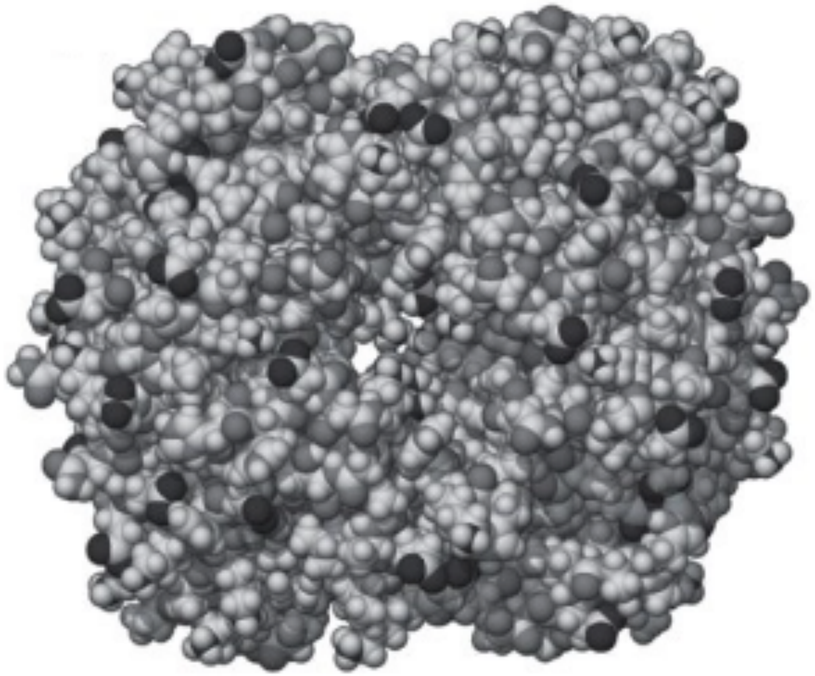
Date	Day (week)	Topic	To do
18.2	Tue (1)	Introductions / syllabus review	Review course content, ask questions
20.2	Thu (GT)	Structure of a scientific paper, critical reading	Look over worksheet, ask questions
25.2	Tue (2)	Introductory unit: Structure	Read PBoC 1.1, 1.2, 8.1, 8.4
27.2	Thu (GT)	Open discussion, Q&A	Ask questions
4.3	Tue (3)	George Feher, Roderick Clayton	Read paper
6.3	Thu (WS)	Discuss paper analysis	Bring completed worksheet
11.3	Tue (4, WS)	Peter Wolynes	Read paper
13.3	Thu (WS)	Discuss paper analysis	Bring completed worksheet
18.3	Tue (5)	Jose Onuchic, Ken Dill Discussion, outlook: Structure	Read paper
20.3	Thu **(GT)**	Discuss paper analysis	Bring completed worksheet
25.3	Tue (6, GT)	Introductory unit: Single molecule mechanics	Read PBoC 8.3

