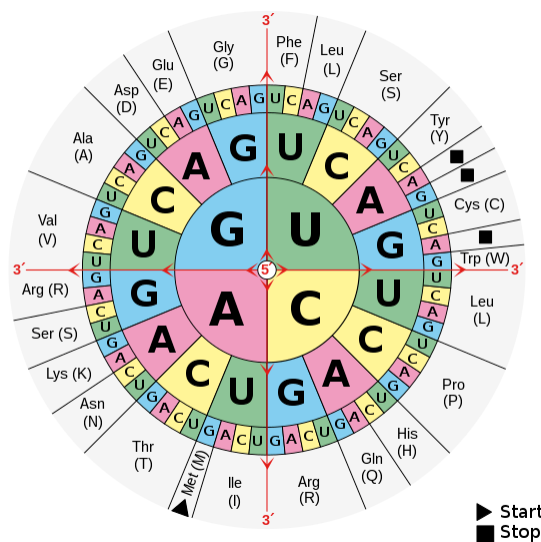


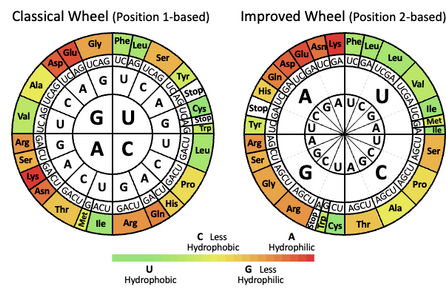
DNA and RNA codon tables

A **codon table** can be used to translate a **genetic code** into a sequence of **amino acids**.^{[1][2]} The standard genetic code is traditionally represented as an **RNA codon table**, because when **proteins** are made in a **cell** by **ribosomes**, it is **messenger RNA** (mRNA) that directs **protein synthesis**.^{[2][3]} The mRNA sequence is determined by the sequence of genomic **DNA**.^[4] In this context, the standard genetic code is referred to as translation table 1.^[3] It can also be represented in a DNA codon table. The DNA codons in such tables occur on the **sense** DNA strand and are arranged in a **5'-to-3'** **direction**. Different tables with alternate codons are used depending on the source of the genetic code, such as from a **cell nucleus**, **mitochondrion**, **plastid**, or **hydrogenosome**.^[5]



The standard RNA codon table organized in a wheel

There are 64 different codons in the genetic code and the below tables; most specify an amino acid.^[6] Three sequences, UAG, UGA, and UAA, known as **stop codons**,^[note 1] do not code for an amino acid but instead signal the release of the nascent **polypeptide** from the ribosome.^[7] In the standard code, the sequence AUG—read as **methionine**—can serve as a **start codon** and, along with sequences such as an **initiation factor**, initiates translation.^{[3][8][9]} In rare instances, start codons in the standard code may also include GUG or UUG; these codons normally represent **valine** and **leucine**, respectively, but as start codons they are translated as **methionine** or **formylmethionine**.^{[3][9]}



The second codon position best determines amino acid hydrophobicity. Color-coding: hydrophobicity from microenvironment in folded proteins [10]

The classical table/wheel of the standard genetic code is arbitrarily organized based on codon position 1. Saier,^[11] following observations from,^[12] showed that reorganizing the wheel based instead on codon position 2 (and reordering from UCAG to UCGA) better arranges the codons by the hydrophobicity of their encoded amino acids. This suggests that early ribosomes read the second codon position most carefully, to control hydrophobicity patterns in protein sequences.

The first table—the standard table—can be used to translate [nucleotide](#) triplets into the corresponding amino acid or appropriate signal if it is a start or stop codon. The second table, appropriately called the inverse, does the opposite: it can be used to deduce a possible triplet code if the amino acid is known. As multiple codons can code for the same amino acid, the [International Union of Pure and Applied Chemistry's](#) (IUPAC) [nucleic acid notation](#) is given in some instances.

