



AMINO ACIDS AND PROTEINS

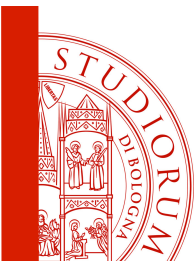
Prof. Alejandro Hochkoeppler
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University of Bologna
E-mail: a.hochkoeppler@unibo.it



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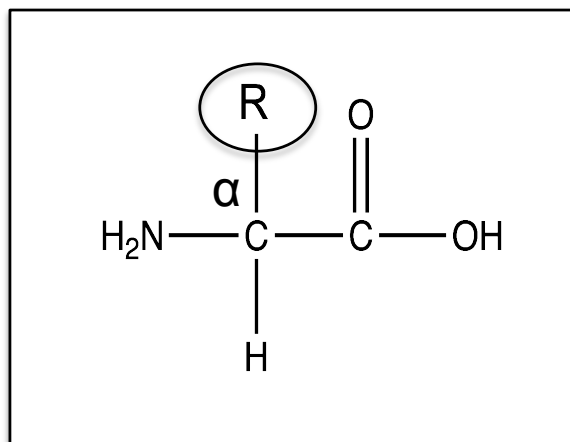
Composition of an *Escherichia coli* cell

Component	% Wet Mass
Water	70
Nucleic Acids	7
Proteins	15
Lipids	2
Polysaccharides	3
Amino Acids (Metabolies)	0.8
Nucleotides (Metabolites)	0.8
Inorganic Ions	1



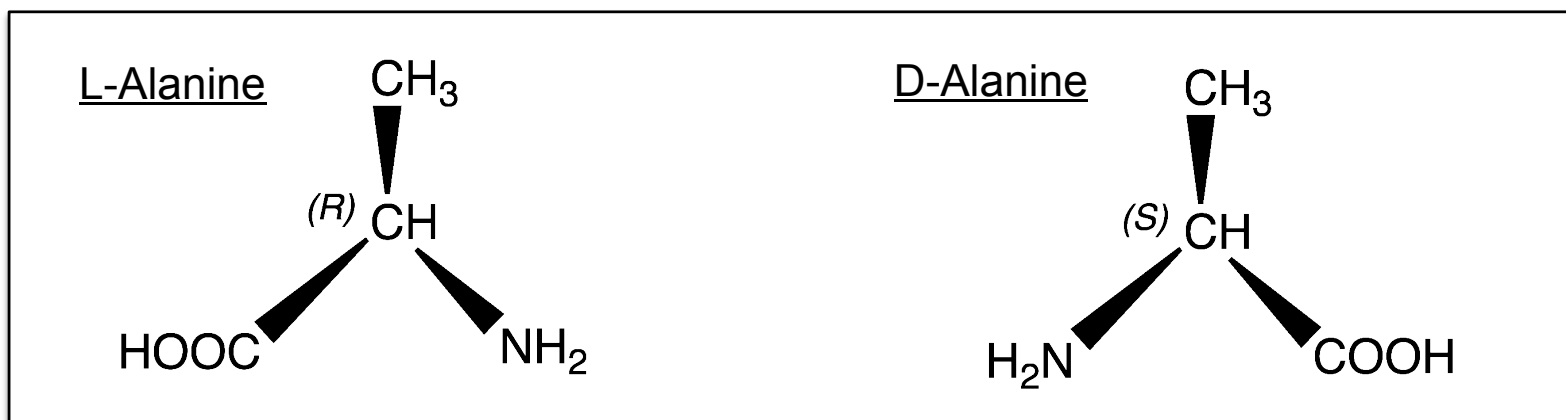
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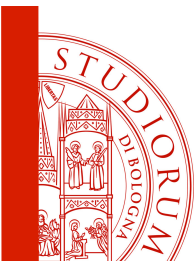
Proteins are composed of α -amino acids



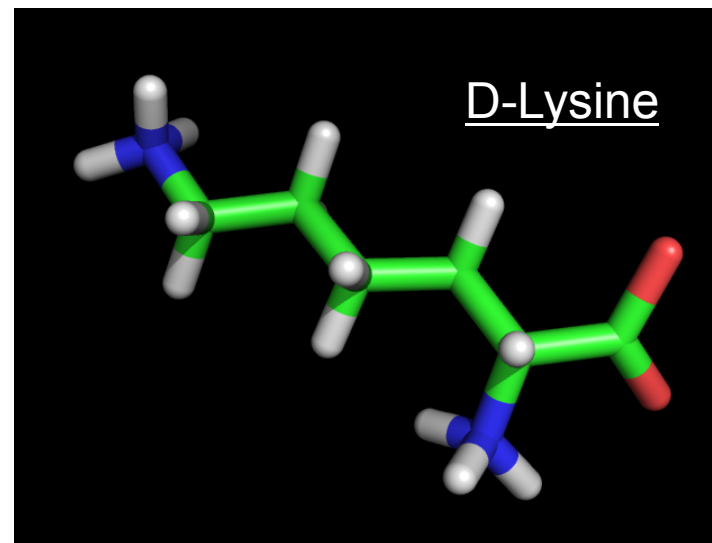
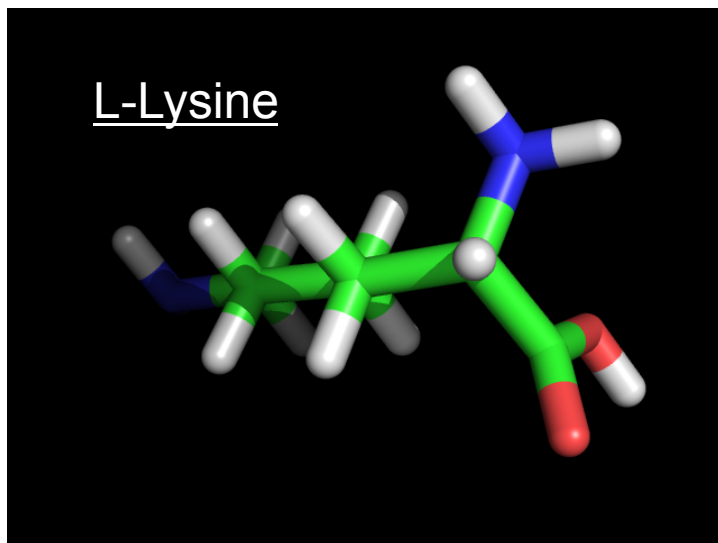
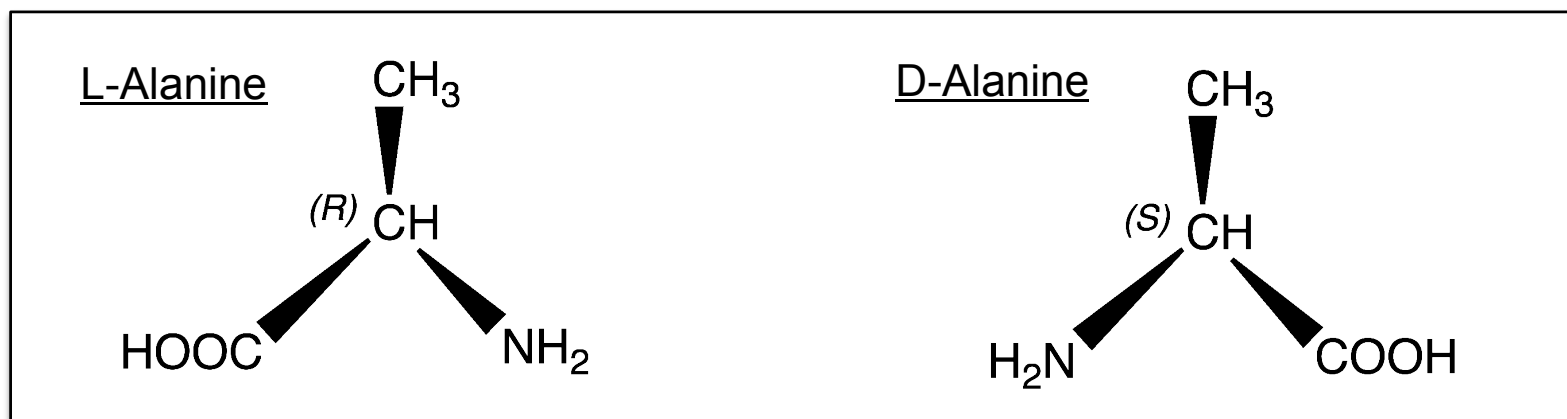
There are 20 types of R groups: 20 different amino acids. Alpha carbon is chiral L- and D-amino acids. Proteins are composed of L-amino acids.

Amino acids are classified according to their R-groups. Three major R groups: hydrophobic, charged, polar. To distinguish between L- and D-amino acids we can look along the H-C α axis. The two configurations are mirrored when we look at them together.