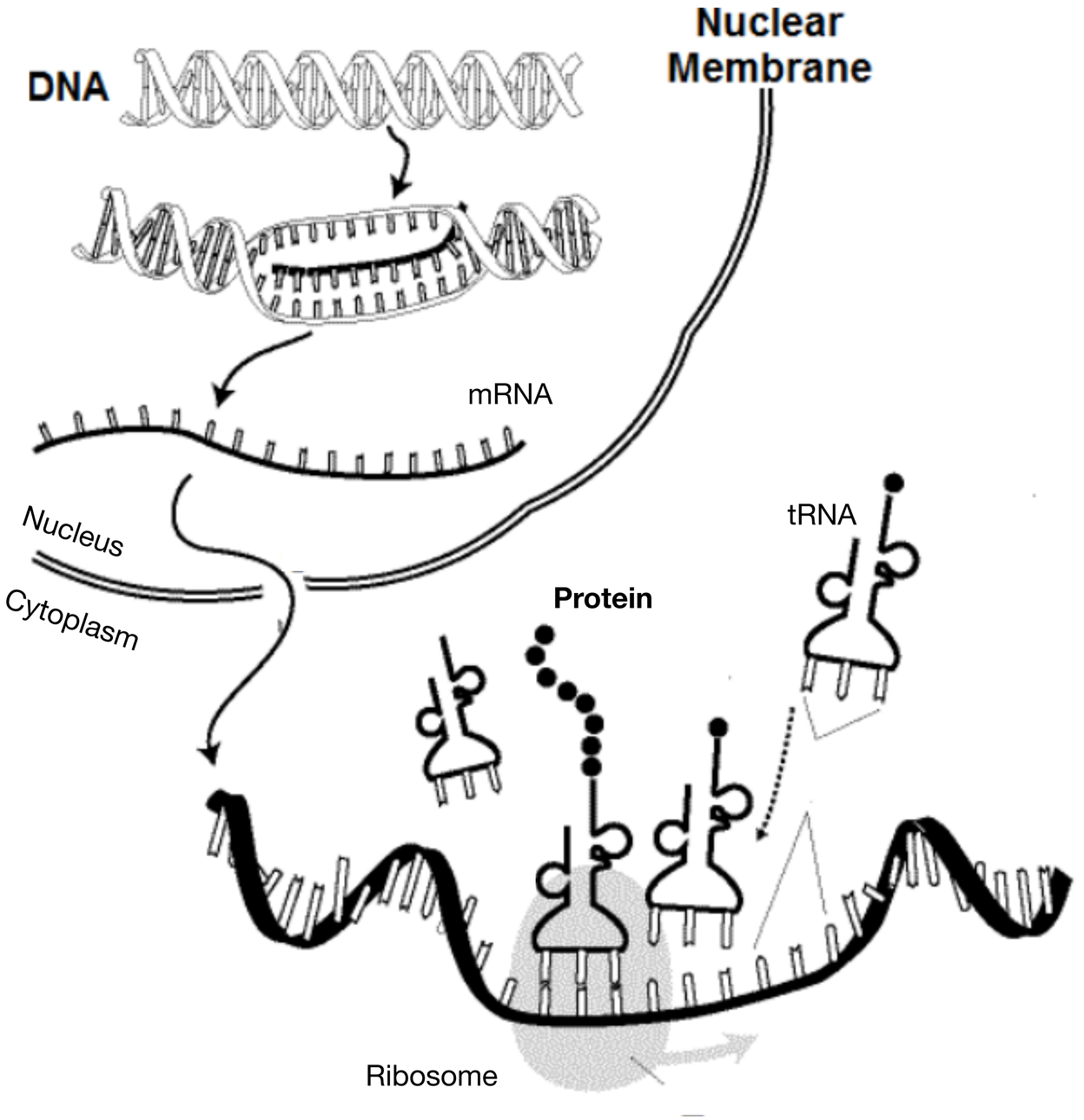


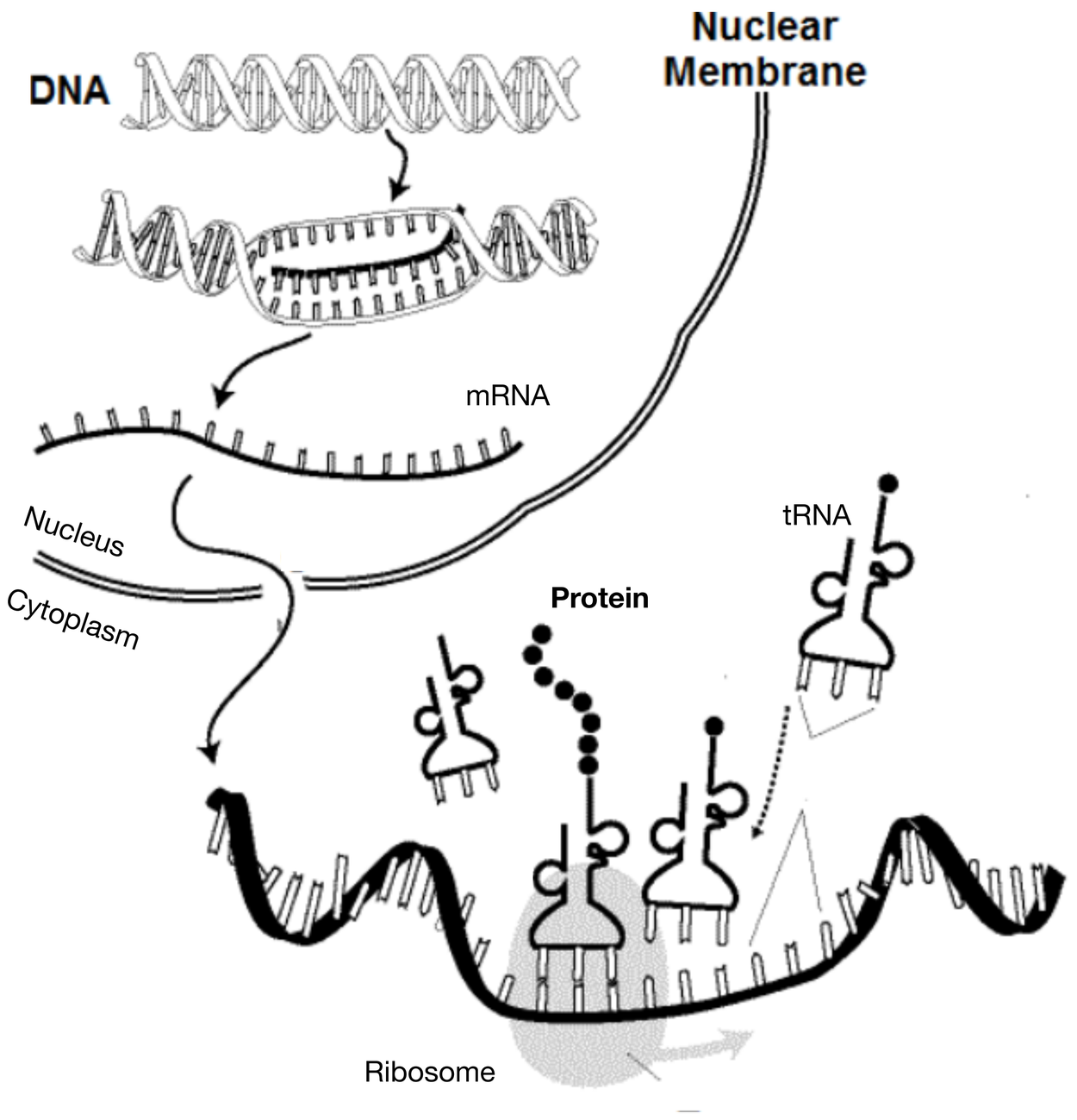
Module 1: Structure

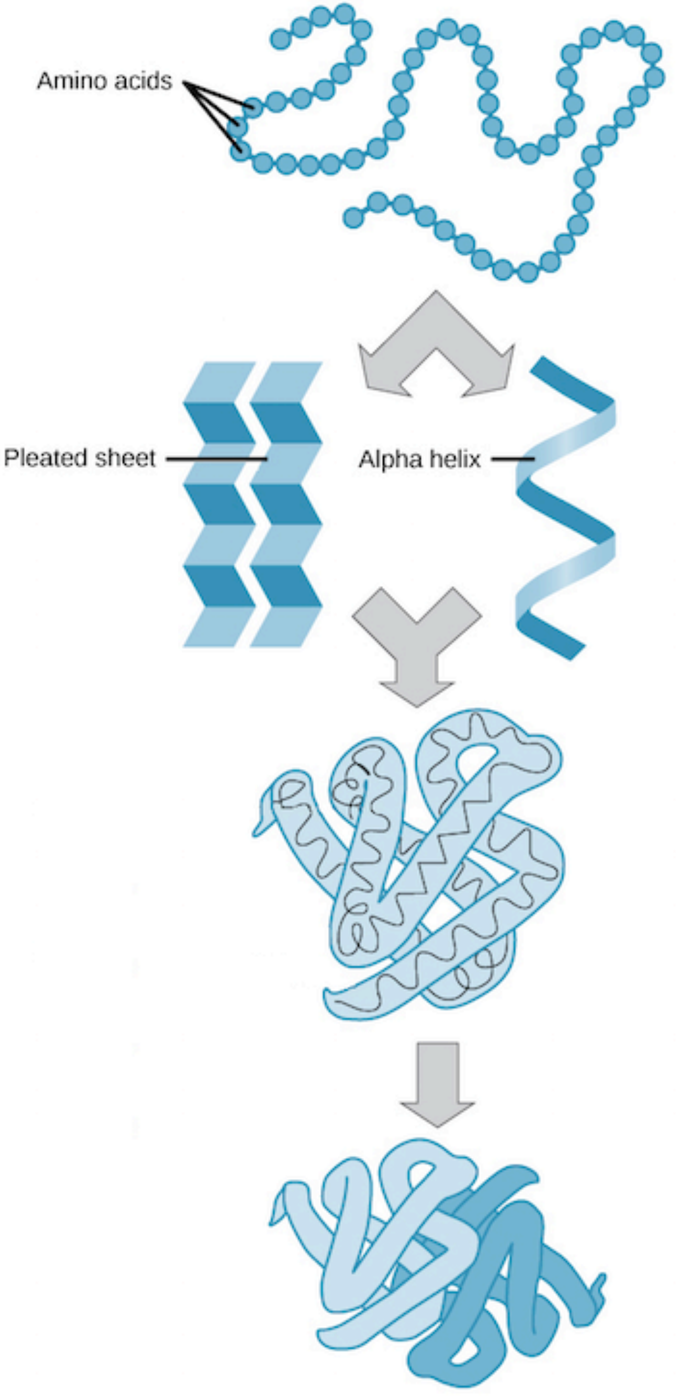
Open discussion, Q&A

Giorgio Tortarolo

Topics in biophysics and physical biology | PHYS-466 | 27.02.2025