Translation table 1

Standard RNA codon table

Amino-acid biochemical properties	Nonpolar (np)	Polar (p)	Basic (b)	Acidic (a)	Termination: stop codon *	Initiation: possible start codon ⇒
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Standard genetic code^{[1][13]}

1st base	2nd base								3rd base
	U		C		A		G		
U	UUU	(Phe/F) Phenylalanine	UCU	(Ser/S) Serine (p)	UAU	(Tyr/Y) Tyrosine (p)	UGU	(Cys/C) Cysteine (p)	U
	UUC	(np)	UCC		UAC		UGC		C
	UUA		UCA		UAA	Stop (Ochre) ★ ^[note 2]	UGA	Stop (Opal) ★ ^[note 2]	A
	UUG ⇒		UCG		UAG	Stop (Amber) ★ ^[note 2]	UGG	(Trp/W) Tryptophan (np)	G
C	CUU	(Leu/L) Leucine (np)	CCU	(Pro/P) Proline (np)	CAU	(His/H) Histidine	CGU	(Arg/R) Arginine (b)	U
	CUC		CCC		CAC	(b)	CGC		C
	CUA		CCA		CAA	(Gln/Q) Glutamine	CGA		A
	CUG		CCG		CAG	(p)	CGG		G
A	AUU	(Ile/I) Isoleucine (np)	ACU	(Thr/T) Threonine (p)	AAU	(Asn/N) Asparagine	AGU	(Ser/S) Serine (p)	U
	AUC		ACC		AAC	(p)	AGC		C
	AUA	(Met/M) Methionine (np)	ACA		AAA	(Lys/K) Lysine (b)	AGA	(Arg/R) Arginine (b)	A
	AUG ⇒		ACG		AAG		AGG		G
G	GUU	(Val/V) Valine (np)	GCU	(Ala/A) Alanine (np)	GAU	(Asp/D) Aspartic acid (a)	GGU	(Gly/G) Glycine (np)	U
	GUC		GCC		GAC		GGC		C
	GUA		GCA		GAA	(Glu/E) Glutamic acid (a)	GGA		A
	GUG ⇒		GCG		GAG		GGG		G

As shown in the above table, NCBI table 1 includes the less-canonical start codons GUG and UUG.^[3]

Inverse RNA codon table

Inverse table for the standard genetic code (compressed using [IUPAC notation](#))^[16]

Amino acid	RNA codons	Compressed	Amino acid	RNA codons	Compressed
Ala, A	GCU, GCC, GCA, GCG	GCN	Ile, I	AUU, AUC, AUA	AUH
Arg, R	CGU, CGC, CGA, CGG; AGA, AGG	CGN, AGR; or CGY, MGR	Leu, L	CUU, CUC, CUA, CUG; UUA, UUG	CUN, UUR; or CUY, YUR
Asn, N	AAU, AAC	AAY	Lys, K	AAA, AAG	AAR
Asp, D	GAU, GAC	GAY	Met, M	AUG	
Asn or Asp, B	AAU, AAC; GAU, GAC	RAY	Phe, F	UUU, UUC	UUY
Cys, C	UGU, UGC	UGY	Pro, P	CCU, CCC, CCA, CCG	CCN
Gln, Q	CAA, CAG	CAR	Ser, S	UCU, UCC, UCA, UCG; AGU, AGC	UCN, AGY
Glu, E	GAA, GAG	GAR	Thr, T	ACU, ACC, ACA, ACG	ACN
Gln or Glu, Z	CAA, CAG; GAA, GAG	SAR	Trp, W	UGG	
Gly, G	GGU, GGC, GGA, GGG	GGN	Tyr, Y	UAU, UAC	UAY
His, H	CAU, CAC	CAY	Val, V	GUU, GUC, GUA, GUG	GUN
START	AUG, CUG, UUG	HUG	STOP	UAA, UGA, UAG	URA, UAG; or UGA, UAR

Standard DNA codon table

Amino-acid biochemical properties	Nonpolar (np)	Polar (p)	Basic (b)	Acidic (a)	Termination: stop codon *	Initiation: possible start codon ⇒
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Standard genetic code^{[17][note 3]}