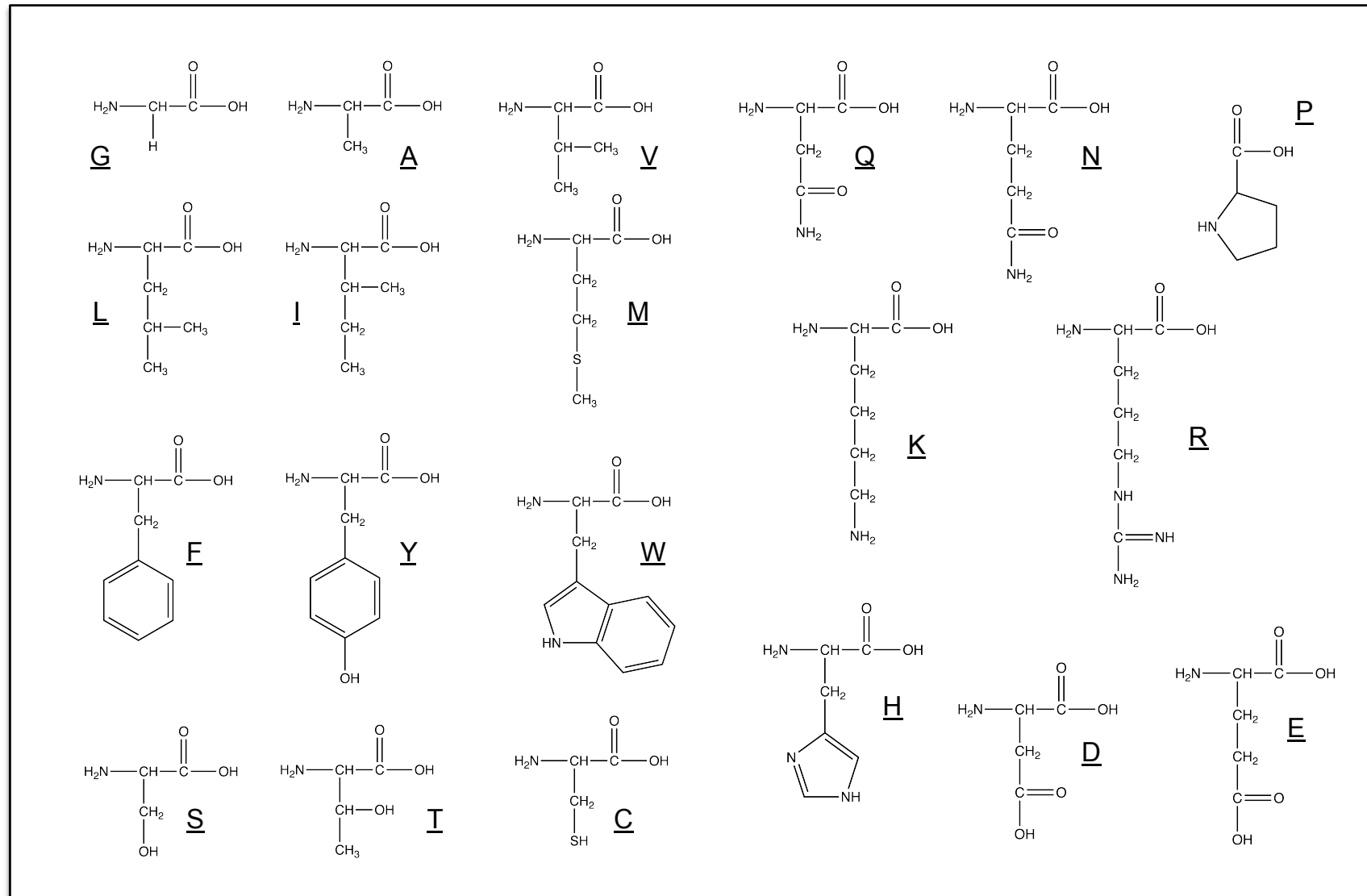


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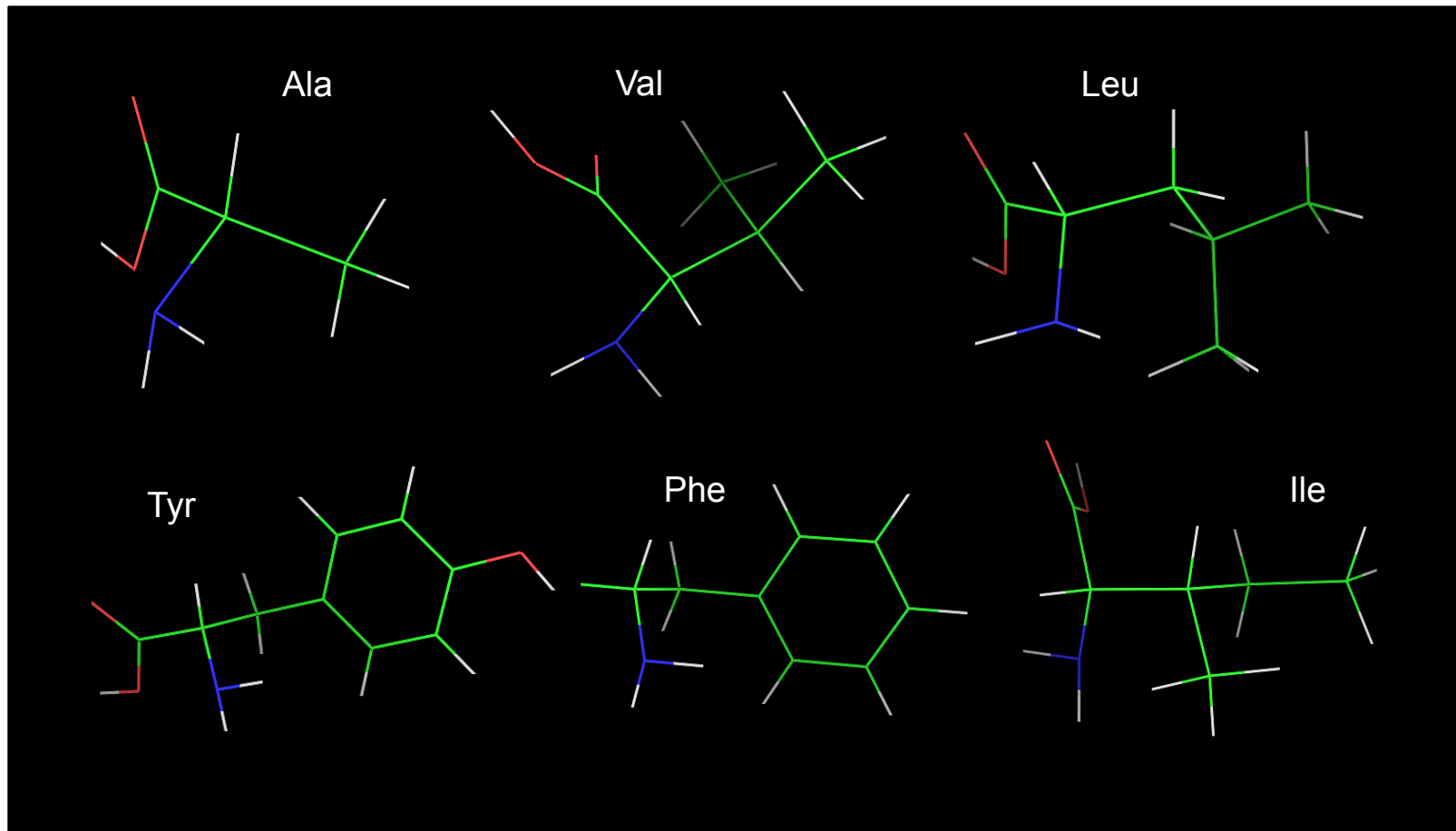
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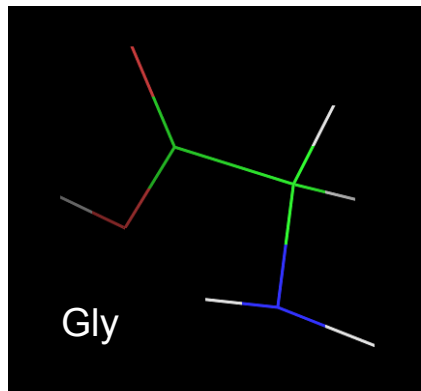
Hydrophobic Amino Acids





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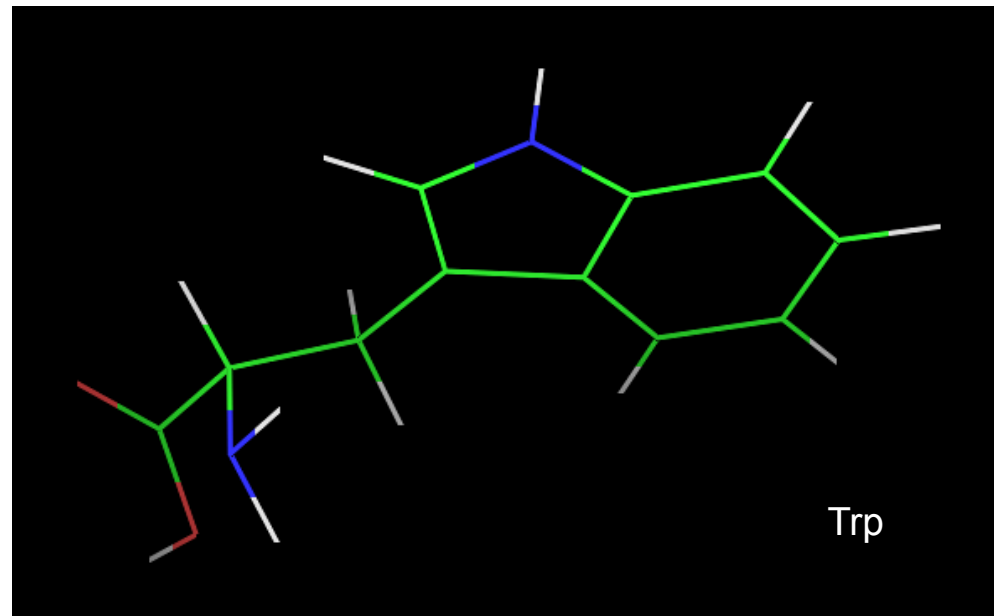
The size of Amino Acids varies considerably



Small Amino Acids

Glycine:

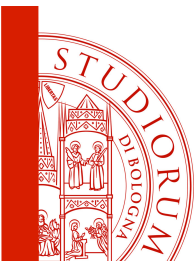
Molecular Mass 75.07 g Mol^{-1}



Large Amino Acids

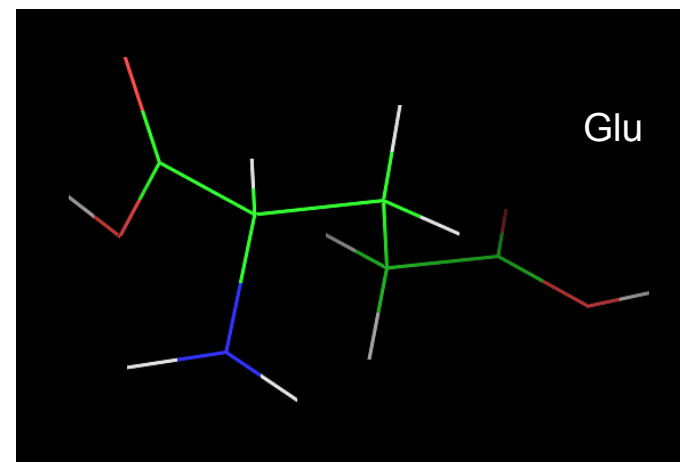
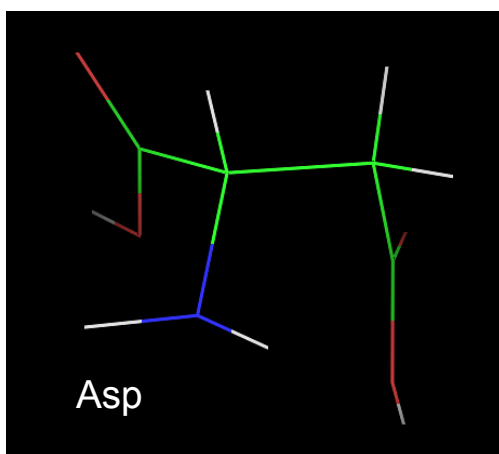
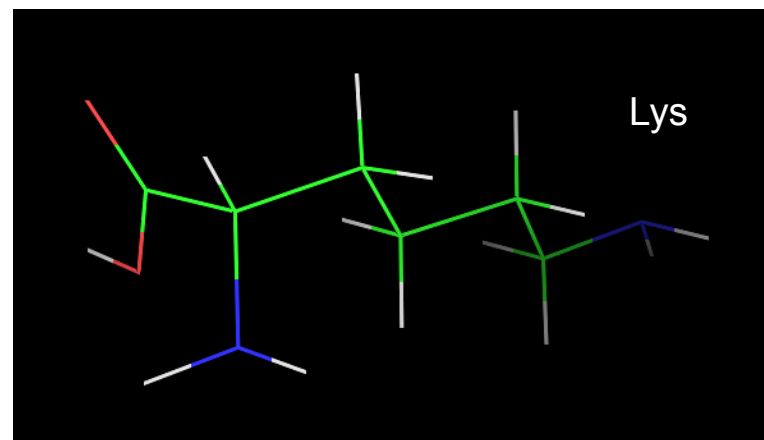
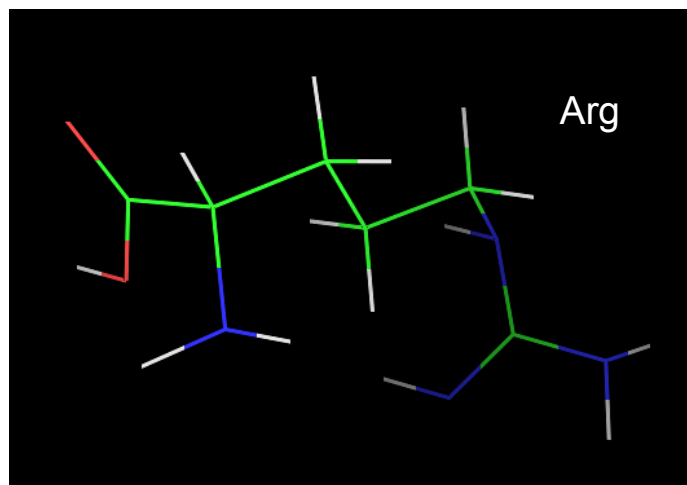
Tryptophan:

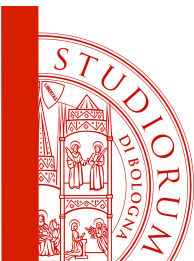
Molecular Mass equal to $204.24 \text{ g Mol}^{-1}$



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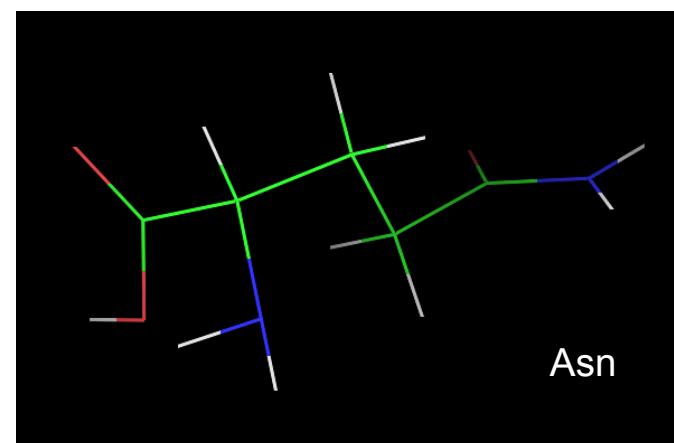
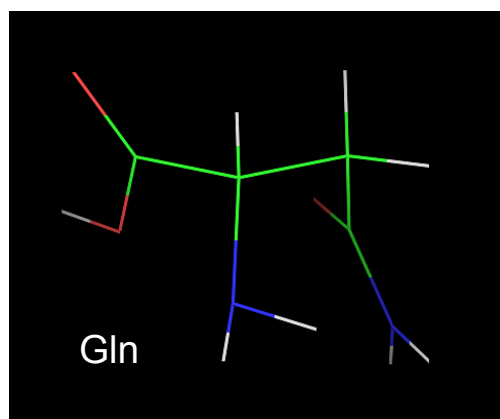
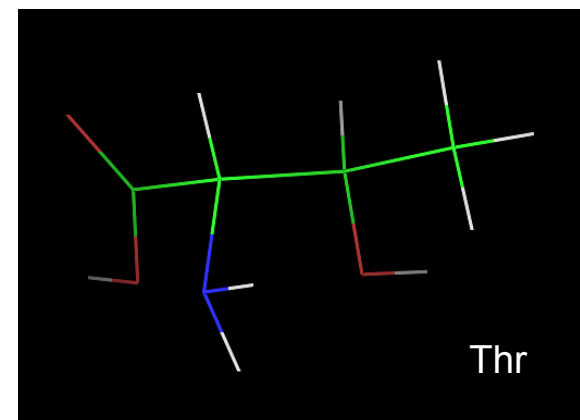
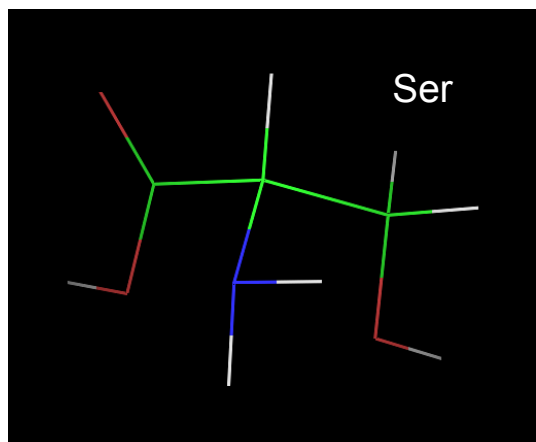
Charged Amino Acids





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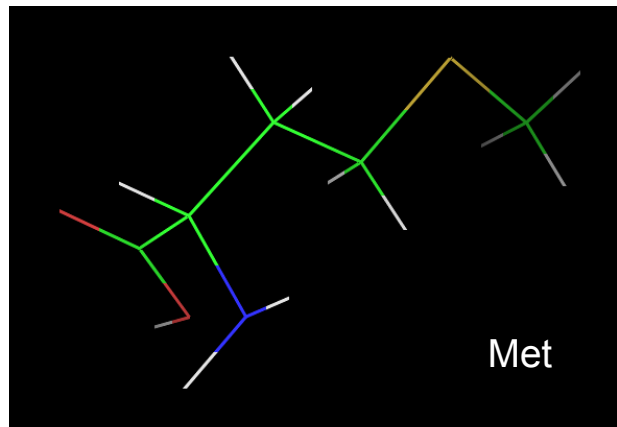
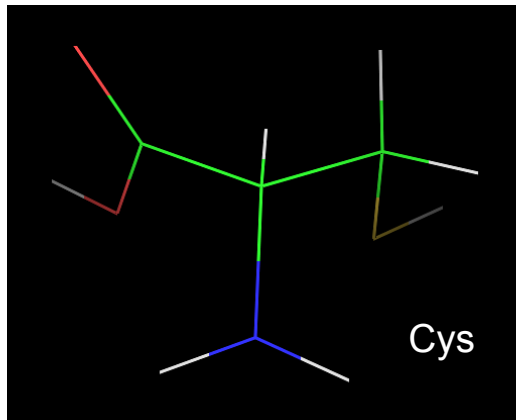
Polar Amino Acids



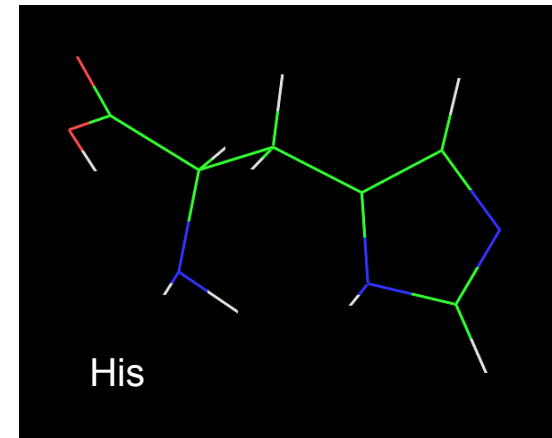


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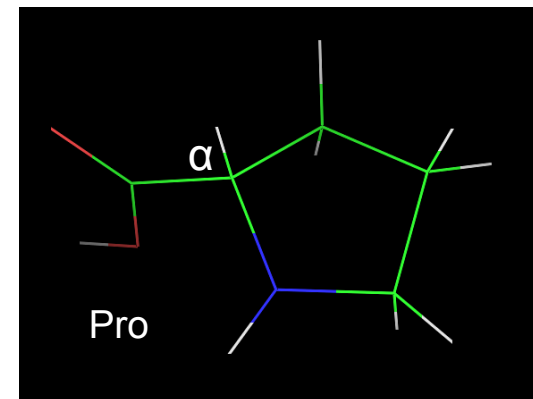
Sulfur-containing Amino Acids