Nuclear
Membrane
DNA
mRNA
Nucleus
Cytoplasm
tRNA
Protein
Ribosome



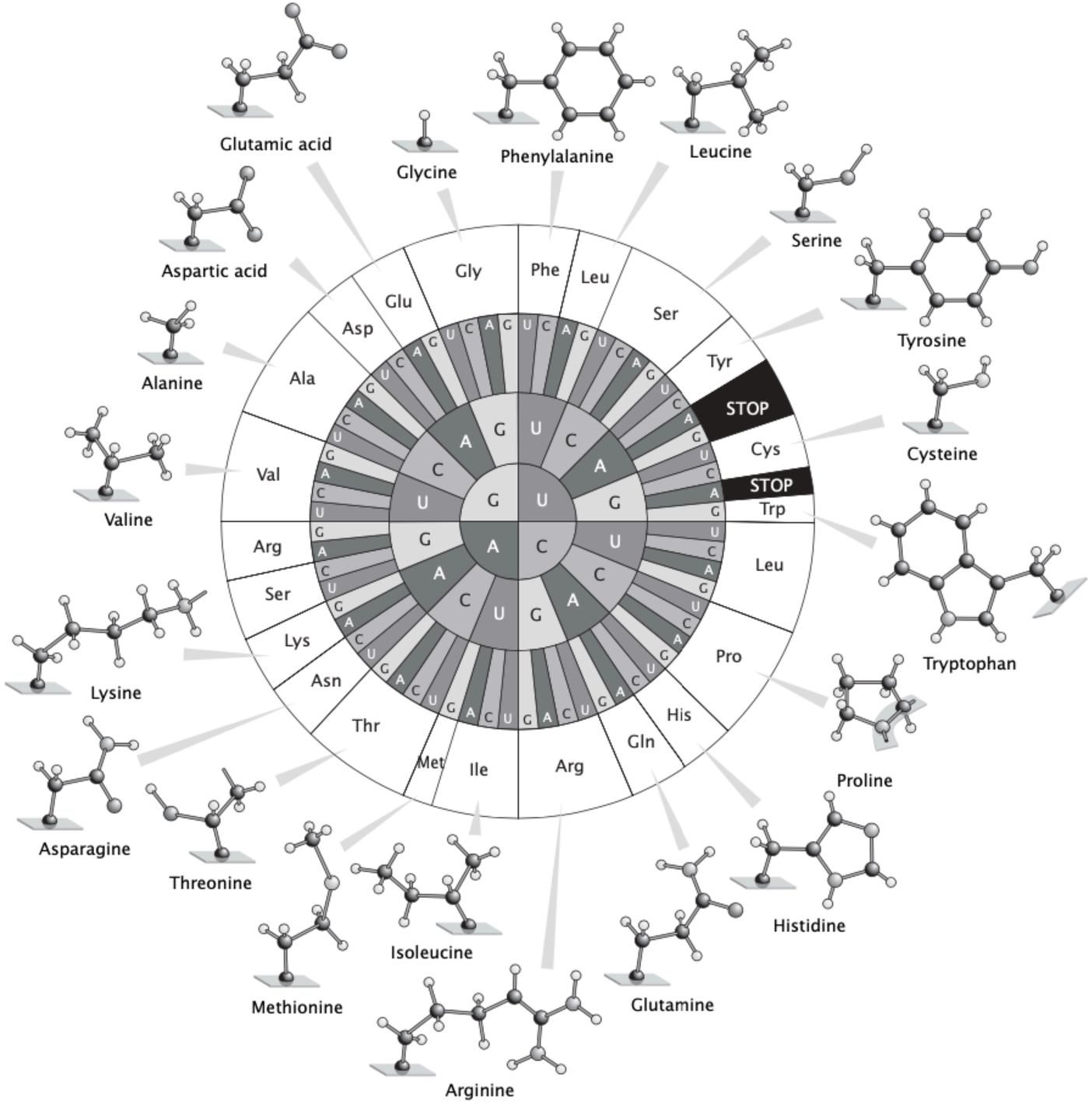


Primary protein structure
sequence of a chain of animo acids

Secondary protein structure
hydrogen bonding of the peptide backbone causes the amino acids to fold into a repeating pattern

Tertiary protein structure
three-dimensional folding pattern of a protein due to side chain interactions

Quaternary protein structure
protein consisting of more than one amino acid chain