1st base	2nd base								3rd base
	T		C		A		G		
T	TTT	(Phe/F) Phenylalanine	TCT	(Ser/S) Serine (p)	TAT	(Tyr/Y) Tyrosine (p)	TGT	(Cys/C) Cysteine	T
	TTC	(np)	TCC		TAC		TGC	(p)	C
	TTA		TCA		TAA	Stop (Ochre) * ^[note 2]	TGA	Stop (Opal) * ^[note 2]	A
	TTG		TCG		TAG	Stop (Amber) * ^[note 2]	TGG	(Trp/W) Tryptophan (np)	G
	⇒								
C	CTT	(Leu/L) Leucine (np)	CCT	(Pro/P) Proline (np)	CAT	(His/H) Histidine	CGT	(Arg/R) Arginine (b)	T
	CTC	CCC	CAC		(b)	CGC	C		
	CTA	CCA	CAA		(Gln/Q) Glutamine	CGA	A		
	CTG	CCG	CAG		(p)	CGG	G		
A	ATT	(Ile/I) Isoleucine (np)	ACT	(Thr/T) Threonine (p)	AAT	(Asn/N) Asparagine	AGT	(Ser/S) Serine (p)	T
	ATC		ACC		AAC	(p)	AGC		C
	ATA		ACA		AAA	(Lys/K) Lysine (b)	AGA	(Arg/R) Arginine (b)	A
	ATG	(Met/M) Methionine (np)	ACG		AAG		AGG		G
⇒									
G	GTT	(Val/V) Valine (np)	GCT	(Ala/A) Alanine (np)	GAT	(Asp/D) Aspartic acid (a)	GGT	(Gly/G) Glycine (np)	T
	GTC		GCC		GAC		GGC		C
	GTA		GCA		GAA	(Glu/E) Glutamic acid (a)	GGA		A
	GTG		GCG		GAG		GGG		G
⇒									

Inverse DNA codon table

Inverse table for the standard genetic code (compressed using [IUPAC notation](#))^[16]

Amino acid	DNA codons	Compressed	Amino acid	DNA codons	Compressed
Ala, A	GCT, GCC, GCA, GCG	GCN	Ile, I	ATT, ATC, ATA	ATH
Arg, R	CGT, CGC, CGA, CGG; AGA, AGG	CGN, AGR; or CGY, MGR	Leu, L	CTT, CTC, CTA, CTG; TTA, TTG	CTN, TTR; or CTY, YTR
Asn, N	AAT, AAC	AAY	Lys, K	AAA, AAG	AAR
Asp, D	GAT, GAC	GAY	Met, M	ATG	
Asn or Asp, B	AAT, AAC; GAT, GAC	RAY	Phe, F	TTT, TTC	TTY
Cys, C	TGT, TGC	TGY	Pro, P	CCT, CCC, CCA, CCG	CCN
Gln, Q	CAA, CAG	CAR	Ser, S	TCT, TCC, TCA, TCG; AGT, AGC	TCN, AGY
Glu, E	GAA, GAG	GAR	Thr, T	ACT, ACC, ACA, ACG	ACN
Gln or Glu, Z	CAA, CAG; GAA, GAG	SAR	Trp, W	TGG	
Gly, G	GGT, GGC, GGA, GGG	GGN	Tyr, Y	TAT, TAC	TAY
His, H	CAT, CAC	CAY	Val, V	GTT, GTC, GTA, GTG	GTN
START	ATG, TTG, GTG, CTG ^[19]	NTG	STOP	TAA, TGA, TAG	TRA, TAR

Alternative codons in other translation tables

The genetic code was once believed to be universal:^[20] a codon would code for the same amino acid regardless of the organism or source. However, it is now agreed that the genetic code evolves,^[21] resulting in discrepancies in how a codon is translated depending on the genetic source.^{[20][21]} For example, in 1981, it was discovered that the use of codons AUA, UGA, AGA and AGG by the coding system in mammalian mitochondria differed from the universal code.^[20] Stop codons can also be affected: in [ciliated protozoa](#), the universal stop codons UAA and UAG code for glutamine.^{[21][note 4]} Four novel alternative genetic codes (numbered here 34–37) were discovered in bacterial genomes by Shulgina and Eddy, revealing the first sense codon changes in bacteria.^[22] The following table displays these alternative codons.

