Orthogonal Ribosomes

Ribo-X

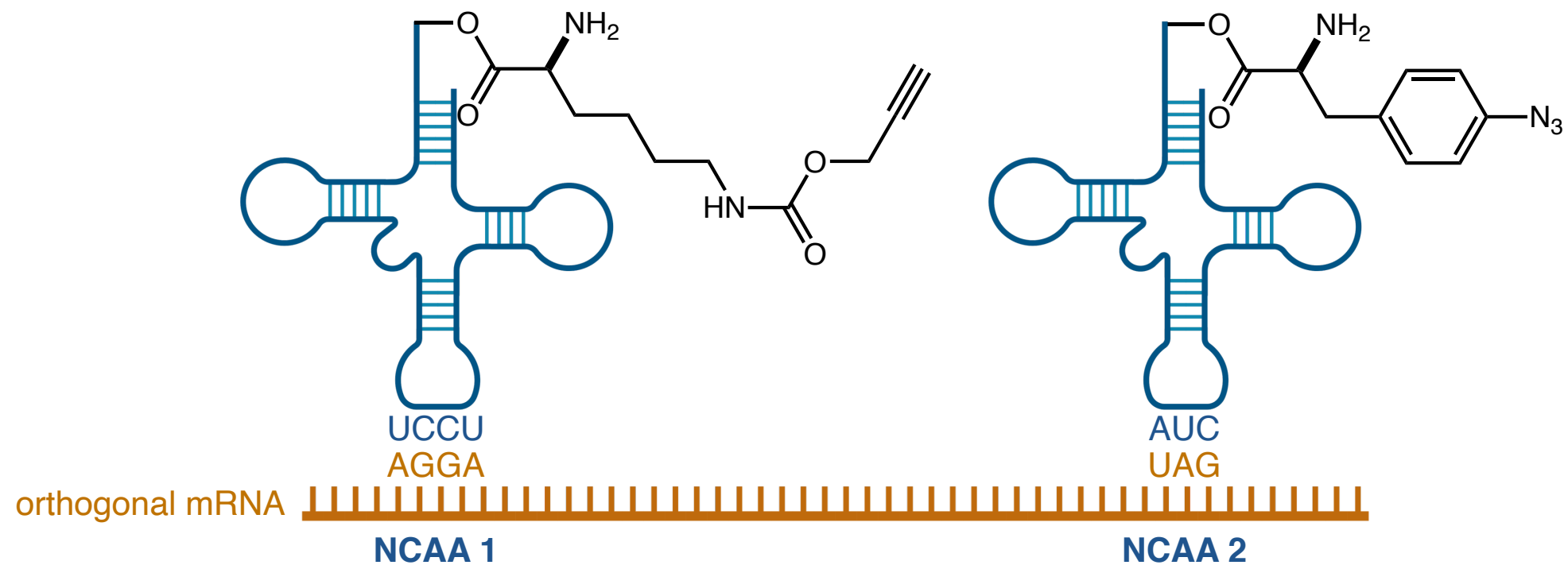
wt-ribosome	+	+	+	+	+	+	+	+	—
Ribo-X	—	—	—	—	+	+	+	+	+
BpaRS/tRNA _{CUA}	+	+	+	+	+	+	+	+	—
Bpa	—	+	—	+	—	+	—	+	+
wt-gst(UAG) _n malE	1	1	2	2	—	—	—	—	—
O-gst(UAG) _n malE	—	—	—	—	1	1	2	2	1



Ribo-X improves noncanonical amino acid incorporation and is hypothesized to decrease ribosomal interaction with Release Factor 1

Orthogonal Ribosomes

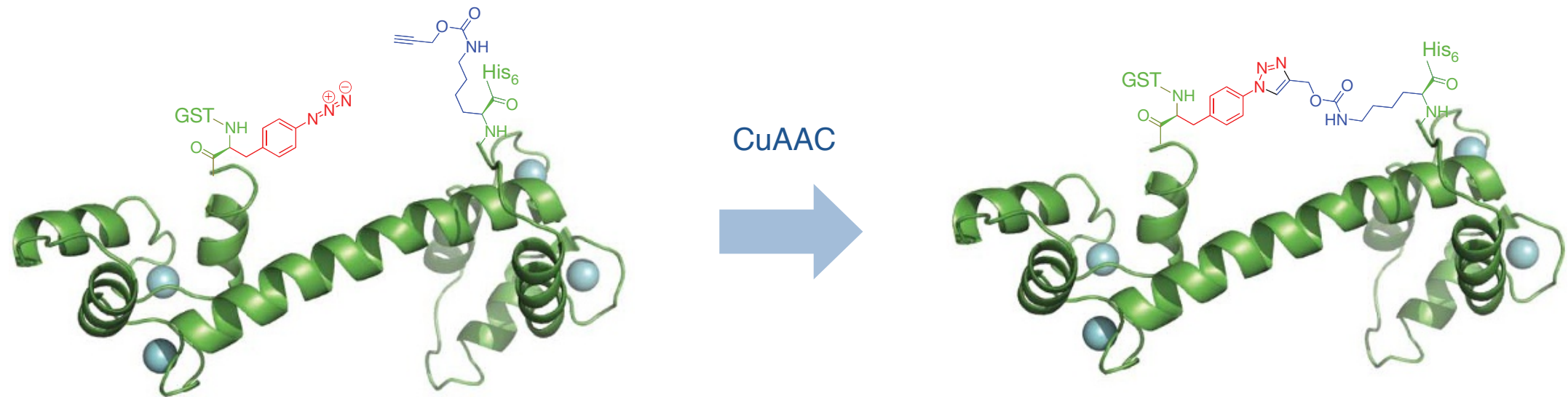
Ribo-Q1



The orthogonal ribosome Ribo-Q1 efficiently decodes quadruplet codons and amber codons

Orthogonal Ribosomes

Ribo-Q1



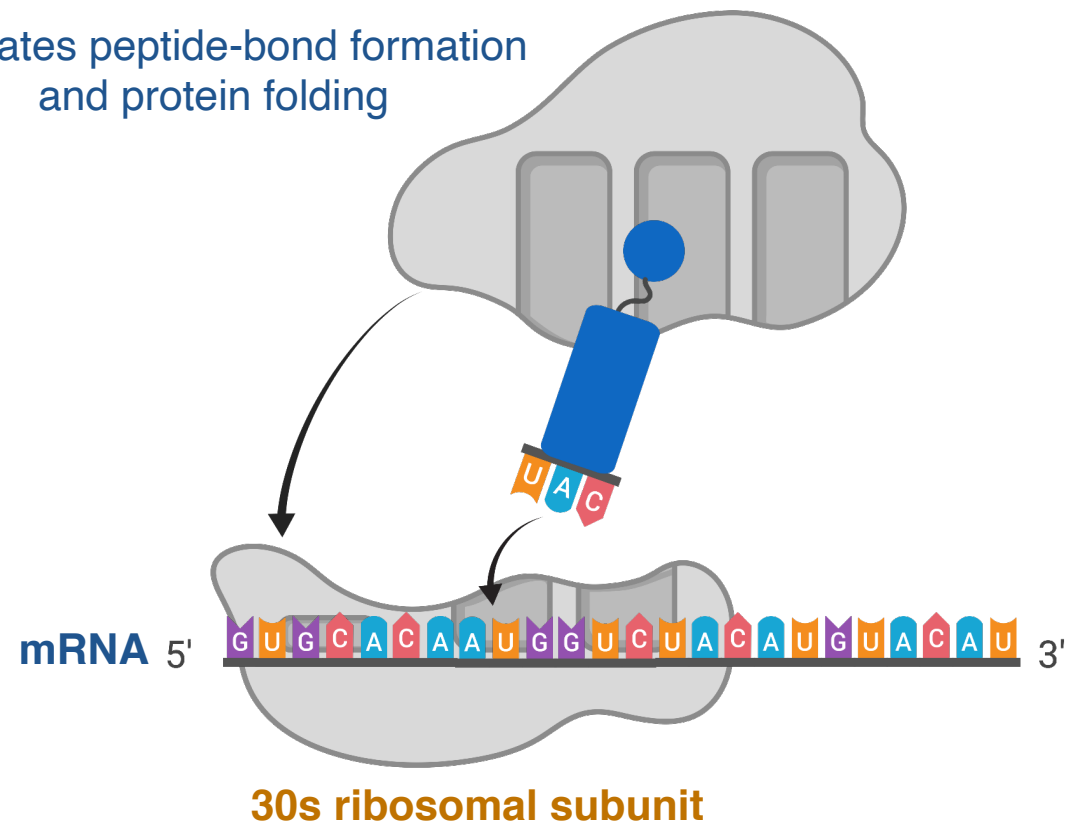
The orthogonal ribosome Ribo-Q1 efficiently decodes quadruplet codons and amber codons