Glutamic acid
Glycine
Phenylalanine
Leucine
Serine
Aspartic acid
Tyrosine
Alanine
Cysteine
Valine
Tryptophan
Lysine
Proline
Asparagine
Threonine
Histidine
Isoleucine
Methionine
Glutamine
Arginine
Gly
Phe
Leu
Ser
Tyr
STOP
Cys
STOP
Trp
Leu
Pro
His
Gln
Arg
Ile
Met
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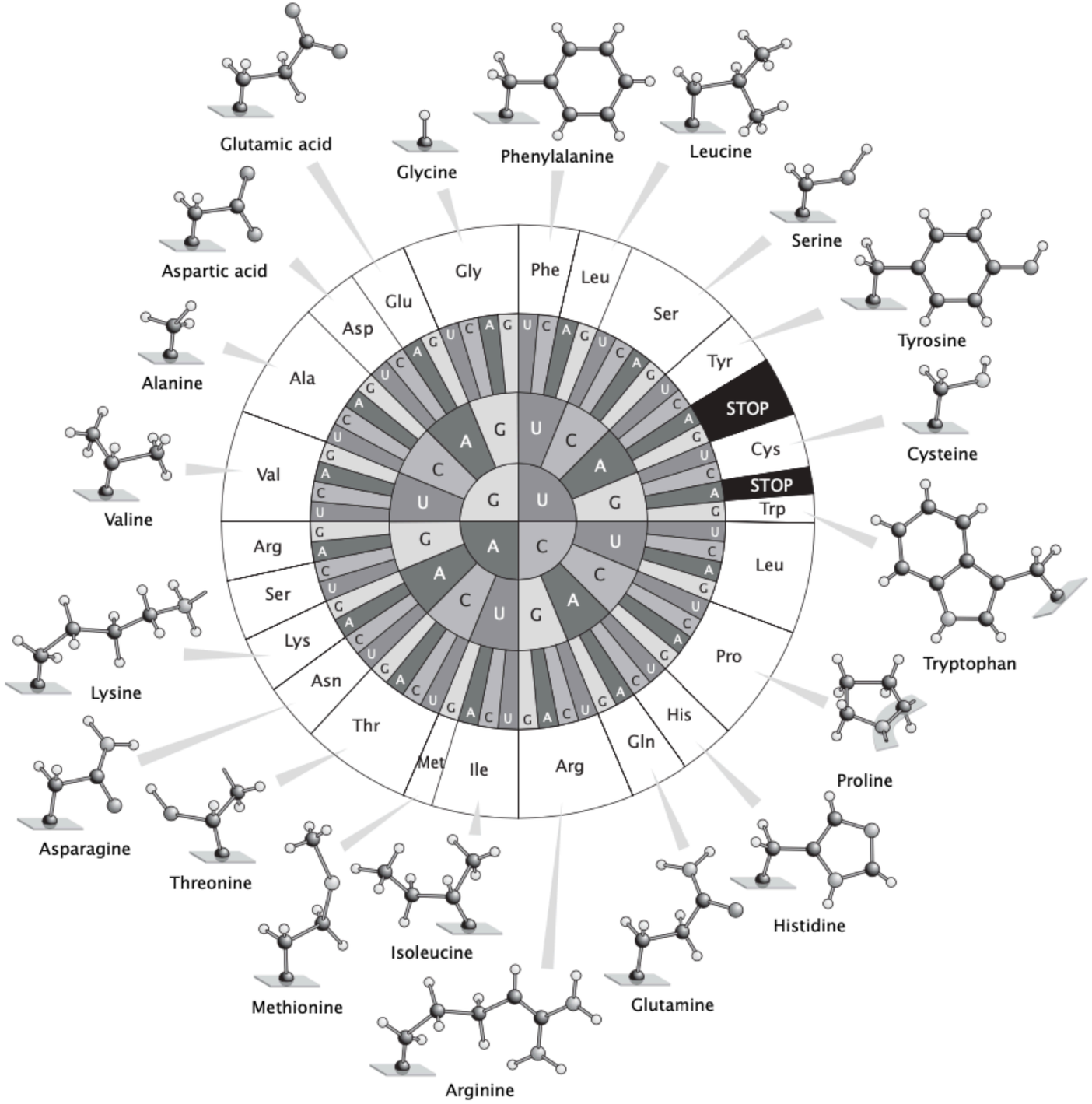
Ser
Arg
Val
Ala
Asp
Glu
U
C
A
G



Degenerate genetic code

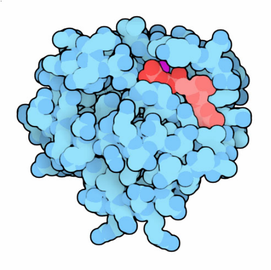
$n = 4$ 4 letters: A G C U

$r = 3$ words of 3 letters each

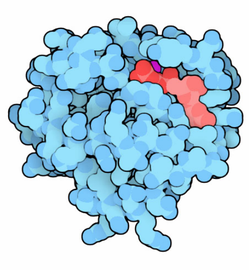
$n^r = 4^3 = 64$ permutations with repetitions