Amino-acid biochemical properties	Nonpolar (np)	Polar (p)	Basic (b)	Acidic (a)	Termination: stop codon *
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Comparison between codon translations with alternative and standard genetic codes^[3]

Code	Translation table	DNA codon involved	RNA codon involved	Translation with this code	Standard translation	Notes
Standard	1					Includes translation table 8 (plant chloroplasts).
Vertebrate mitochondrial	2	AGA	AGA	Stop *	Arg (R) (b)	
		AGG	AGG	Stop *	Arg (R) (b)	
		ATA	AUA	Met (M) (np)	Ile (I) (np)	
		TGA	UGA	Trp (W) (np)	Stop *	
Yeast mitochondrial	3	ATA	AUA	Met (M) (np)	Ile (I) (np)	
		CTT	CUU	Thr (T) (p)	Leu (L) (np)	
		CTC	CUC	Thr (T) (p)	Leu (L) (np)	
		CTA	CUA	Thr (T) (p)	Leu (L) (np)	
		CTG	CUG	Thr (T) (p)	Leu (L) (np)	
		TGA	UGA	Trp (W) (np)	Stop *	
		CGA	CGA	absent	Arg (R) (b)	
		CGC	CGC	absent	Arg (R) (b)	
Mold, protozoan, and coelenterate mitochondrial + Mycoplasma / Spiroplasma	4	TGA	UGA	Trp (W) (np)	Stop *	Includes the translation table 7 (kinetoplasts).
Invertebrate mitochondrial	5	AGA	AGA	Ser (S) (p)	Arg (R) (b)	
		AGG	AGG	Ser (S) (p)	Arg (R) (b)	
		ATA	AUA	Met (M) (np)	Ile (I) (np)	
		TGA	UGA	Trp (W) (np)	Stop *	
Ciliate, dasycladacean and Hexamita nuclear	6	TAA	UAA	Gln (Q) (p)	Stop *	
		TAG	UAG	Gln (Q) (p)	Stop *	
Echinoderm and flatworm mitochondrial	9	AAA	AAA	Asn (N) (p)	Lys (K) (b)	
		AGA	AGA	Ser (S) (p)	Arg (R) (b)	
		AGG	AGG	Ser (S) (p)	Arg (R) (b)	
		TGA	UGA	Trp (W) (np)	Stop *	
Euplotid nuclear	10	TGA	UGA	Cys (C) (p)	Stop *	

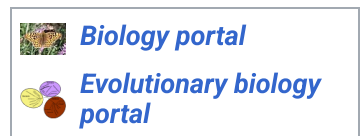
Code	Translation table	DNA codon involved	RNA codon involved	Translation with this code	Standard translation	Notes
Bacterial, archaeal and plant plastid	11					See translation table 1 .
Alternative yeast nuclear	12	CTG	CUG	Ser (S) (p)	Leu (L) (np)	
Ascidian mitochondrial	13	AGA	AGA	Gly (G) (np)	Arg (R) (b)	
		AGG	AGG	Gly (G) (np)	Arg (R) (b)	
		ATA	AUA	Met (M) (np)	Ile (I) (np)	
		TGA	UGA	Trp (W) (np)	Stop *	
Alternative flatworm mitochondrial	14	AAA	AAA	Asn (N) (p)	Lys (K) (b)	
		AGA	AGA	Ser (S) (p)	Arg (R) (b)	
		AGG	AGG	Ser (S) (p)	Arg (R) (b)	
		TAA	UAA	Tyr (Y) (p)	Stop *	
		TGA	UGA	Trp (W) (np)	Stop *	
<i>Blepharisma</i> nuclear	15	TAG	UAG	Gln (Q) (p)	Stop *	As of Nov. 18, 2016: absent from the NCBI update. Similar to translation table 6 .
Chlorophycean mitochondrial	16	TAG	UAG	Leu (L) (np)	Stop *	
Trematode mitochondrial	21	TGA	UGA	Trp (W) (np)	Stop *	
		ATA	AUA	Met (M) (np)	Ile (I) (np)	
		AGA	AGA	Ser (S)	Arg (R) (b)	
		AGG	AGG	Ser (S) (p)	Arg (R) (b)	
		AAA	AAA	Asn (N) (p)	Lys (K) (b)	
<i>Scenedesmus obliquus</i> mitochondrial	22	TCA	UCA	Stop *	Ser (S) (p)	
		TAG	UAG	Leu (L) (np)	Stop *	
<i>Thraustochytrium</i> mitochondrial	23	TTA	UUA	Stop *	Leu (L) (np)	Similar to translation table 11 .
Pterobranchia mitochondrial	24	AGA	AGA	Ser (S) (p)	Arg (R) (b)	
		AGG	AGG	Lys (K) (b)	Arg (R) (b)	