Orthogonal Ribosomes

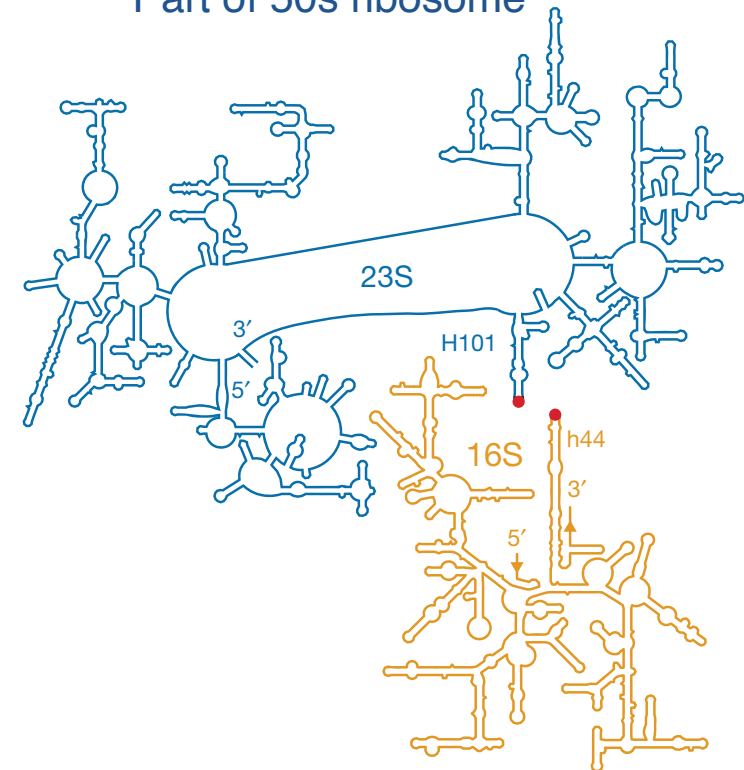
oRibo-T

50s ribosomal subunit

facilitates peptide-bond formation and protein folding



Part of 50s ribosome



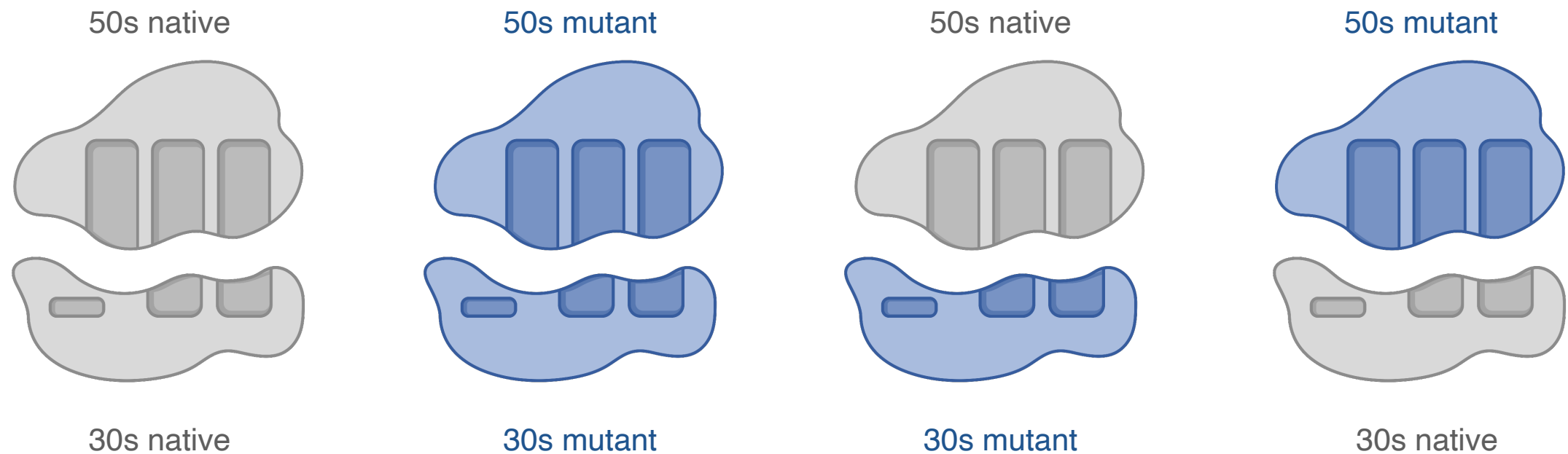
Part of 30s ribosome

Previous work: Engineering of 16s rRNA of the 30s ribosomal subunit

Can the 23s rRNA of the 50s ribosomal subunit be engineered as well to improve noncanonical amino acid incorporation?

Orthogonal Ribosomes

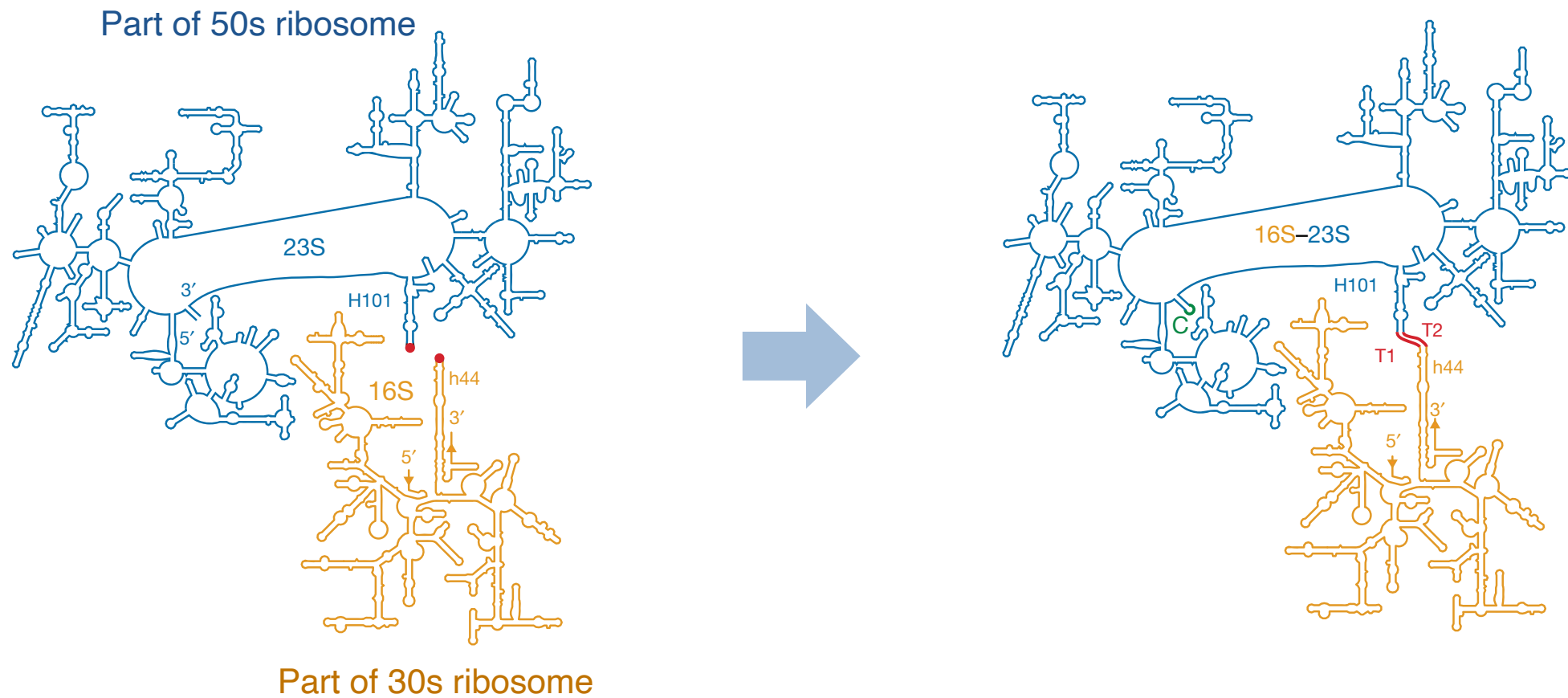
oRibo-T



Problem: Engineered rRNA of the 50s / 30s ribosomal subunits can interact with endogenous 30s / 50s subunits