Histidine: acid-base catalysis

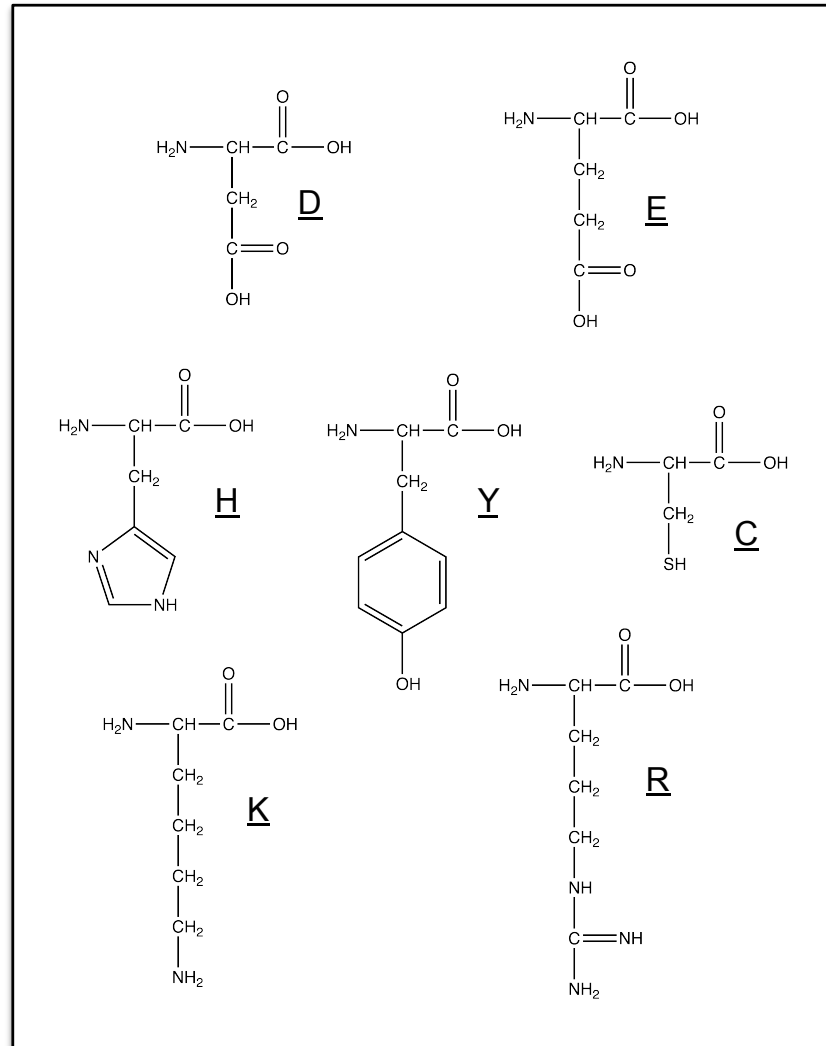


Proline: peculiar α carbon





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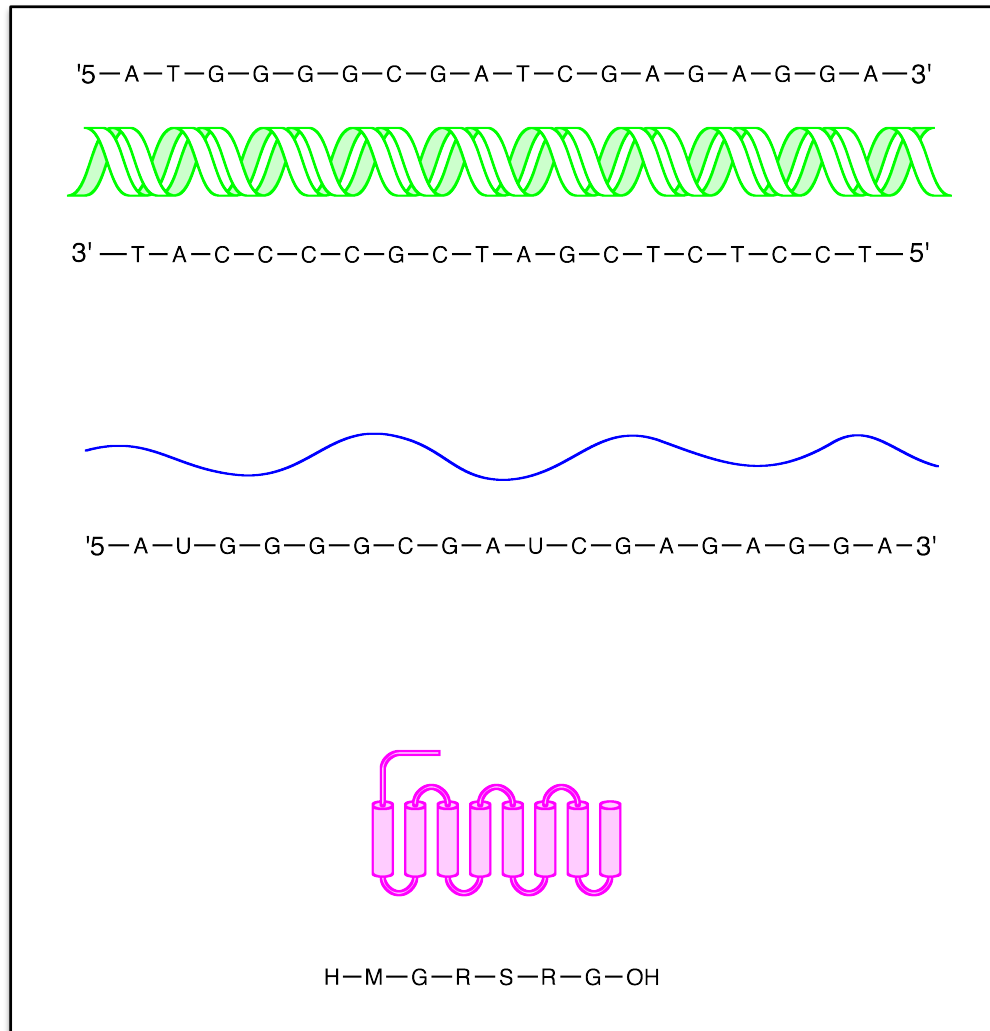
Amino Acid	pKa
Aspartate (D)	3.90
Glutamate (E)	4.07
Histidine (H)	6.04
Tyrosine (Y)	10.13
Cysteine (C)	10.46
Lysine (K)	10.79
Arginine (R)	12.48

Only Histidine features a pKa near physiological pH.

Cysteine is engaged in disulfide bridges.



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One strand of DNA is transcribed
(5' to 3' direction)



Messenger RNA (mRNA)

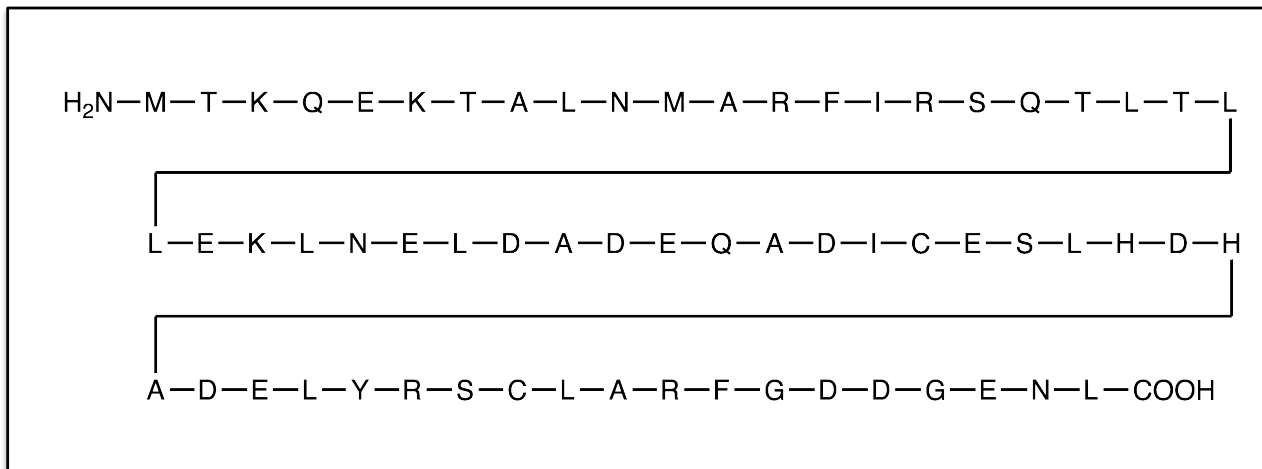


mRNA is translated into protein
(5' to 3' direction)
Protein synthesis from N- to C-ter



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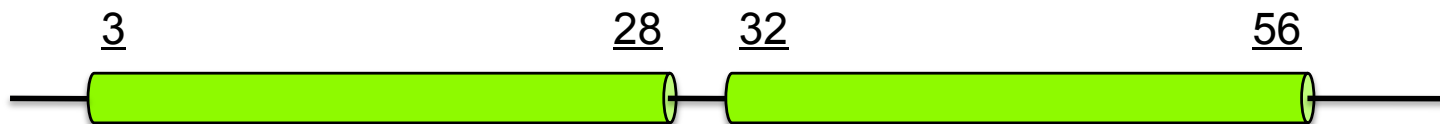
Escherichia coli Rop protein: 63 amino acids



The sequence of amino acids (N- to C-ter, left to right) is denoted as “primary structure”. Primary structures can be compared: sequences of proteins are aligned and identity or homology are revealed

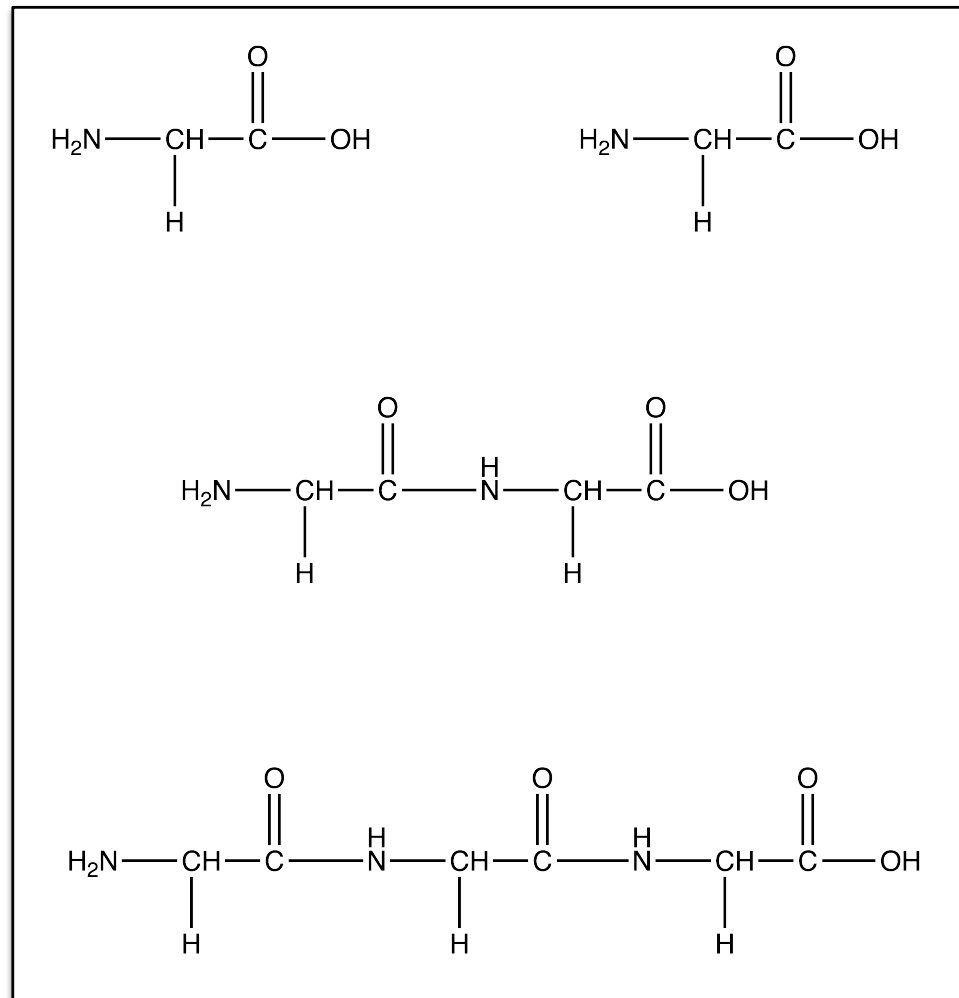
Secondary structure of Rop protein:

two secondary structural elements (alpha helices, H) are present (H1 3 to 28, H2 32 to 56)





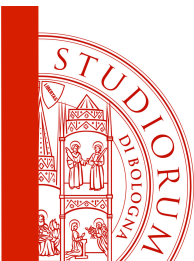
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A dehydration reaction leads to the formation of peptide bond: a carboxylate and an amino group are linked into an amide.

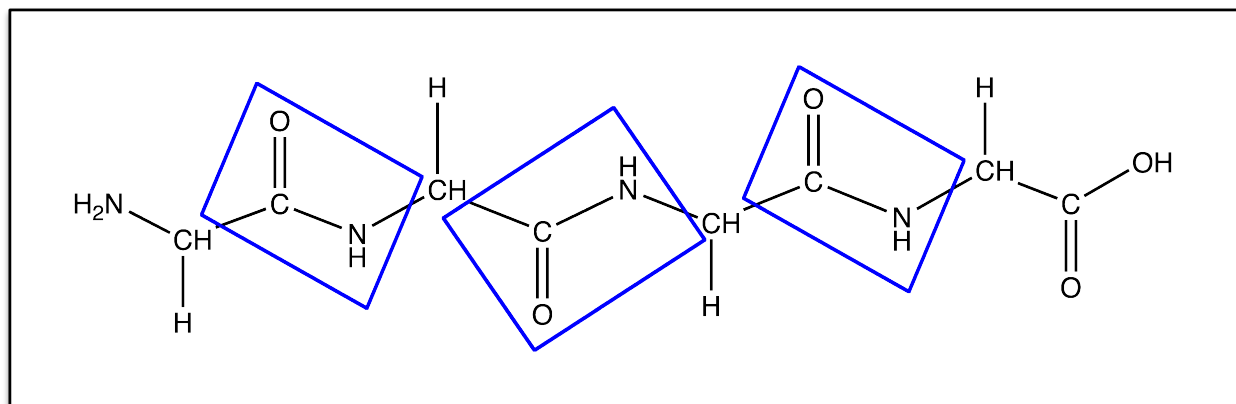
One acidic function (carboxylate) and one basic function (amino) are lost upon peptide bond formation. The remaining amino and carboxy function are denominated: N- and C-terminus, respectively.

By convention the sequence of a peptide (or protein) is written from left to right in the N-ter to C-ter direction.



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Alpha carbon features sp_3 hybridization. Carbon C' is sp_2 -hybridized.



Amino nitrogen is conjugated with C' carbon.