Code	Translation table	DNA codon involved	RNA codon involved	Translation with this code			Standard translation	Notes
		TGA	UGA	Trp (W) (np)			Stop *	
Candidate division SR1 and Gracilibacteria	25	TGA	UGA	Gly (G) (np)			Stop *	
<i>Pachysolen tannophilus</i> nuclear	26	CTG	CUG	Ala (A) (np)			Leu (L) (np)	
Karyorelict nuclear	27	TAA	UAA	Gln (Q) (p)			Stop *	
		TAG	UAG	Gln (Q) (p)			Stop *	
		TG	UGA	Stop *	or	Trp (W) (np)	Stop *	
<i>Condyllostoma</i> nuclear	28	TAA	UAA	Stop *	or	Gln (Q) (p)	Stop *	
		TAG	UAG	Stop *	or	Gln (Q) (p)	Stop *	
		TGA	UGA	Stop *	or	Trp (W) (np)	Stop *	
<i>Mesodinium</i> nuclear	29	TAA	UAA	Tyr (Y) (p)			Stop *	
		TAG	UAG	Tyr (Y) (p)			Stop *	
Peritrich nuclear	30	TA	UAA	Glu (E) (a)			Stop *	
		TAG	UAG	Glu (E) (a)			Stop *	
<i>Blastocrithidia</i> nuclear	31	TAA	UAA	Stop *	or	Glu (E) (a)	Stop *	
		TAG	UAG	Stop *	or	Glu (E) (a)	Stop *	
		TGA	UGA	Trp (W) (np)			Stop *	
Cephalodiscidae mitochondrial code	33	AGA	AGA	Ser (S) (p)			Arg (R) (b)	Similar to translation table 24.
		AGG	AGG	Lys (K) (b)			Arg (R) (b)	
		TAA	UAA	Tyr (Y) (p)			Stop *	
		TGA	UGA	Trp (W) (np)			Stop *	
Enterosoma ^[22]	34	AGG	AGG	Met (M) (np)			Arg (R) (b)	
<i>Peptacetobacter</i> ^[22]	35	CGG	CGG	Gln (Q) (p)			Arg (R) (b)	

Code	Translation table	DNA codon involved	RNA codon involved	Translation with this code	Standard translation	Notes
<i>Anaerococcus and Onthovivens</i> ^[22]	36	CGG	CGG	Trp (W) (np)	Arg (R) (b)	
<i>Absconditabacteraceae</i> ^[22]	37	CGA	CGA	Trp (W) (np)	Arg (R) (b)	
		CGG	CGG	Trp (W) (np)	Arg (R) (b)	
		TGA	UGA	Gly (G) (np)	Stop *	

See also

- Bioinformatics
- List of genetic codes



Notes

- Each stop codon has a specific name: UAG is *amber*, UGA is *opal* or *umber*, and UAA is *ochre*.^[7] In DNA, these stop codons are TAG, TGA, and TAA, respectively.
- The historical basis for designating the [stop codons as amber, ochre and opal](#) is described in the autobiography of [Sydney Brenner](#)^[14] and in a historical article by Bob Edgar.^[15]
- The major difference between DNA and RNA is that [thymine](#) (T) is only found in the former. In RNA, it is replaced with [uracil](#) (U).^[18] This is the only difference between the standard RNA codon table and the standard DNA codon table.
- Euplotes octacarinatus* is an exception.^[21]

References

- "Amino Acid Translation Table" (<https://web.archive.org/web/20200529000711/http://sites.science.oregonstate.edu/genbio/otherresources/aminoacidtranslation.htm>) . Oregon State University. Archived from the original (<http://sites.science.oregonstate.edu/genbio/otherresources/aminoacidtranslation.htm>) on 29 May 2020. Retrieved 2 December 2020.
- Bartee, Lisa; Brook, Jack. *MHCC Biology 112: Biology for Health Professions* (<https://mhccbiology112.pressbooks.com>) . Open Oregon. p. 42. Archived (<https://web.archive.org/web/20201206173711/https://mhccbiology112.pressbooks.com/>) from the original on 6 December 2020. Retrieved 6 December 2020.