Orthogonal Ribosomes

oRibo-T



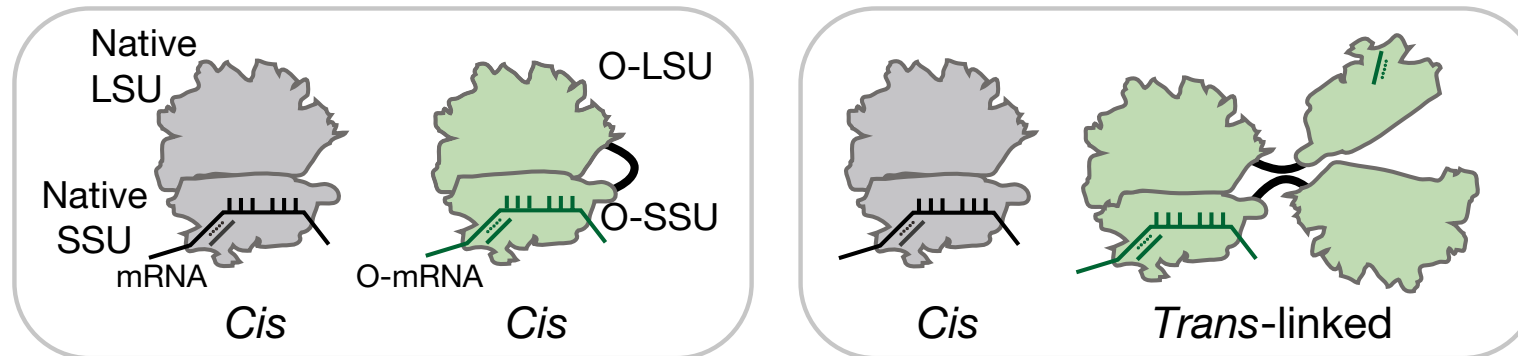
Solution: 'Stapled ribosomes' link 16S and 23S rRNA together

This work: The first fully orthogonal ribosome (both subunits)

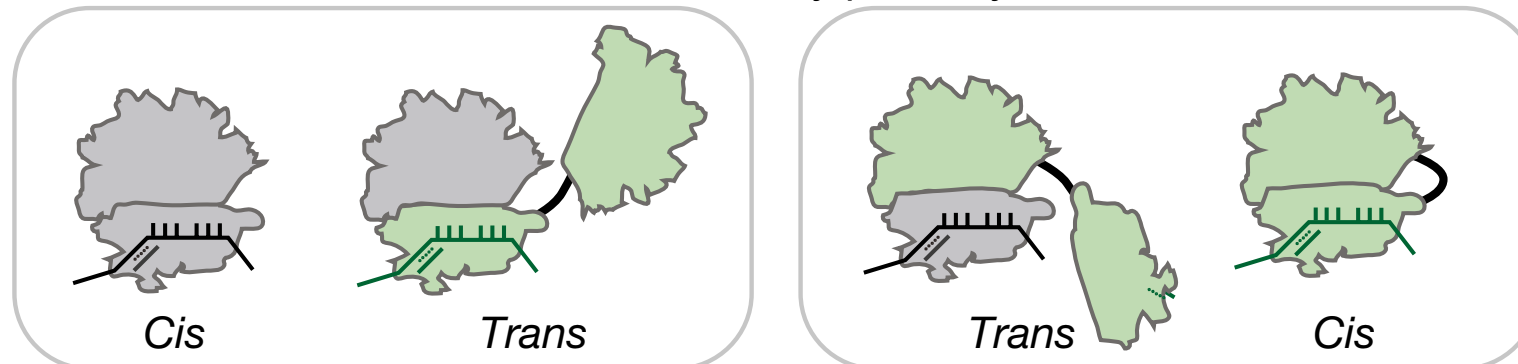
Problem: Low activity

Orthogonal Ribosomes

Orthogonal translation pathways



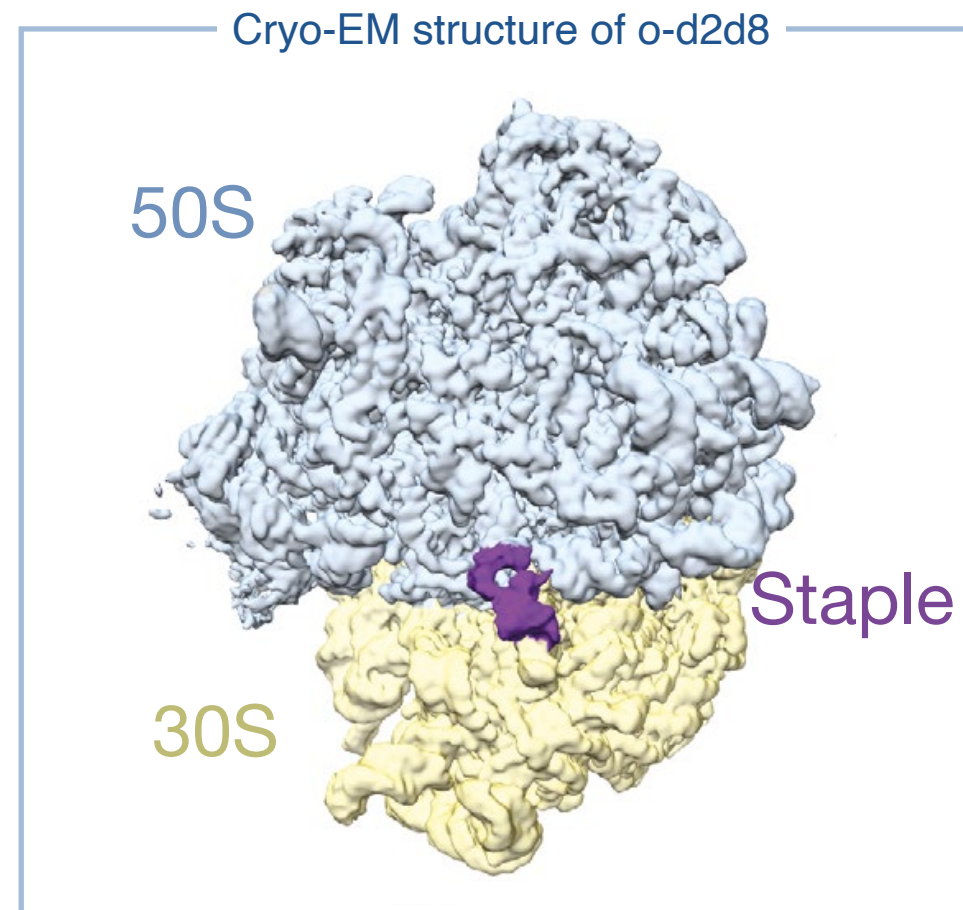
Cross-assembly pathways



‘Stapled ribosomes’ can still interact with endogenous 50s and 30s subunits

Orthogonal Ribosomes

o-d2d8



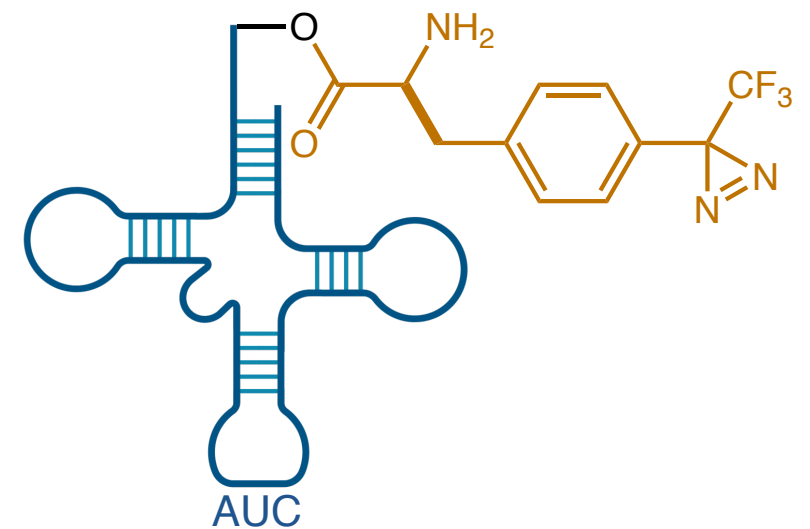
This work: Engineer a 'stapled ribosome' that does not associate with endogenous subunits