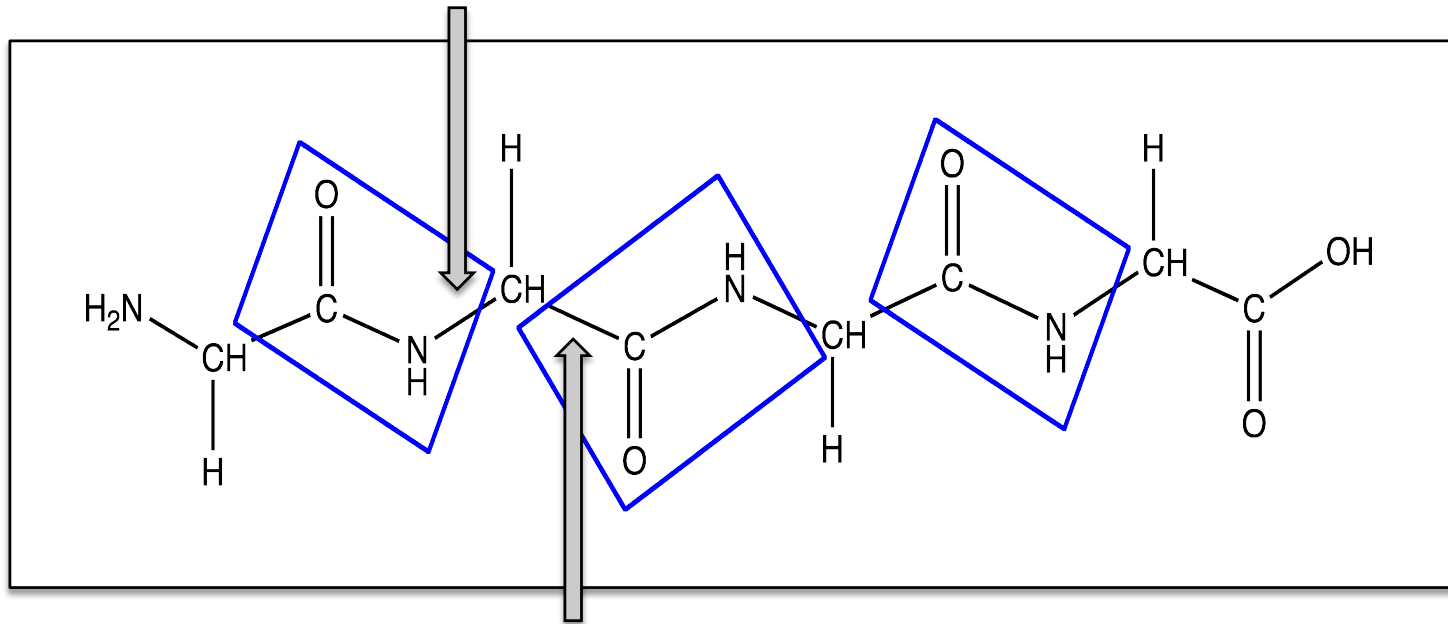
Peptide unit: alpha carbon i , C' carbon i , amino nitrogen $i+1$, alpha carbon $i+1$

Due to delocalization of nitrogen doublet, the peptide unit is planar.
Rotation around alpha carbon is responsible of protein conformation



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Rotation of alphaC-amideN: phi angle



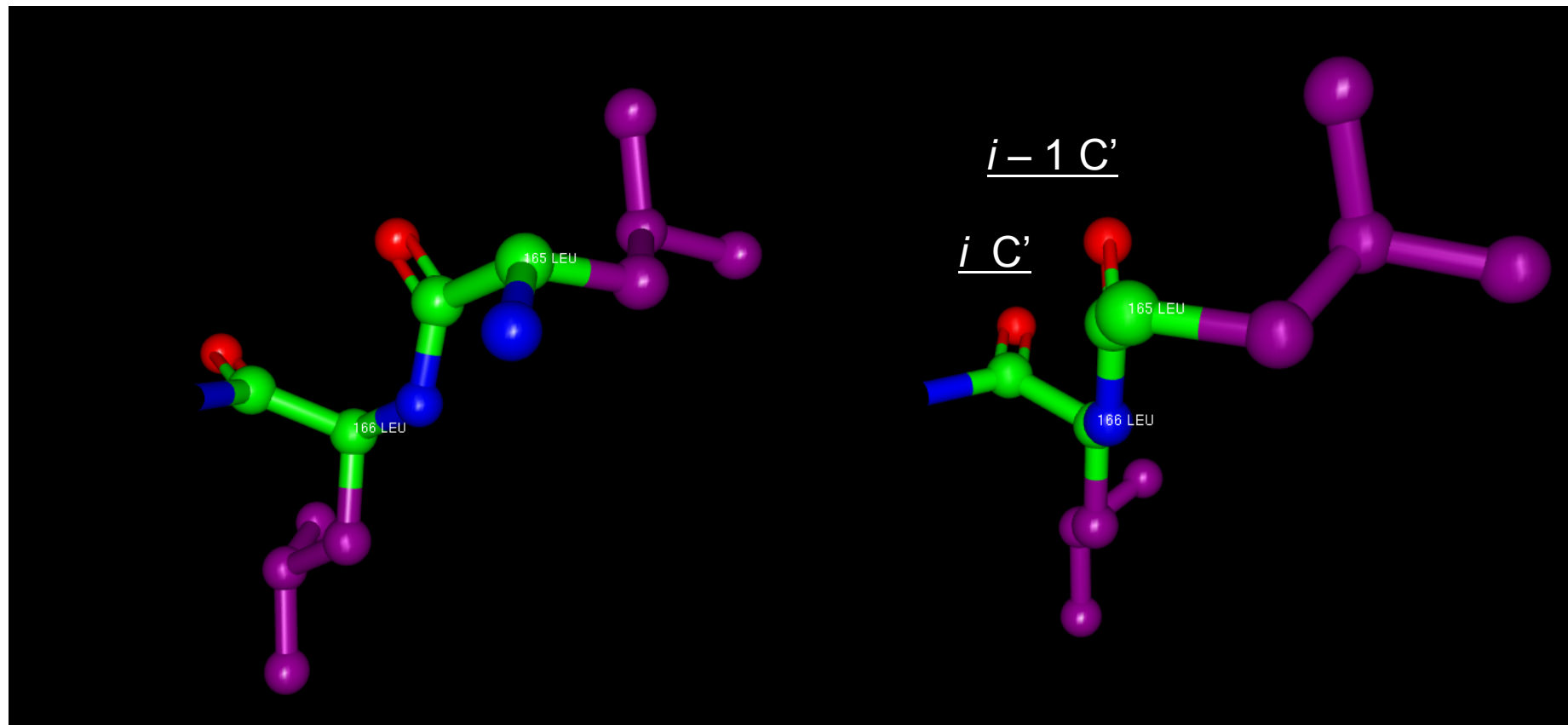
Rotation of alphaC-C'carbon: psi angle

How are phi and psi angles defined?



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Looking along the amideN-alphaC axis (perpendicular):

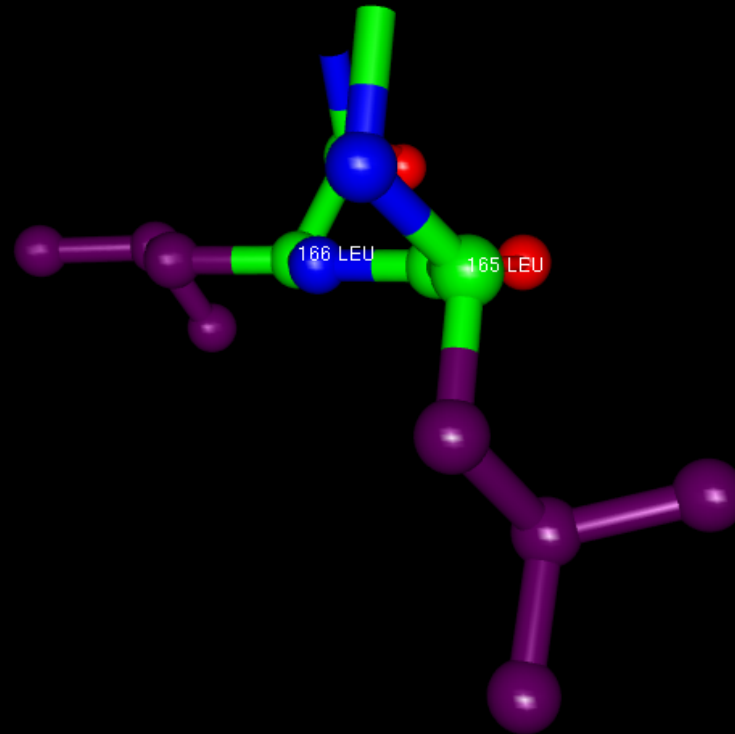


The i C' lies to the left of $i-1$ C': phi angle is negative



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Looking along the alphaC-C' axis:

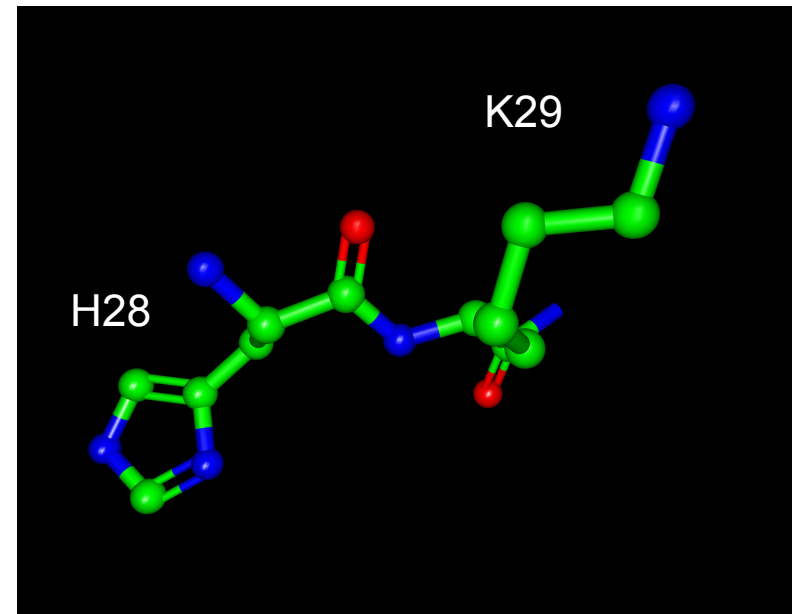
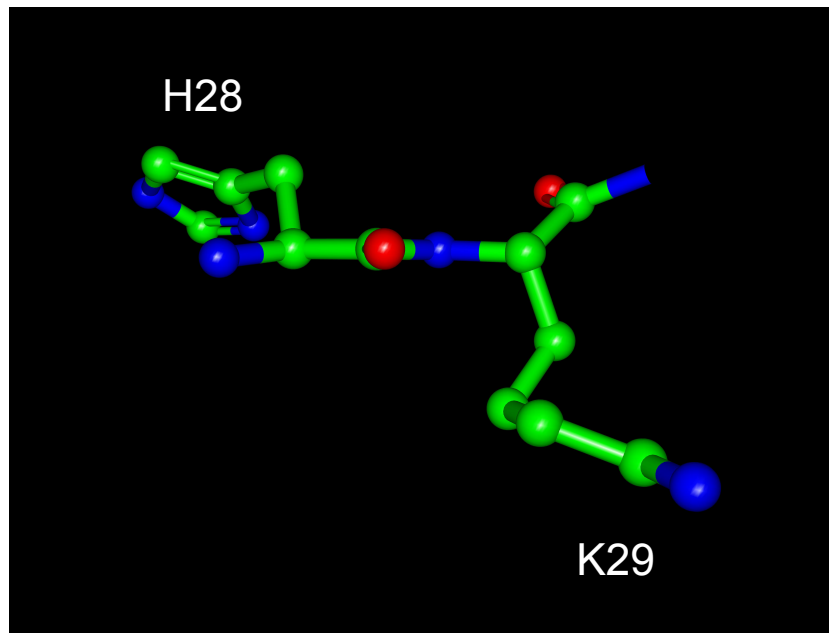


The $i + 1$ N lies to the left of i N: psi angle is negative



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The peptide unit in proteins is usually in trans conformation



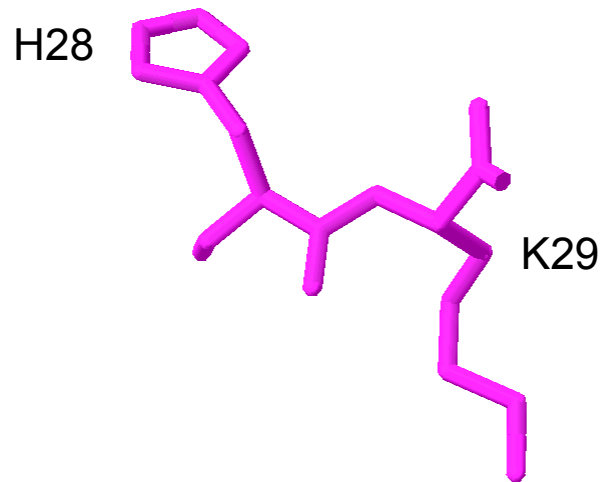
H28 enters to the peptide unit from the back, K29 exits to the front. Steric clash between R groups is avoided in the trans conformation.