3. Elzanowski A, Ostell J (7 January 2019). "The Genetic Codes" (<https://web.archive.org/web/20201005105339/https://www.ncbi.nlm.nih.gov/Taxonomy/Utils/wprintgc.cgi>) . National Center for Biotechnology Information. Archived from the original (<https://www.ncbi.nlm.nih.gov/Taxonomy/Utils/wprintgc.cgi>) on 5 October 2020. Retrieved 21 February 2019.
4. "RNA Functions" (<https://www.nature.com/scitable/topicpage/rna-functions-352/>) . Scitable. Nature Education. Archived (<https://web.archive.org/web/20081018170459/https://www.nature.com/scitable/topicpage/rna-functions-352/>) from the original on 18 October 2008. Retrieved 5 January 2021.
5. "The Genetic Codes" (<https://www.ncbi.nlm.nih.gov/Taxonomy/Utils/wprintgc.cgi>) . National Center for Biotechnology Information. Archived (<https://web.archive.org/web/20110513014234/http://www.ncbi.nlm.nih.gov/Taxonomy/Utils/wprintgc.cgi>) from the original on 13 May 2011. Retrieved 2 December 2020.
6. "Codon" (<https://www.genome.gov/genetics-glossary/Codon>) . National Human Genome Research Institute. Archived (<https://web.archive.org/web/20201022081214/https://www.genome.gov/genetics-glossary/Codon>) from the original on 22 October 2020. Retrieved 10 October 2020.
7. Maloy S. (29 November 2003). "How nonsense mutations got their names" (<https://web.archive.org/web/20200923075442/http://www.sci.sdsu.edu/~smaloy/MicrobialGenetics/topics/rev-sup/amber-name.html>) . *Microbial Genetics Course*. San Diego State University. Archived from the original (<http://www.sci.sdsu.edu/~smaloy/MicrobialGenetics/topics/rev-sup/amber-name.html>) on 23 September 2020. Retrieved 10 October 2020.
8. Hinnebusch AG (2011). "Molecular Mechanism of Scanning and Start Codon Selection in Eukaryotes" (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3165540>) . *Microbiology and Molecular Biology Reviews*. **75** (3): 434–467. doi:10.1128/MMBR.00008-11 (<https://doi.org/10.1128%2FMMBR.00008-11>) . PMC 3165540 (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3165540>) . PMID 21885680 (<https://pubmed.ncbi.nlm.nih.gov/21885680>) .
9. Touriol C, Bornes S, Bonnal S, Audigier S, Prats H, Prats AC, Vagner S (2003). "Generation of protein isoform diversity by alternative initiation of translation at non-AUG codons" (<https://doi.org/10.1016%2FS0248-4900%2803%2900033-9>) . *Biology of the Cell*. **95** (3–4): 169–78. doi:10.1016/S0248-4900(03)00033-9 (<https://doi.org/10.1016%2FS0248-4900%2803%2900033-9>) . PMID 12867081 (<https://pubmed.ncbi.nlm.nih.gov/12867081>) .

10. Bandyopadhyay, Debashree; Mehler, Ernest L. (August 2008). "Quantitative expression of protein heterogeneity: Response of amino acid side chains to their local environment". *Proteins*. **72** (2): 646–59. doi:10.1002/prot.21958 (<https://doi.org/10.1002%2Fprot.21958>) . PMID 18247345 (<https://pubmed.ncbi.nlm.nih.gov/18247345>) .
11. Saier, Milton H. Jr. (10 July 2019). "Understanding the Genetic Code" (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6620406>) . *J Bacteriol.* **201** (15): e00091-19. doi:10.1128/JB.00091-19 (<https://doi.org/10.1128%2FJB.00091-19>) . PMC 6620406 (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6620406>) . PMID 31010904 (<https://pubmed.ncbi.nlm.nih.gov/31010904>) .
12. Muto, A.; Osawa, S. (January 1987). "The guanine and cytosine content of genomic DNA and bacterial evolution" (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC304163>) . *Proc Natl Acad Sci USA*. **84** (1): 166–9. Bibcode:1987PNAS...84..166M (<https://ui.adsabs.harvard.edu/abs/1987PNAS...84..166M>) . doi:10.1073/pnas.84.1.166 (<https://doi.org/10.1073%2Fpnas.84.1.166>) . PMC 304163 (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC304163>) . PMID 3467347 (<https://pubmed.ncbi.nlm.nih.gov/3467347>) .
13. "The Information in DNA Determines Cellular Function via Translation" (<https://www.nature.com/scitable/topicpage/the-information-in-dna-determines-cellular-function-6523228/>) . Scitable. Nature Education. Archived (<https://web.archive.org/web/20170923100645/http://www.nature.com/scitable/topicpage/the-information-in-dna-determines-cellular-function-6523228>) from the original on 23 September 2017. Retrieved 5 December 2020.
14. Brenner, Sydney; Wolpert, Lewis (2001). *A Life in Science*. Biomed Central Limited. pp. 101–104. ISBN 9780954027803.
15. Edgar B (2004). "The genome of bacteriophage T4: an archeological dig" (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC1448817>) . *Genetics*. **168** (2): 575–82. doi:10.1093/genetics/168.2.575 (<https://doi.org/10.1093%2Fgenetics%2F168.2.575>) . PMC 1448817 (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC1448817>) . PMID 15514035 (<https://pubmed.ncbi.nlm.nih.gov/15514035>) . see pages 580–581
16. IUPAC—IUB Commission on Biochemical Nomenclature. "Abbreviations and Symbols for Nucleic Acids, Polynucleotides and Their Constituents" (<http://publications.iupac.org/pac/1974/pdf/4003x0277.pdf>) (PDF). International Union of Pure and Applied Chemistry. Archived (<https://web.archive.org/web/20210709183441/http://publications.iupac.org/pac/1974/pdf/4003x0277.pdf>) (PDF) from the original on 9 July 2021. Retrieved 5 December 2020.