Orthogonal 'stapled' ribosomes have activities comparable to that of the parent orthogonal ribosome

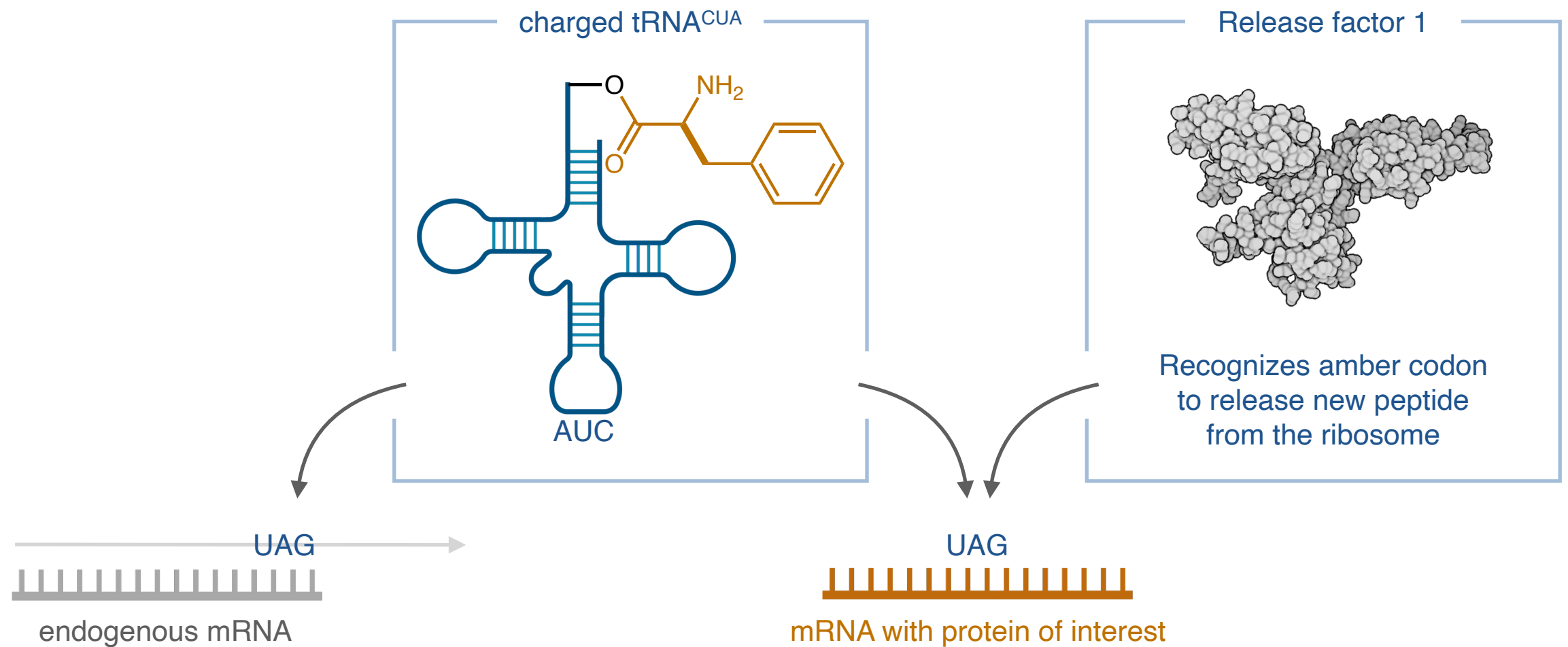
Schmied, W. H.; Tnimov, Z.; Uttapmapinant, C.; Rae, C. D.; Fried, S. D.; Chin, J. W. *Nature* **2018**, 564, 444.

Expanding the Genetic Code

- The traditional genetic code
- Expanding the genetic code
 - In vitro
 - In eukaryotes, prokaryotes, and mammalian cells
- Orthogonal ribosomes
- Genetically recoded organisms and synonymous codon compression
- Outlook



Genomically Recoded Organisms



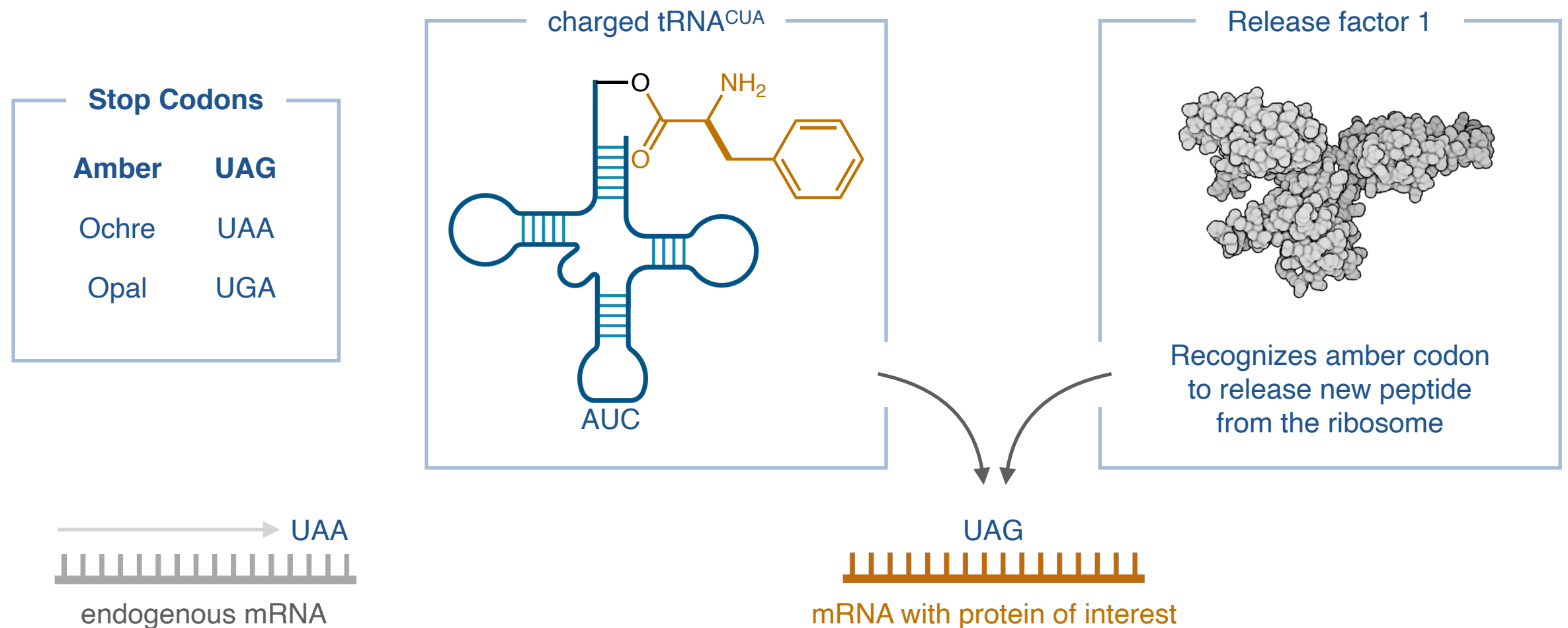
Problems with amber suppression

Release factors compete with tRNA^{CUA}, diminishing amber suppression efficiency