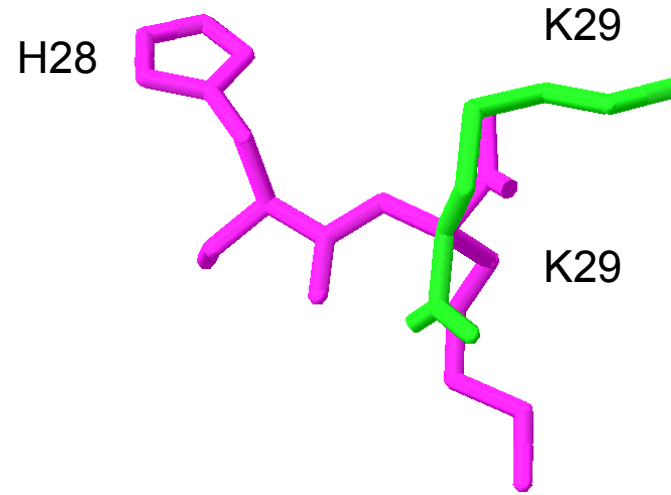
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Native conformation (purple)

Altered conformation (green)



ϕ angle: 7.7

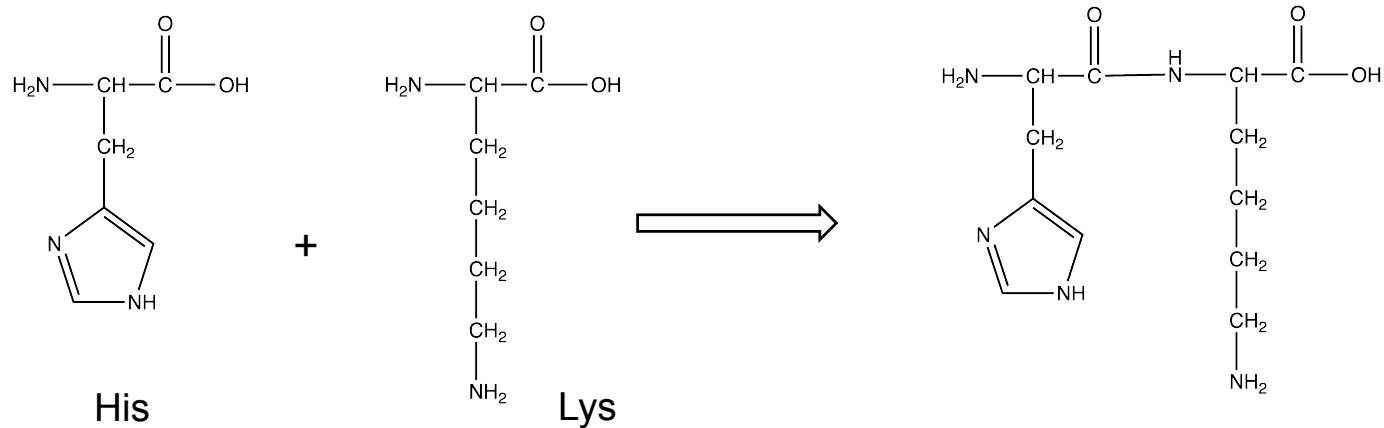


ϕ angle: -141.8

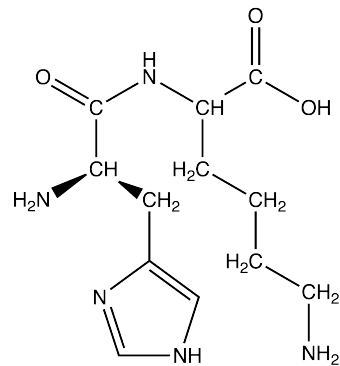
Native conformaion is in trans, altered conformation is in cis



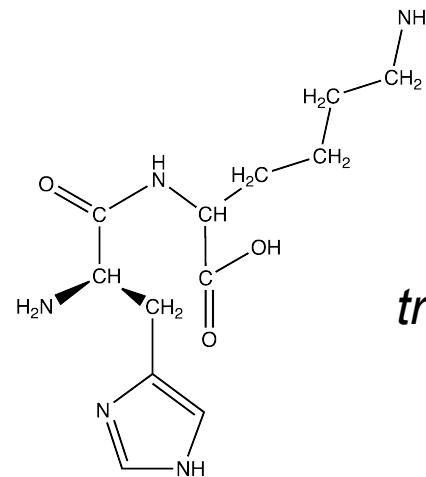
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cis



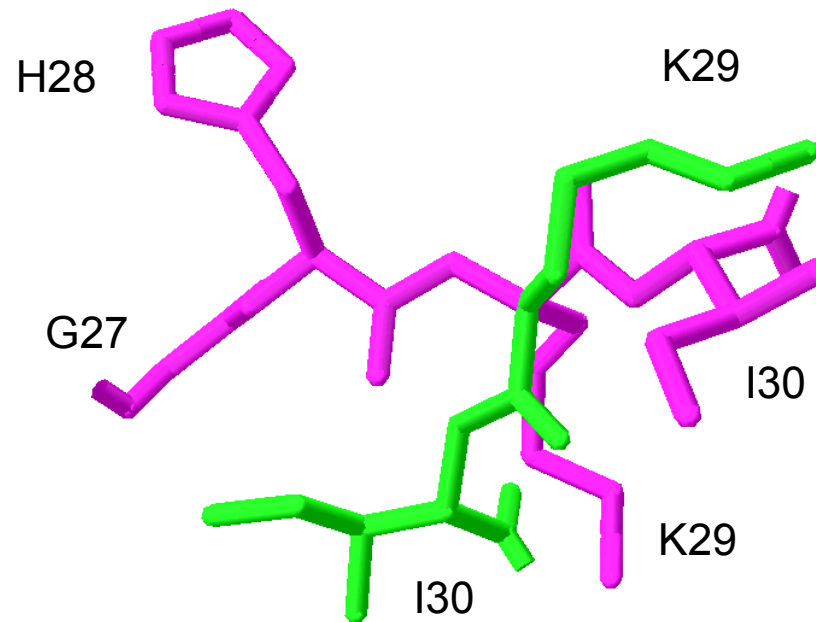
trans

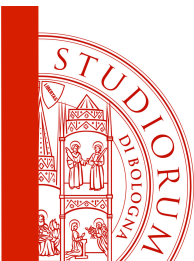




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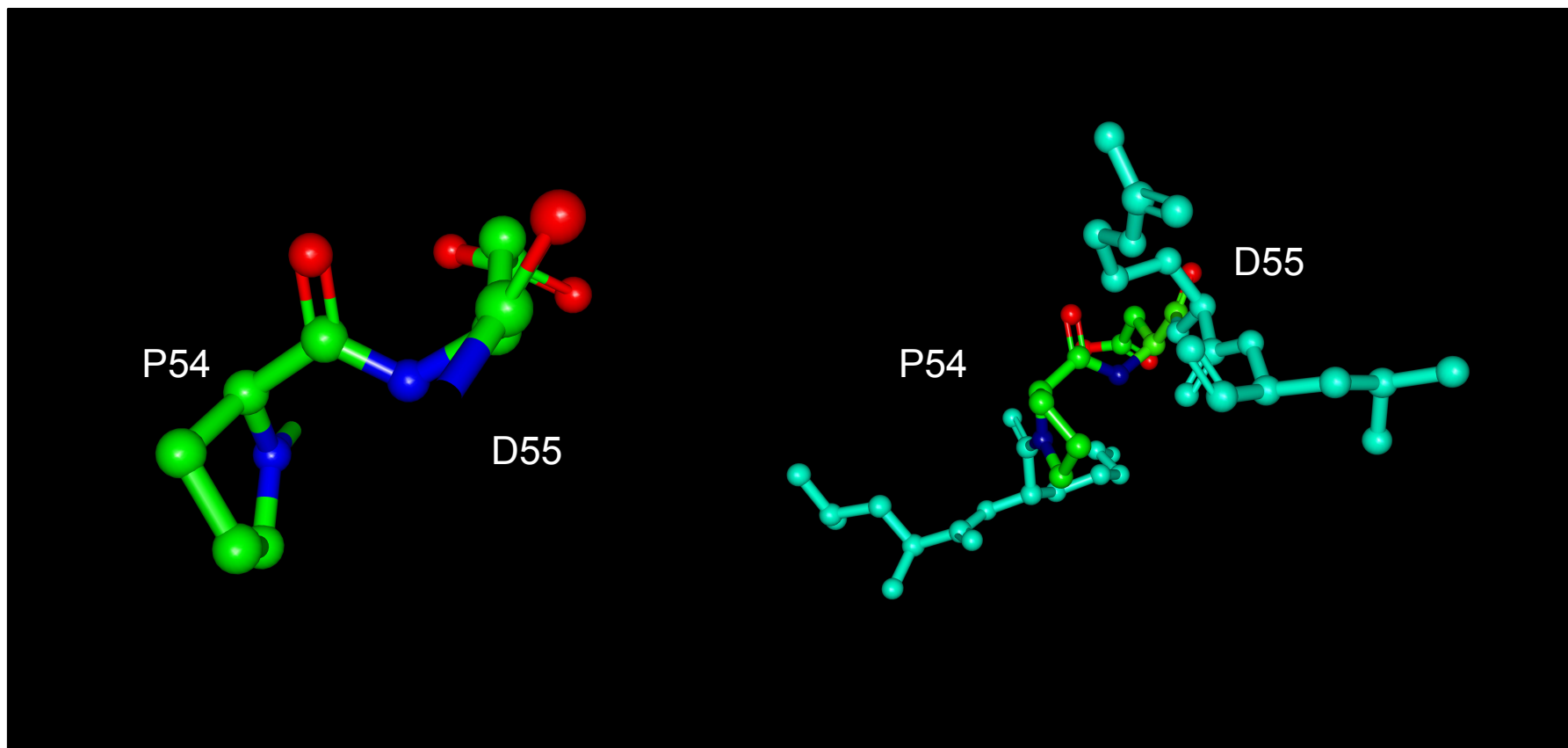
Neighbour amino acids (G27 and I 30). Trans or cis conformation?