17. "What does DNA do?" (<https://web.archive.org/web/20201129044637/https://www.yourgenome.org/facts/what-does-dna-do>) . *Your Genome*. Welcome Genome Campus. Archived from the original (<https://www.yourgenome.org/facts/what-does-dna-do>) on 29 November 2020. Retrieved 12 January 2021.
18. "Genes" (<https://sphweb.bumc.bu.edu/otlt/MPH-Modules/PH/DNA-Genetics/DNA-Genetics3.html>) . *DNA, Genetics, and Evolution*. Boston University. Archived (<https://web.archive.org/web/20200428050259/http://sphweb.bumc.bu.edu/otlt/MPH-Modules/PH/DNA-Genetics/DNA-Genetics3.html>) from the original on 28 April 2020. Retrieved 10 December 2020.
19. "Choose a start codon" (<https://depts.washington.edu/agro/genomes/students/stanstart.htm>) . *depts.washington.edu*. Retrieved 2024-08-14.
20. Osawa, A (November 1993). "Evolutionary changes in the genetic code" (<https://pubmed.ncbi.nlm.nih.gov/8281749/>) . *Comparative Biochemistry and Physiology*. **106** (2): 489–94. doi:10.1016/0305-0491(93)90122-I (<https://doi.org/10.1016%2F0305-0491%2893%2990122-I>) . PMID 8281749 (<https://pubmed.ncbi.nlm.nih.gov/8281749/>) . Archived (<https://web.archive.org/web/20201206173716/https://pubmed.ncbi.nlm.nih.gov/8281749/>) from the original on 2020-12-06. Retrieved 2020-12-05.
21. Osawa S, Jukes TH, Watanabe K, Muto A (March 1992). "Recent evidence for evolution of the genetic code" (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC372862>) . *Microbiological Reviews*. **56** (1): 229–64. doi:10.1128/MR.56.1.229-264.1992 (<https://doi.org/10.1128%2FMR.56.1.229-264.1992>) . PMC 372862 (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC372862>) . PMID 1579111 (<https://pubmed.ncbi.nlm.nih.gov/1579111/>) .
22. Shulgina, Yekaterina; Eddy, Sean R. (9 November 2021). "A computational screen for alternative genetic codes in over 250,000 genomes" (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8629427>) . *eLife*. **10**. doi:10.7554/eLife.71402 (<https://doi.org/10.7554%2FeLife.71402>) . PMC 8629427 (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8629427>) . PMID 34751130 (<https://pubmed.ncbi.nlm.nih.gov/34751130/>) .

Further reading

- Chevance FV, Hughes KT (2 May 2017). "Case for the genetic code as a triplet of triplets" (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5422812>) . *Proceedings of the National Academy of Sciences of the United States of America*. **114** (18): 4745–4750. Bibcode:2017PNAS..114.4745C (<https://ui.adsabs.harvard.edu/abs/2017PNAS..114.4745C>) . doi:10.1073/pnas.1614896114 (<https://doi.org/10.1073%2Fpnas.1614896114>) . JSTOR 26481868 (<https://www.jstor.org/stable/26481868>) .