Charged tRNA^{CUA} suppress endogenous UAG stop codons

Solution: Recode endogenous UAG (amber codon) to UAA and delete Release Factor 1

Genomically Recoded Organisms



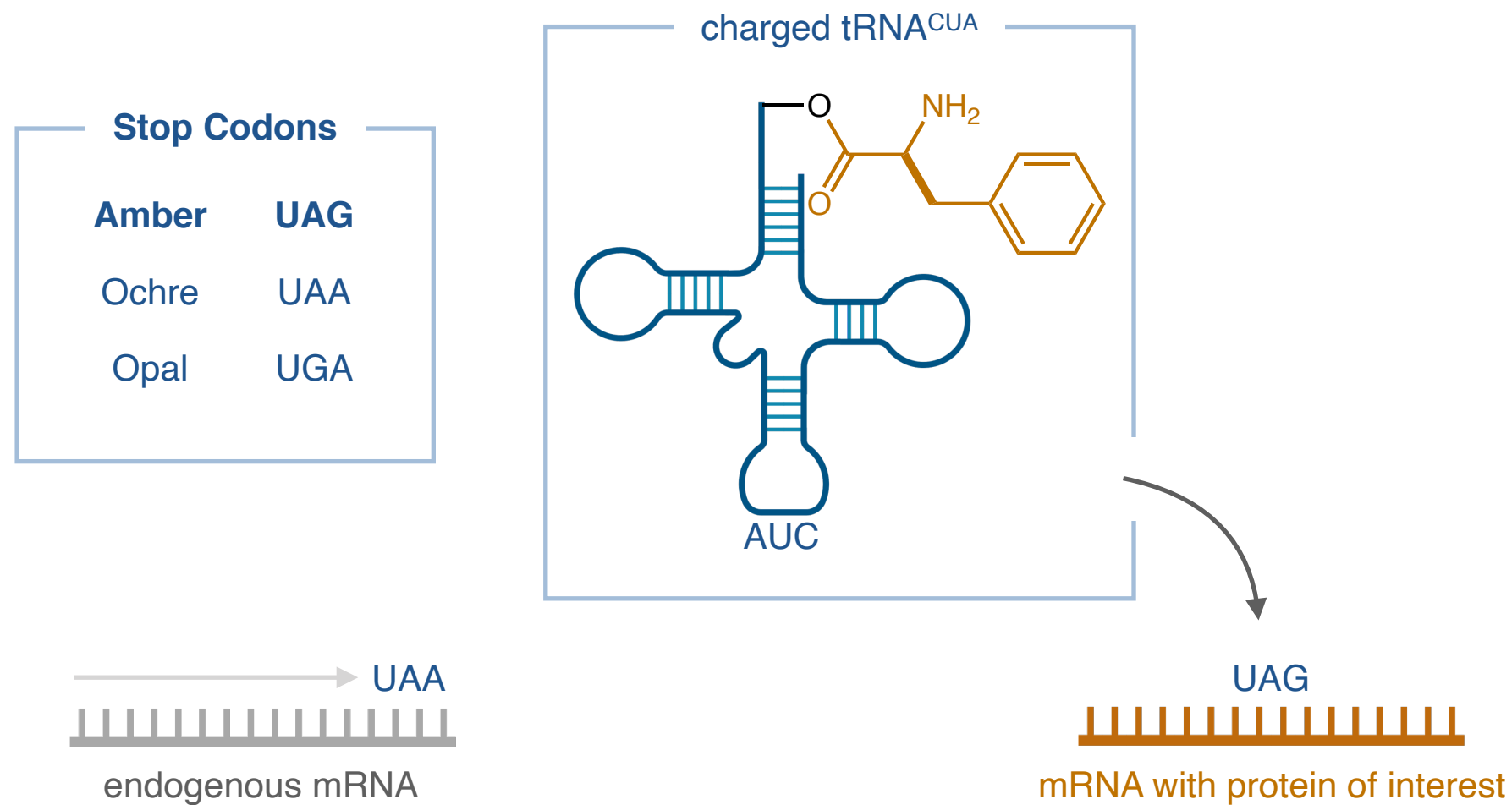
Problems with amber suppression

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Genomically Recoded Organisms



Problems with amber suppression

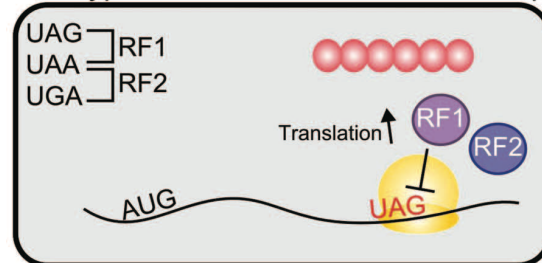
Release factors compete with tRNA^{CUA}, diminishing amber suppression efficiency

Charged tRNA^{CUA} suppress endogenous UAG stop codons

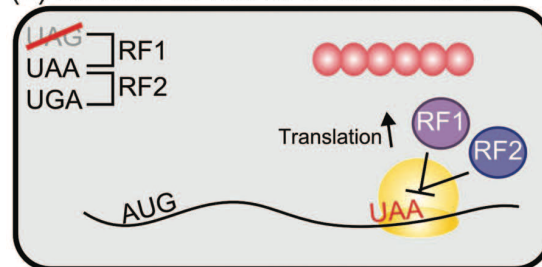
Solution: Recode endogenous UAG (amber codon) to UAA and delete Release Factor 1