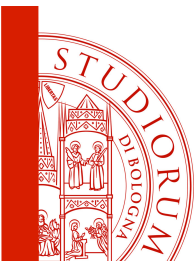




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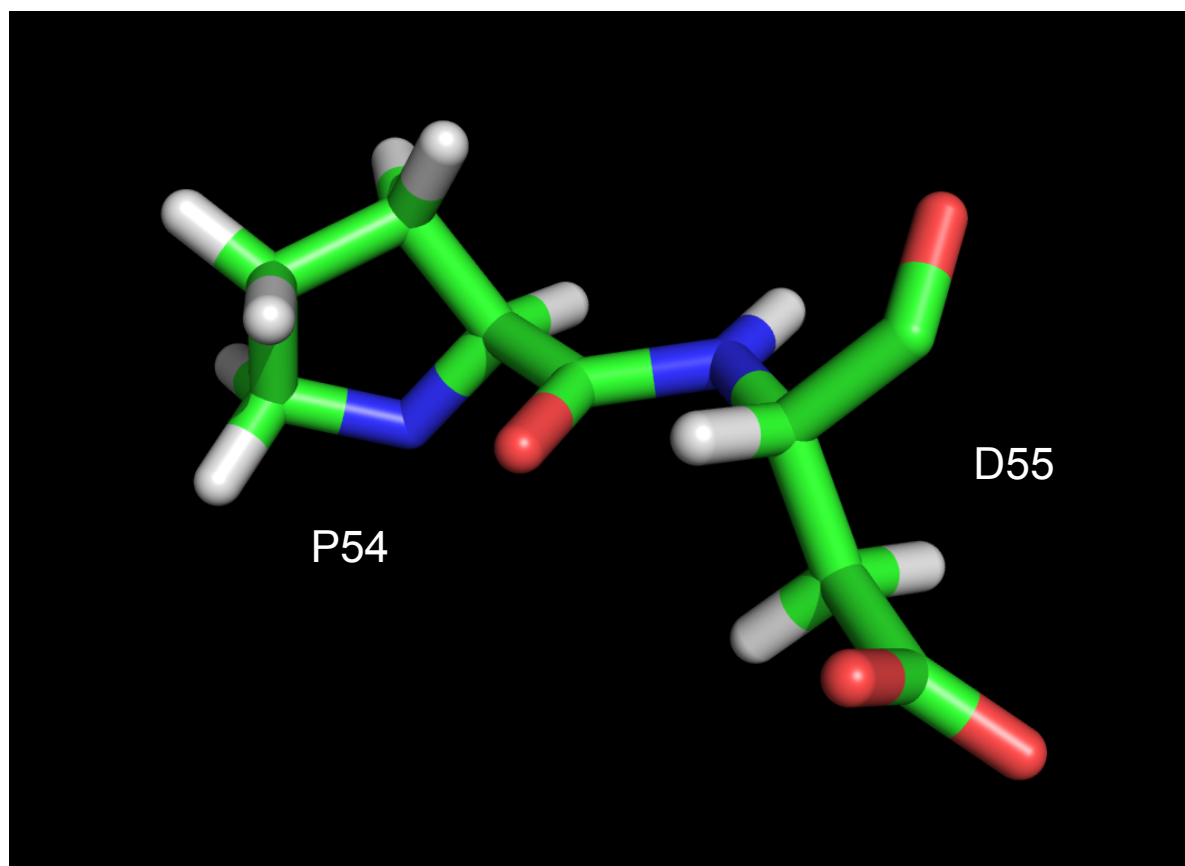
The Pro-X unit features trans or cis configuration. Trans-cis interconversion?





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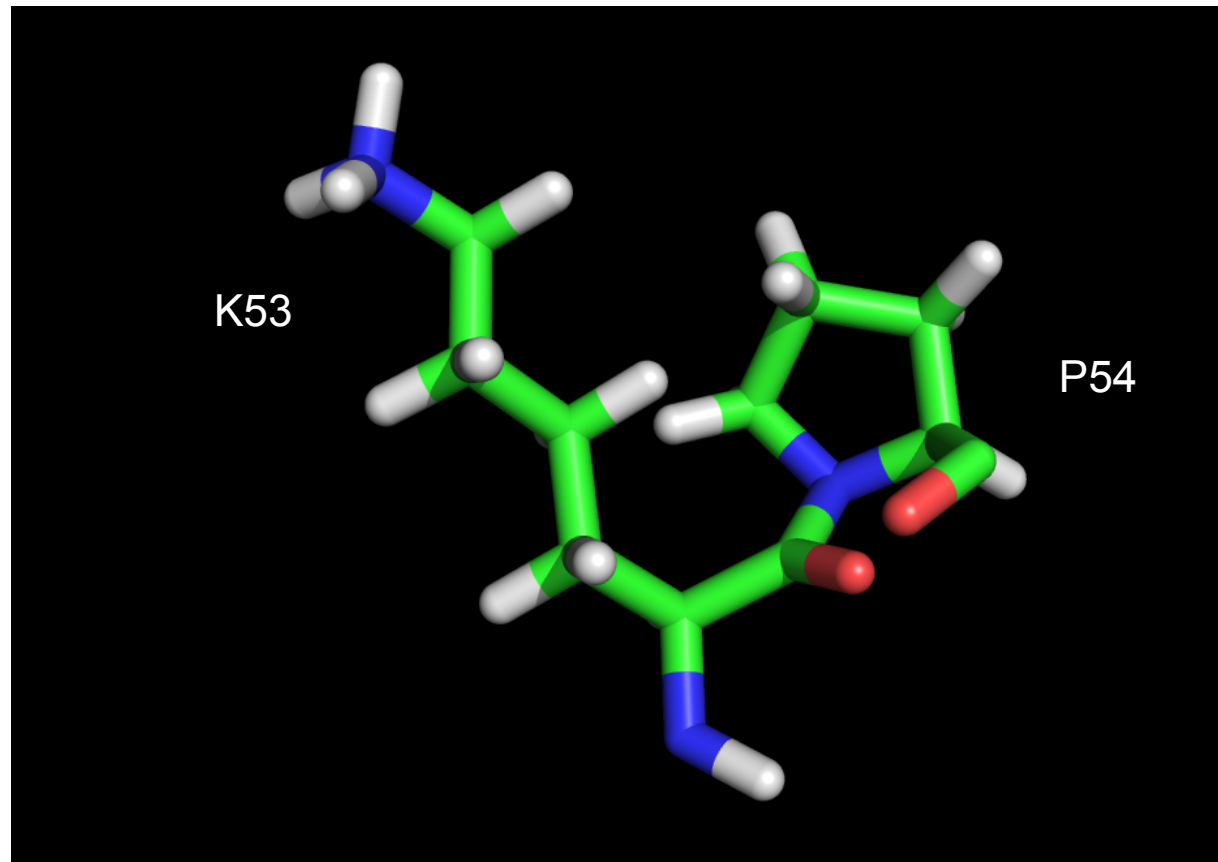
The Pro-X unit features trans or cis configuration. Trans-cis interconversion?

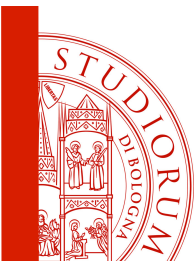




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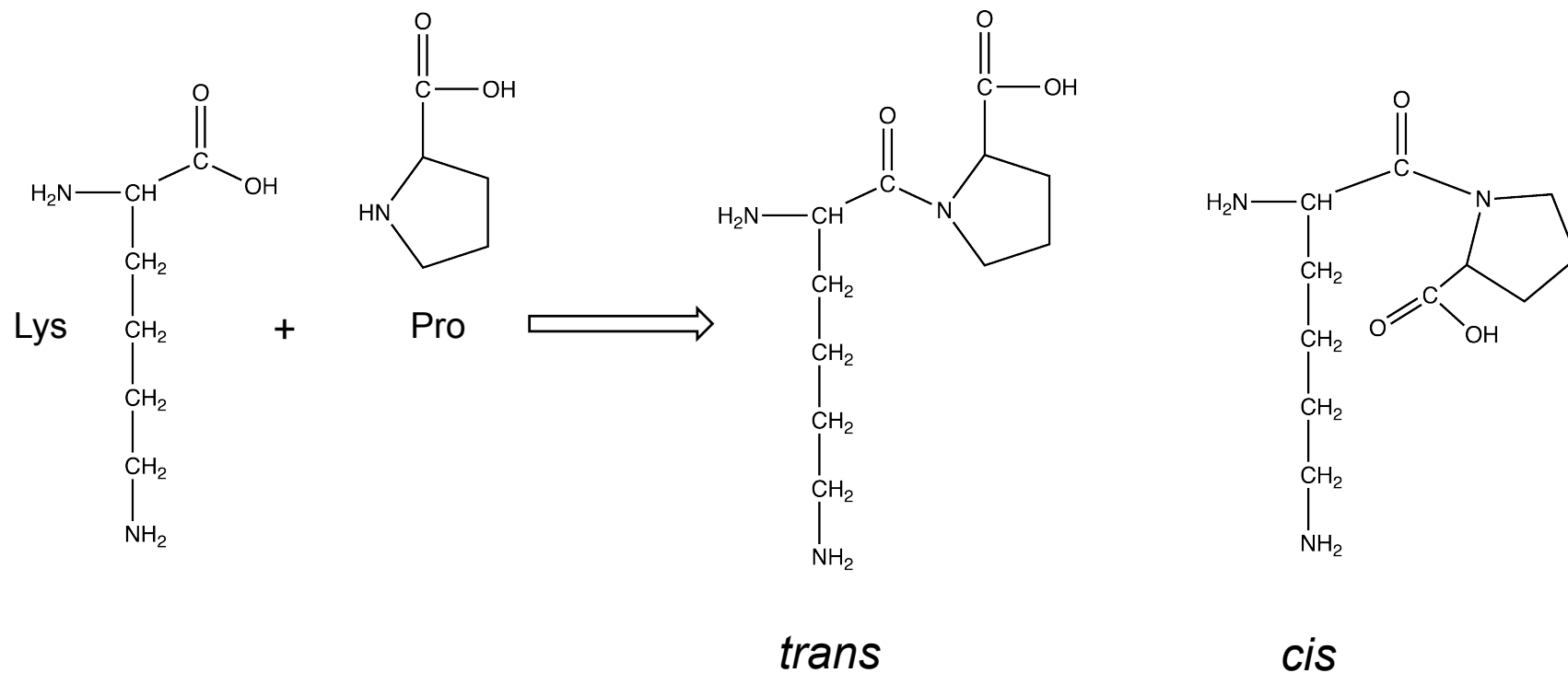
The X-Pro unit features trans or cis configuration. Trans-cis interconversion?