481868) . PMC 5422812 (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5422812>) .
PMID 28416671 (<https://pubmed.ncbi.nlm.nih.gov/28416671>) .

- Dever TE (29 June 2012). "A New Start for Protein Synthesis" (<https://zenodo.org/record/1230920>) . *Science*. **336** (6089). American Association for the Advancement of Science: 1645–1646. Bibcode:2012Sci...336.1645D (<https://ui.adsabs.harvard.edu/abs/2012Sci...336.1645D>) . doi:10.1126/science.1224439 (<https://doi.org/10.1126/science.1224439>) . JSTOR 41585146 (<https://www.jstor.org/stable/41585146>) . PMID 22745408 (<https://pubmed.ncbi.nlm.nih.gov/22745408>) . S2CID 44326947 (<https://api.semanticscholar.org/CorpusID:44326947>) . Archived (<https://web.archive.org/web/20220608001506/https://zenodo.org/record/1230920>) from the original on 8 June 2022. Retrieved 17 October 2020.
- Gardner RS, Wahba AJ, Basilio C, Miller RS, Lengyel P, Speyer JF (December 1962). "Synthetic polynucleotides and the amino acid code. VII" (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC221128>) . *Proceedings of the National Academy of Sciences of the United States of America*. **48** (12): 2087–2094. Bibcode:1962PNAS...48.2087G (<https://ui.adsabs.harvard.edu/abs/1962PNAS...48.2087G>) . doi:10.1073/pnas.48.12.2087 (<https://doi.org/10.1073/pnas.48.12.2087>) . PMC 221128 (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC221128>) . PMID 13946552 (<https://pubmed.ncbi.nlm.nih.gov/13946552>) .
- Nakamoto T (March 2009). "Evolution and the universality of the mechanism of initiation of protein synthesis". *Gene*. **432** (1–2): 1–6. doi:10.1016/j.gene.2008.11.001 (<https://doi.org/10.1016/j.gene.2008.11.001>) . PMID 19056476 (<https://pubmed.ncbi.nlm.nih.gov/19056476>) .
- Wahba AJ, Gardner RS, Basilio C, Miller RS, Speyer JF, Lengyel P (January 1963). "Synthetic polynucleotides and the amino acid code. VIII" (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC300638>) . *Proceedings of the National Academy of Sciences of the United States of America*. **49** (1): 116–122. Bibcode:1963PNAS...49..116W (<https://ui.adsabs.harvard.edu/abs/1963PNAS...49..116W>) . doi:10.1073/pnas.49.1.116 (<https://doi.org/10.1073/pnas.49.1.116>) . PMC 300638 (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC300638>) . PMID 13998282 (<https://pubmed.ncbi.nlm.nih.gov/13998282>) .
- Yanofsky C (9 March 2007). "Establishing the Triplet Nature of the Genetic Code" (<https://doi.org/10.1016/j.cell.2007.02.029>) . *Cell*. **128** (5): 815–818. doi:10.1016/j.cell.2007.02.029 (<https://doi.org/10.1016/j.cell.2007.02.029>) . PMID 17350564 (<https://pubmed.ncbi.nlm.nih.gov/17350564>) . S2CID 14249277 (<https://api.semanticscholar.org/CorpusID:14249277>) .
- Zaneveld J, Hamady M, Sueoka N, Knight R (28 February 2009). "CodonExplorer: An Interactive Online Database for the Analysis of Codon Usage and Sequence Composition". *Bioinformatics for DNA Sequence Analysis*. Methods in Molecular Biology. Vol. 537. pp. 207–232. doi:10.1007/978-1-

59745-251-9_10 (https://doi.org/10.1007%2F978-1-59745-251-9_10) . ISBN 978-1-58829-910-9. PMC 2953947 (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2953947>) . PMID 19378146 (<https://pubmed.ncbi.nlm.nih.gov/19378146>) .

External links

- DNA codon chart organized in a wheel (<https://web.archive.org/web/20160321090602/https://www.yourgenome.org/sites/default/files/downloads/activities/kras-cancer-mutation/krascodonwheel.pdf>)