Genomically Recoded Organisms

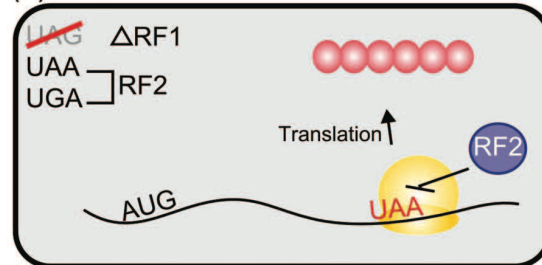
Wild type UAG denotes translation stop



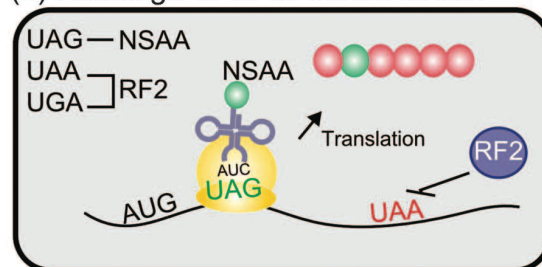
(1) Recode all native UAGs to UAA



(2) Eliminate UAG termination: Δ RF1

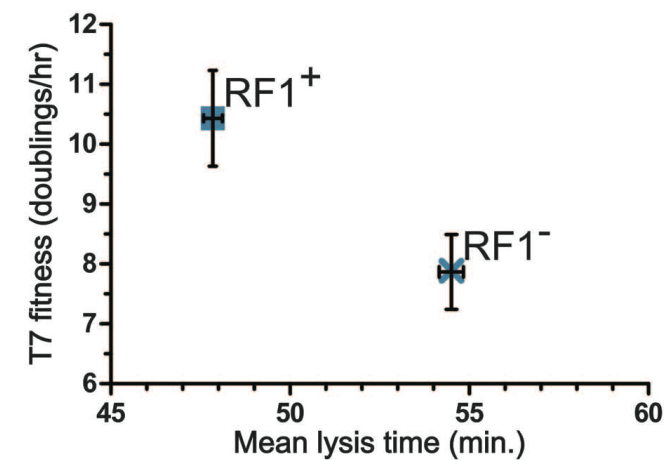


(3) Reassign UAG as sense codon



Project resulted in the *E. coli* species **C321. Δ A**

Phages rely on host to express proteins necessary for propagation



T7 virus fitness is reduced when release factor 1 is removed

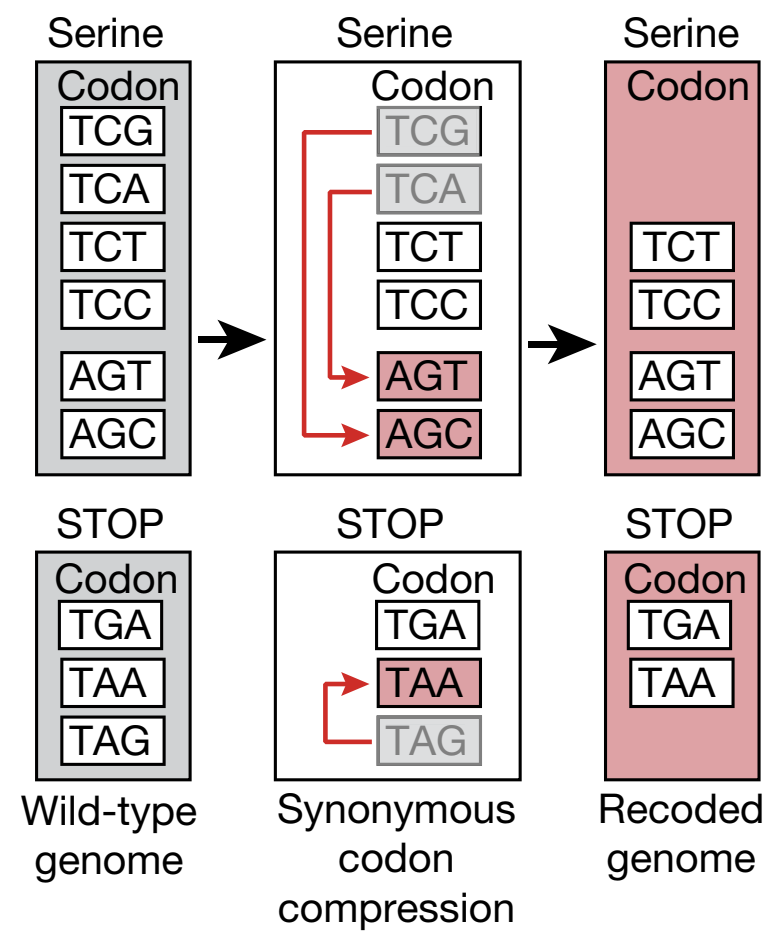
ARTICLE

<https://doi.org/10.1038/s41586-019-1192-5>

Total synthesis of *Escherichia coli* with a recoded genome

Julius Fredens^{1,4}, Kaihang Wang^{1,2,4}, Daniel de la Torre^{1,4}, Louise F. H. Funke^{1,4}, Wesley E. Robertson^{1,4}, Yonka Christova¹, Tiongsun Chia¹, Wolfgang H. Schmied¹, Daniel L. Dunkelmann¹, Václav Beránek¹, Chayasith Uttamapinant^{1,3}, Andres Gonzalez Llamazares¹, Thomas S. Elliott¹ & Jason W. Chin^{1*}

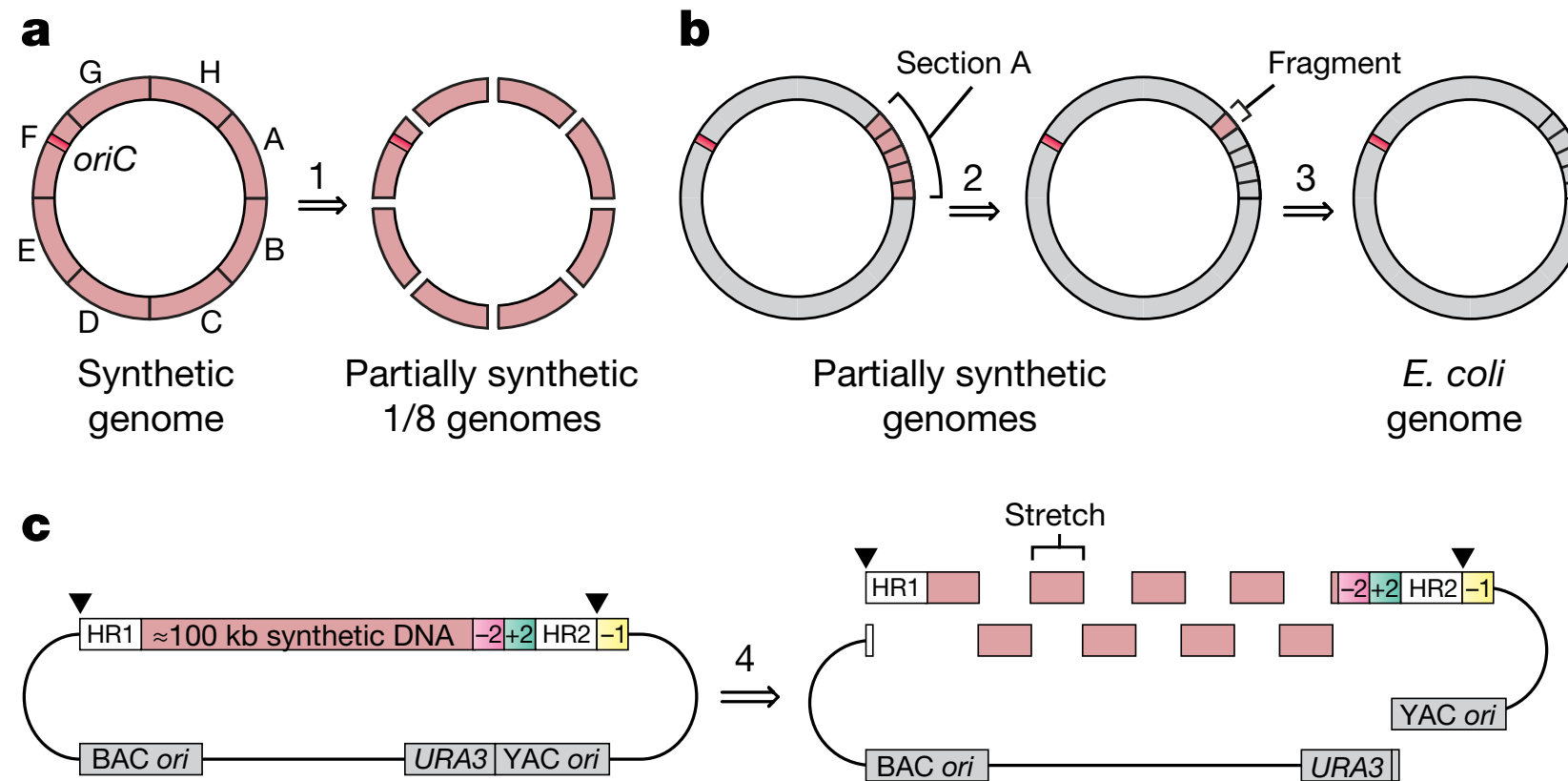
Total Synthesis of *E. coli* with a Recoded Genome