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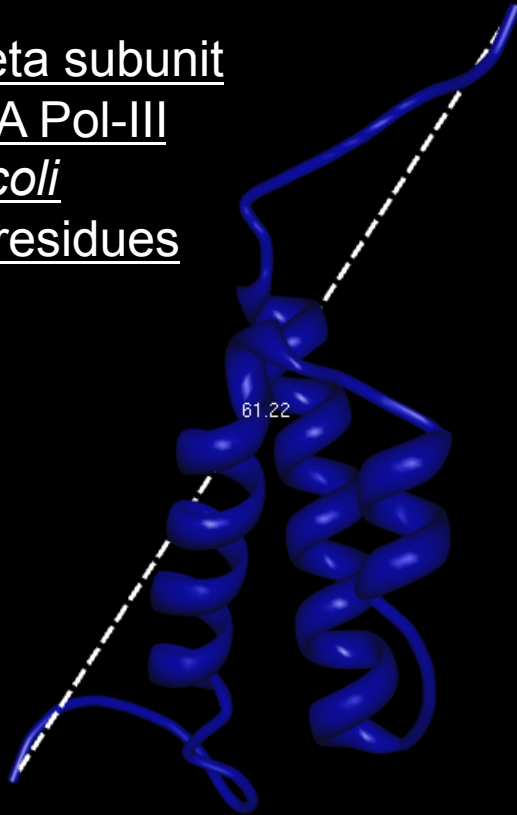
Cleavage of the peptide bond for *cis-trans* isomerization of Lys-Pro





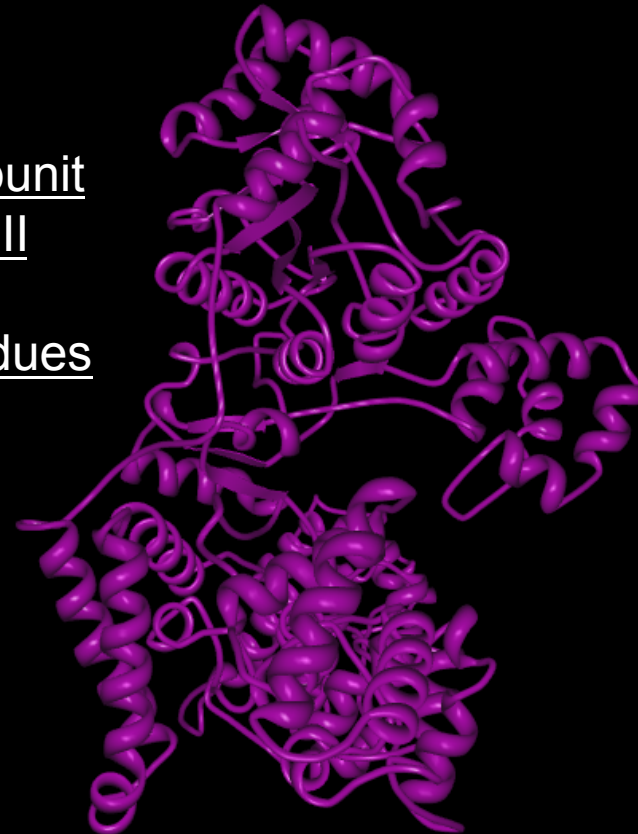
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Theta subunit
DNA Pol-III
E. coli
76 residues



61.22 Angstroms
1 Å = 0.1 nm

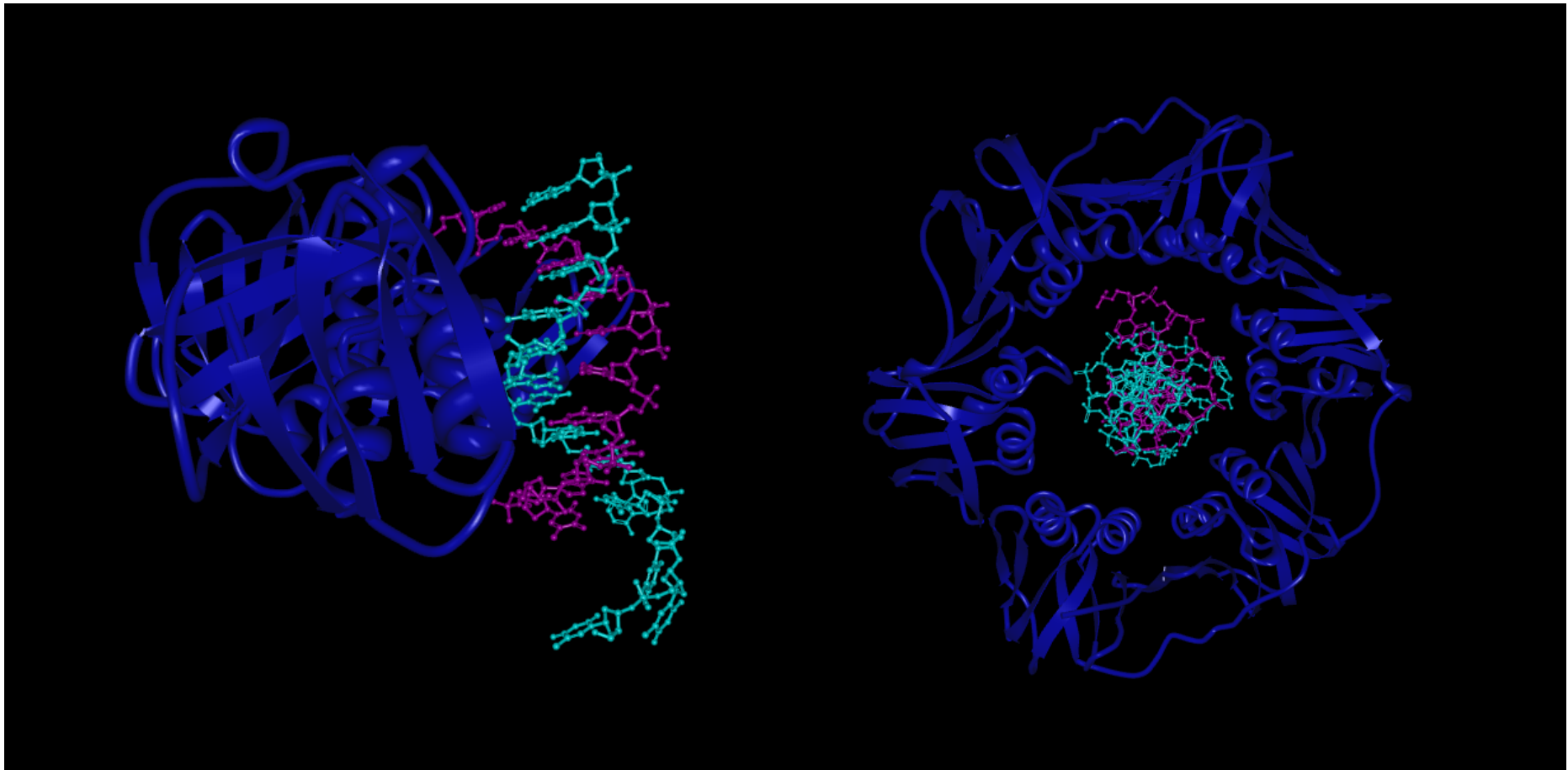
Alpha subunit
DNA Pol-III
E. coli
1160 residues





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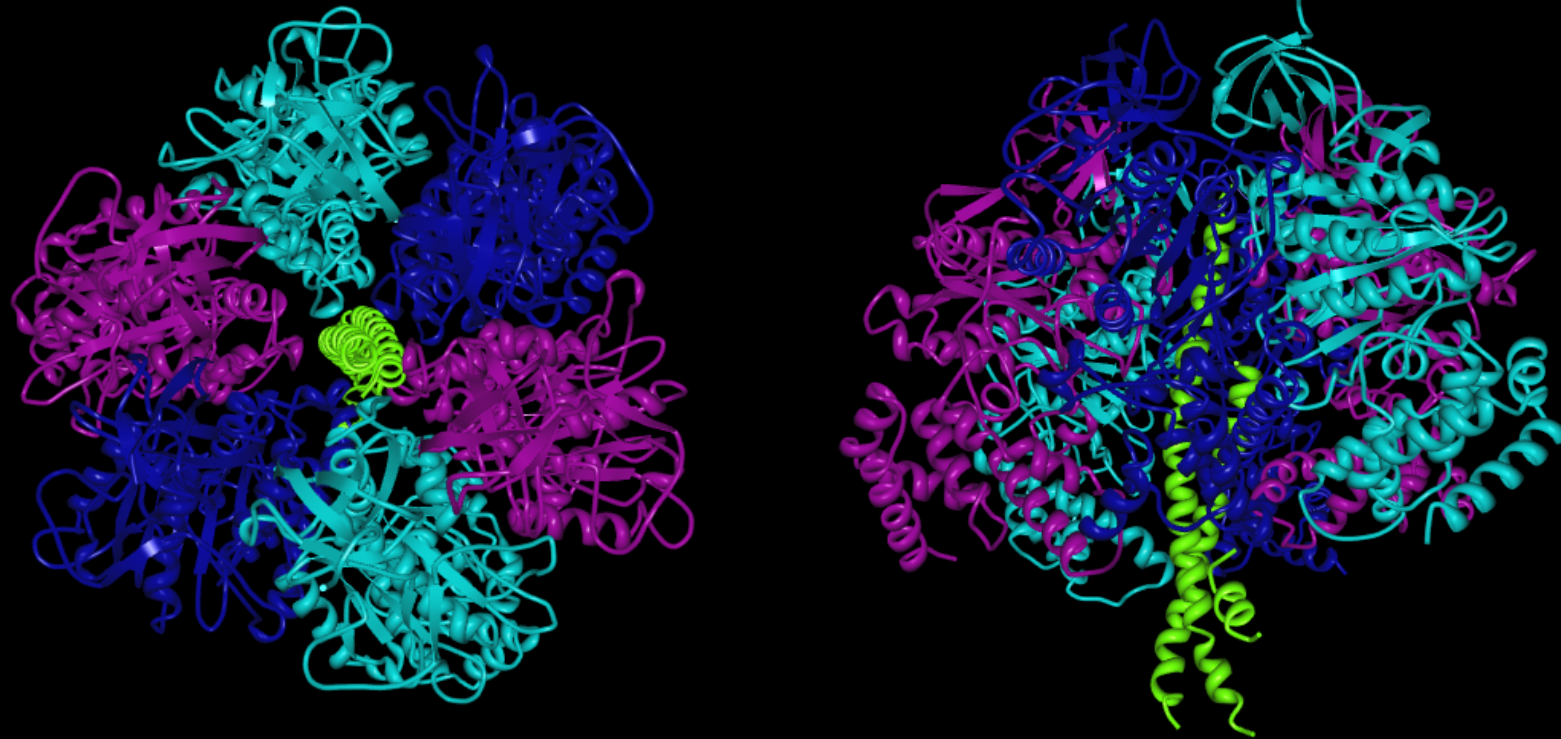
Beta clamp of DNA Pol-III *E. coli*: 366 amino acids. Homodimer.





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F₀-F₁ ATPase: complex enzyme, membrane-associated (F₀).





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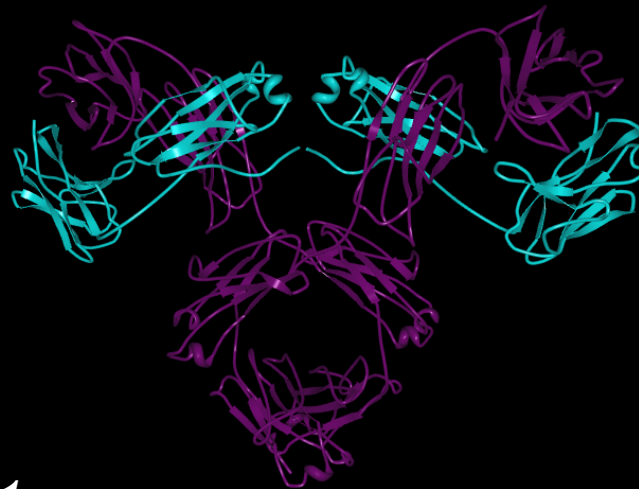


Tubulin
Structural protein

Trypsin



An enzyme



IgG1
Binds an antigen