But only 20 amino acids

The motivation to understand protein structure



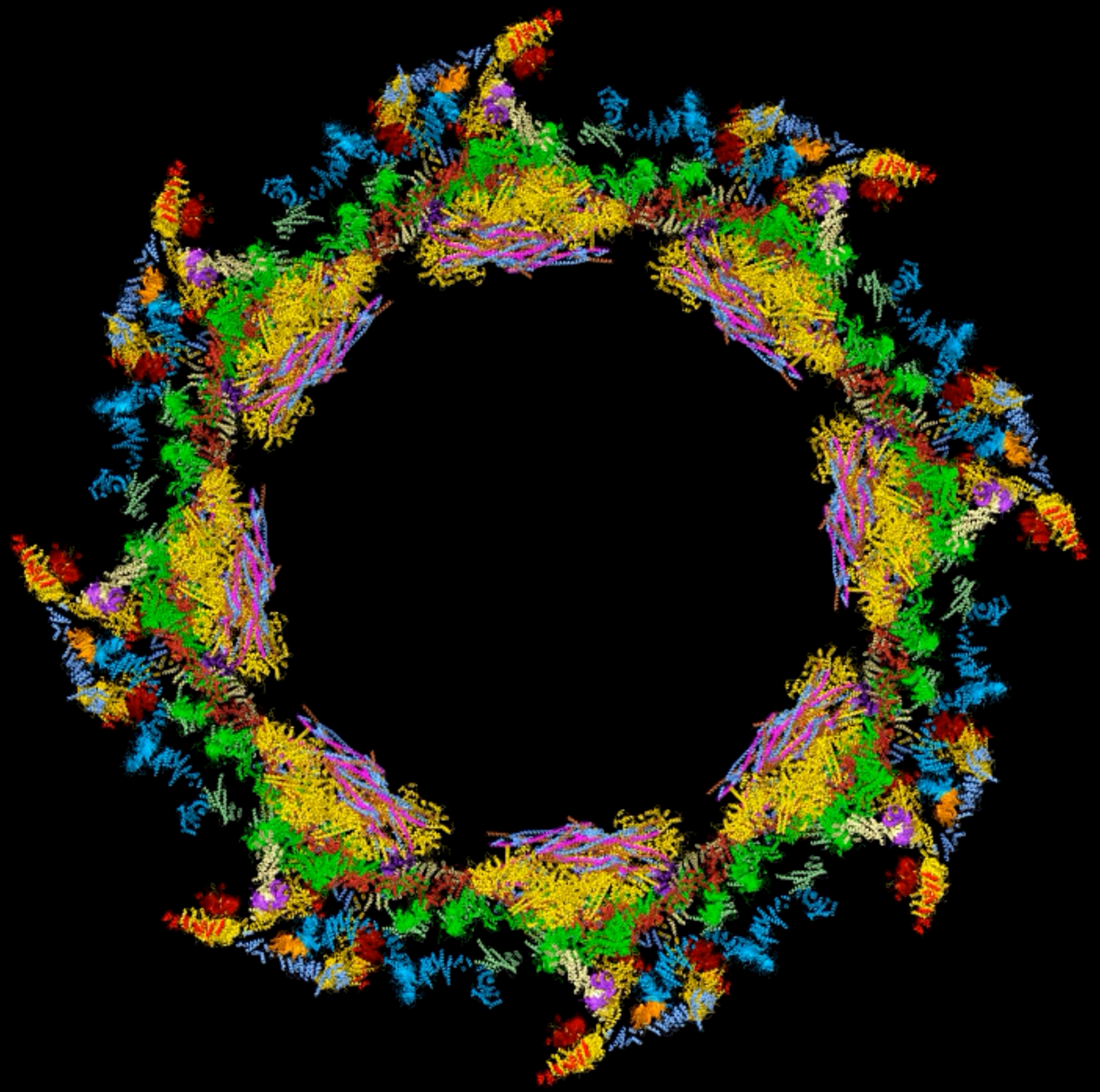
Protein folding: questions



(i) What is the physical code by which an amino acid sequence dictates a protein's native structure?