Serine: TCA = AGT and TCG = AGC

Stop codon: TAG = TAA

Total Synthesis of *E. coli* with a Recoded Genome

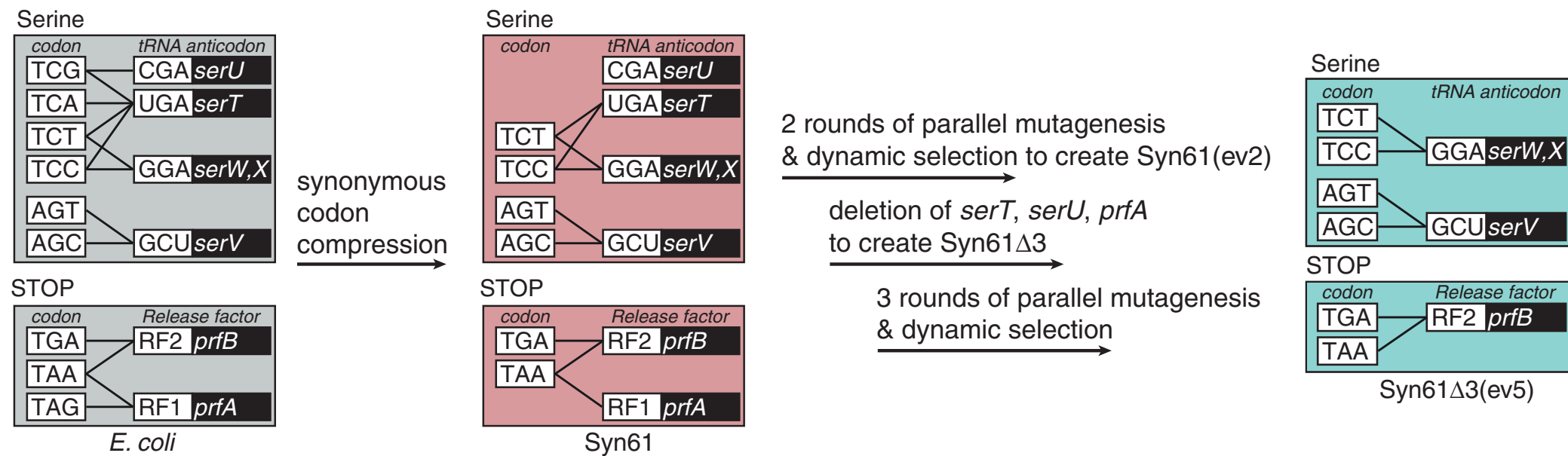


E. coli genome was divided into 8 fragments which were created using REXER

Project resulted in the successful creation of the *E. coli* species **Syn61**

Total Synthesis of *E. coli* with a Recoded Genome

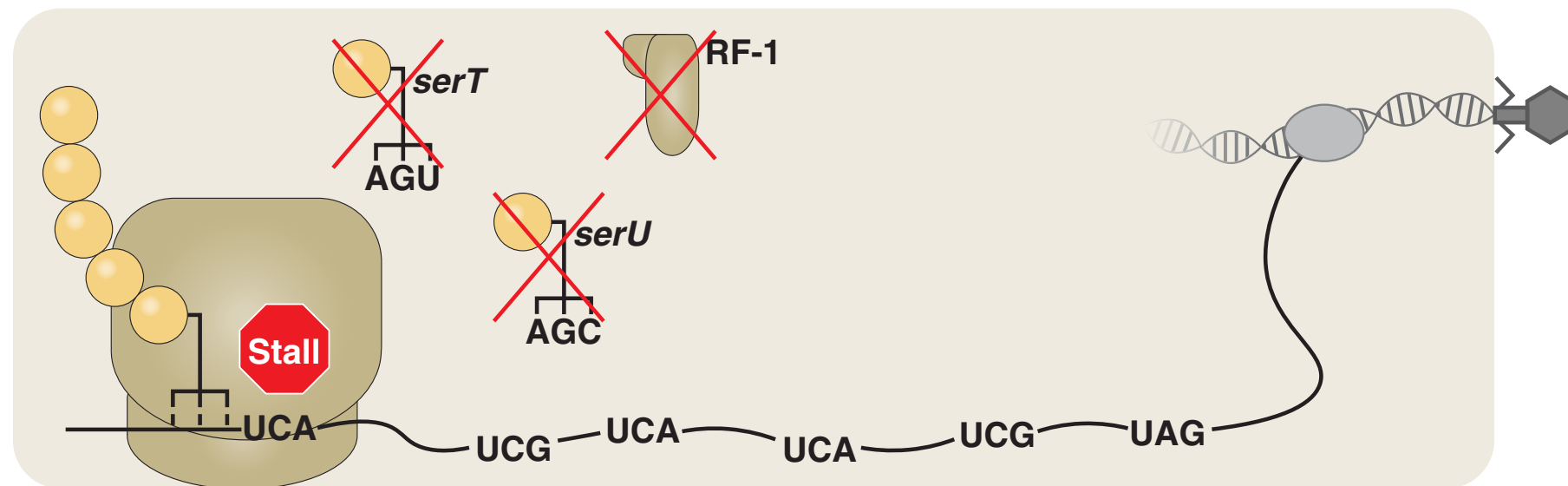
Syn61 Δ 3



Syn61 can be evolved to remove serine tRNAs and release factor 1

Total Synthesis of *E. coli* with a Recoded Genome

Syn61 Δ 3



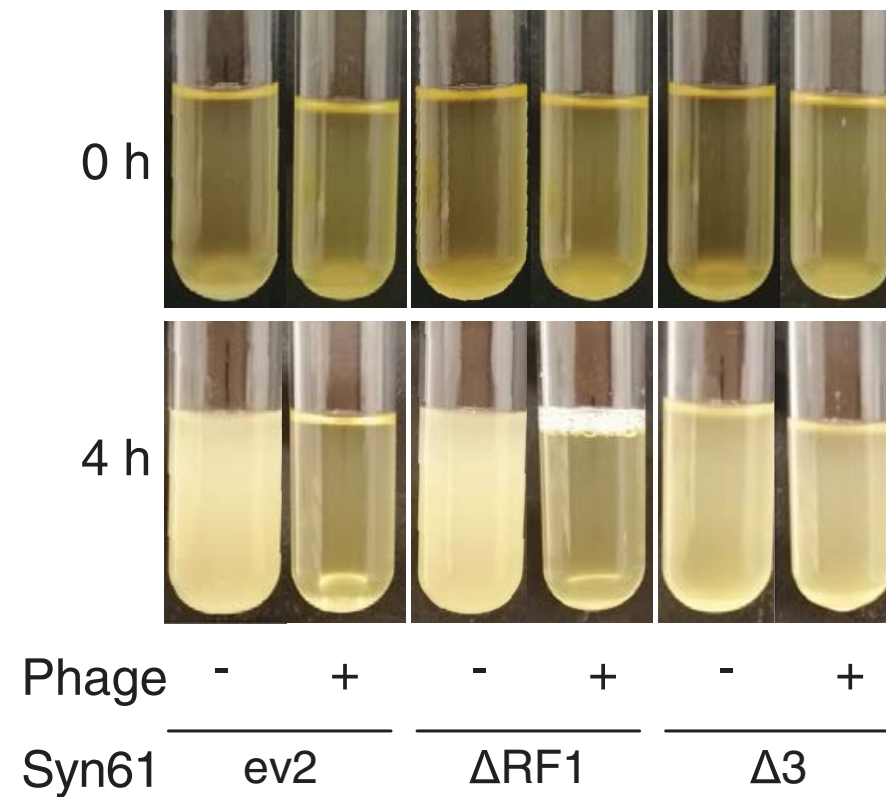
Phages use endogenous translation machinery to reproduce

What happens when phages try to infect Syn61 Δ 3?

Total Synthesis of *E. coli* with a Recoded Genome

Syn61 Δ 3

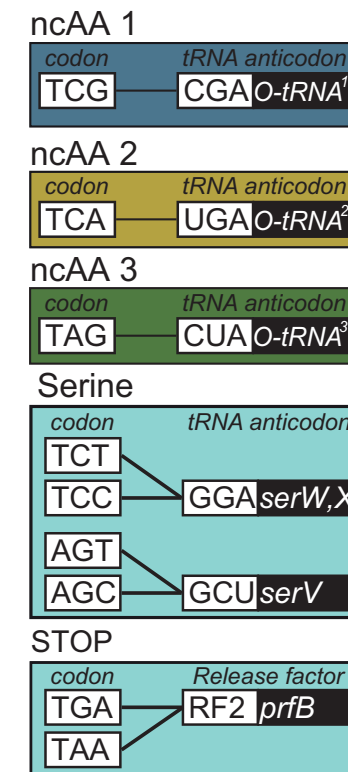
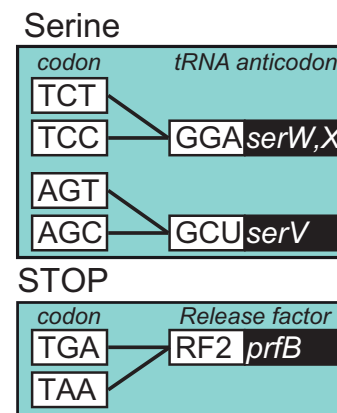
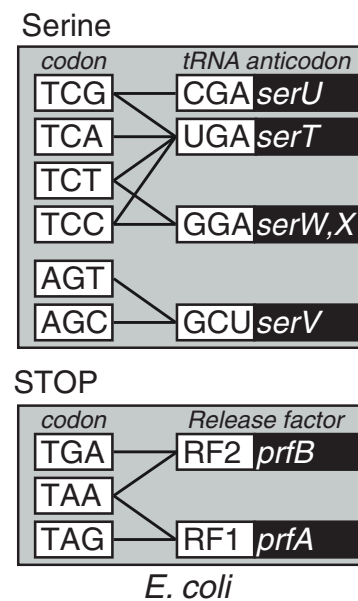
λ +P1 vir+T4+T6+T7