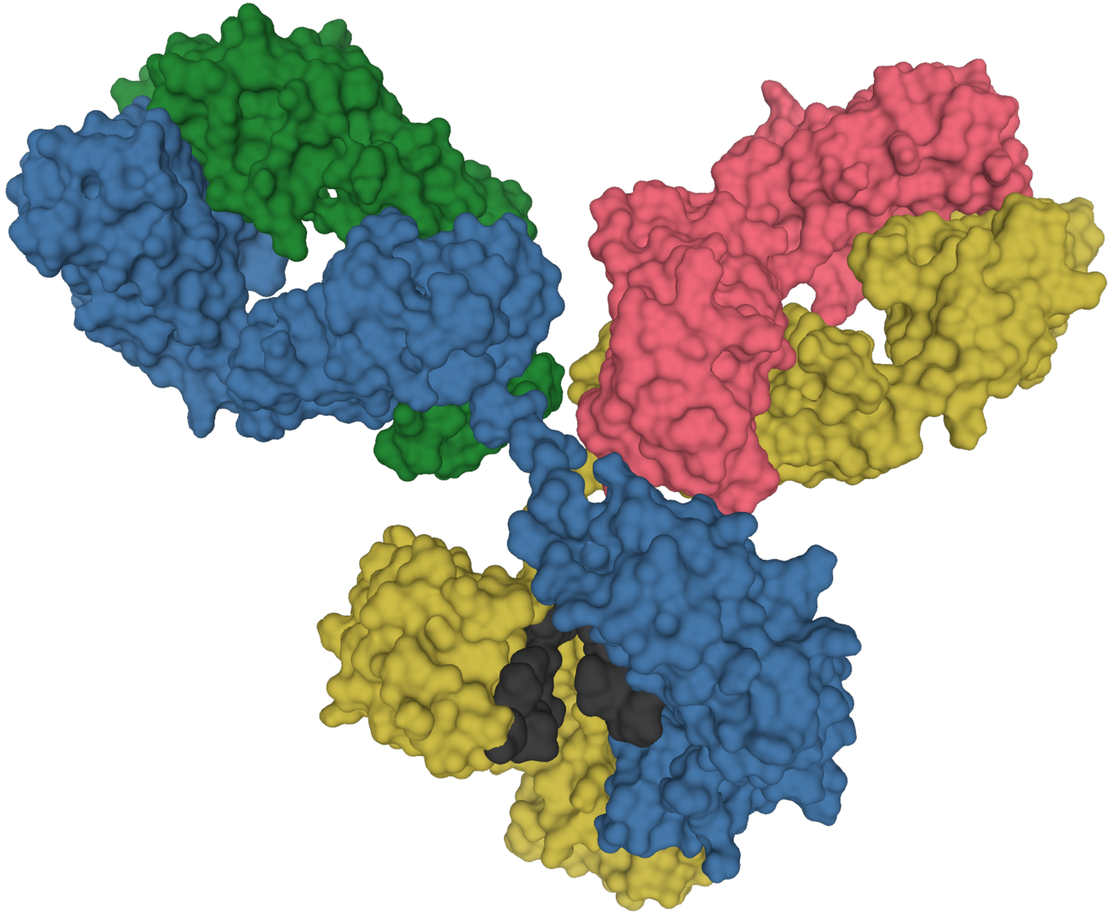
(ii) How can proteins fold so fast?

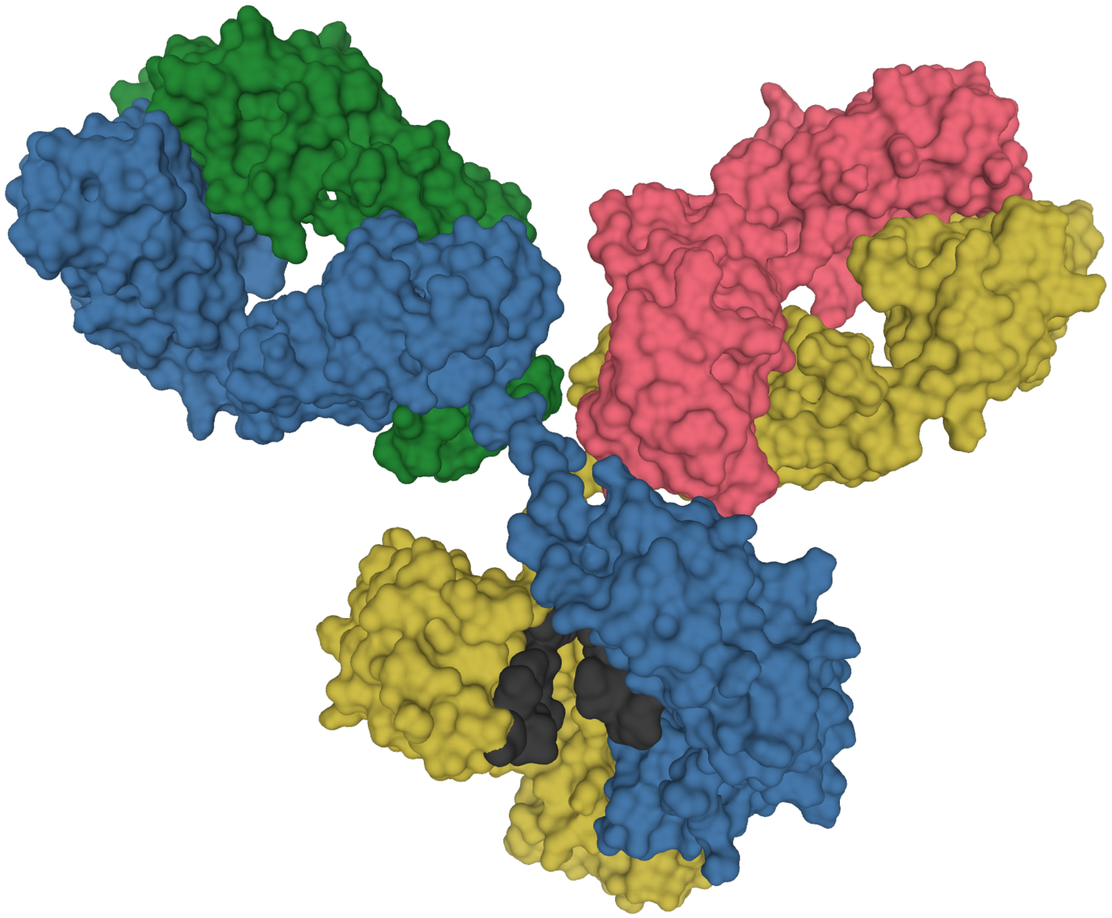
(iii) Can we devise a computer algorithm to predict protein structures from their sequence?

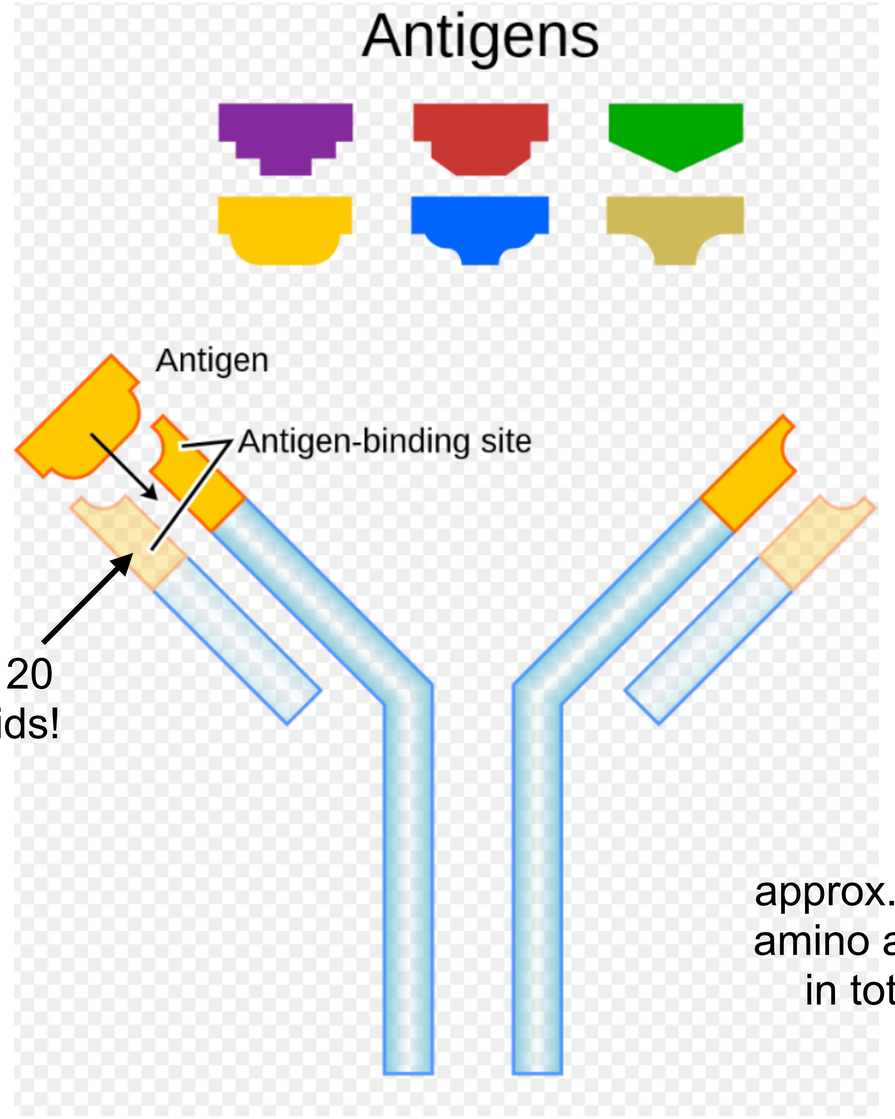


Christian E. Zimmerli et al., *Nuclear pores dilate and constrict in cellulo.* **Science 374**


Pausa (k)






Antigens
Antigen
Antigen-binding site
approx. 120
amino acids!
approx. 700
amino acids
in total

Open discussion

Awardees of the “Structure” module

Roderick K. Clayton and George Feher - 1982

*“For their many contributions to the understanding of the **physics of photosynthesis**; specifically, for their role in the pioneering of the concept of reaction enters in photosynthetic bacteria, their isolation, their spectroscopy and their structural characterisation.”*

Peter Wolynes - 2004

*"For his conceptual breakthroughs in **protein dynamics and protein folding**, and his critical insights toward the understanding of how proteins work at the most fundamental level."*

Ken A. Dill and Jose Nelson Onuchic - 2019

*"For independent contributions to **a new view of protein folding**, from the introduction and exploration of simple models, to detailed confrontations between theory and experiment."*