Syn61 Δ 3 is more resistant to phage infection

Total Synthesis of *E. coli* with a Recoded Genome

Syn61Δ3

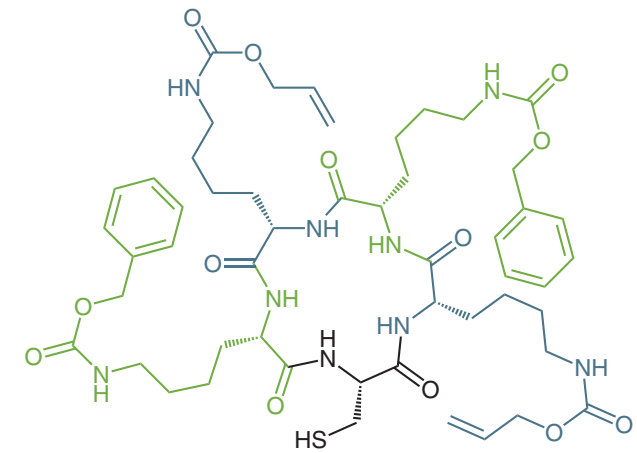
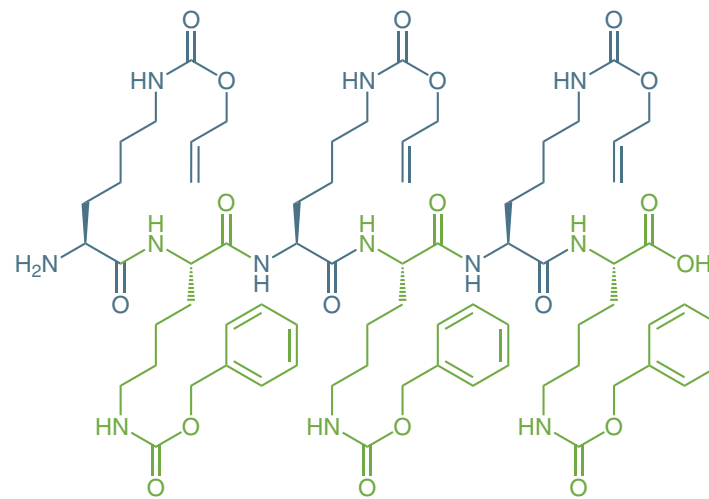
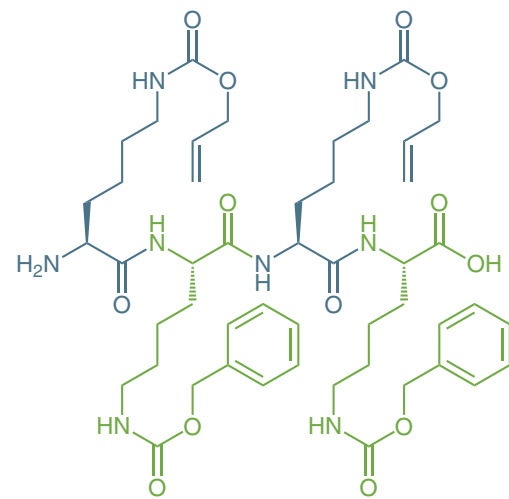


The codons TCG, TCA, and TAG are no longer present in the genome

TCG, TCA, and TAG can be recoded to incorporate three different noncanonical amino acids

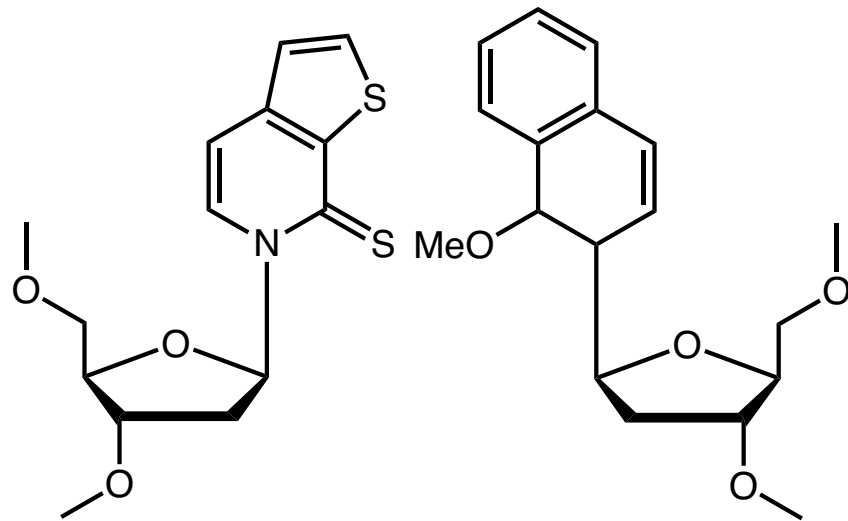
Total Synthesis of *E. coli* with a Recoded Genome

Syn61 Δ 3



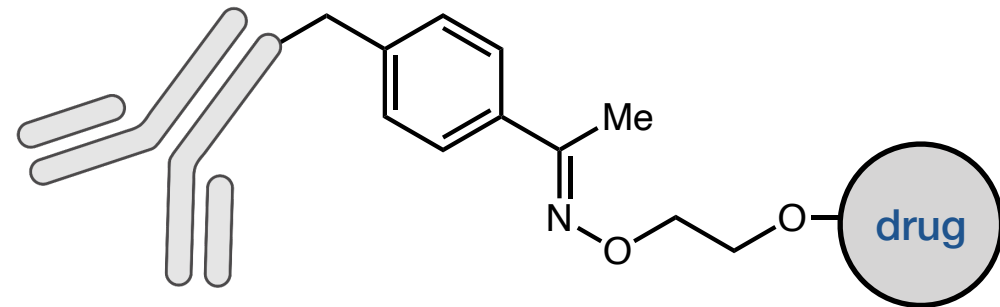
Syn61 Δ 3 can be used to synthesize noncanonical heteropolymers and macrocycles

New Conceptual Applications and the Future of Genetic Code Expansion



Non-natural nucleic acid base pairs

Nature **2014**, 509, 385.



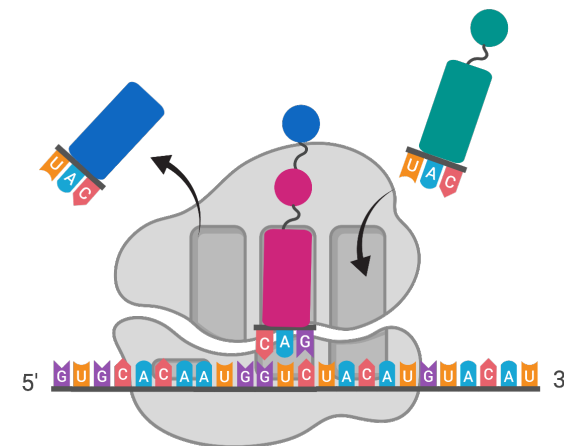
antibody-drug conjugate generation

Proc. Natl. Acad. Sci **2014**, 111, 1766.

Serine	
<i>codon</i>	<i>tRNA anticodon</i>
TCT	GGA _{serW,X}
TCC	
AGT	GCU _{serV}
AGC	

STOP	
<i>codon</i>	<i>Release factor</i>
TGA	RF2 _{prfB}
TAA	

Genomically recoded mammalian cells?



Additional mechanistic exploration to improve noncanonical amino acid incorporation

Shandell, M. A.; Tan, Z.; Cornish, V. W. et al. *Biochemistry* **2021**, 60, 3455.

Questions?

