

Peptides And Proteins

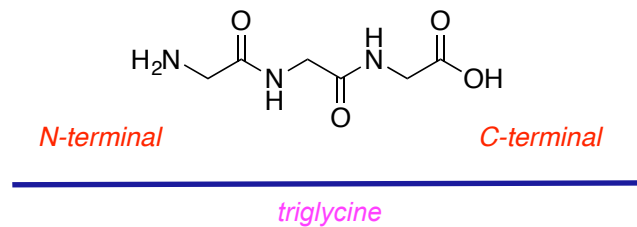
from chapter(s) _____ in the recommended text

A. Introduction

B. Nomenclature And Conventions

by *amide* bonds.

on the *left*,
right.



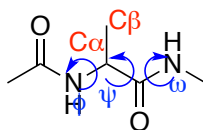
amine,
acid.

ammonium and a C-terminal *carboxylate*.

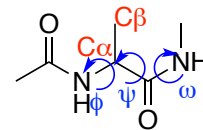
trans (based on the *peptide polyamide backbone alkenes*).

local conformations

like ϕ (the $N-C\alpha$ dihedral) ψ ($C\alpha-CO$), and ω ($CO-NH$)
 ω because of amide



trans



cis

C. Primary Structures

sequence of amino

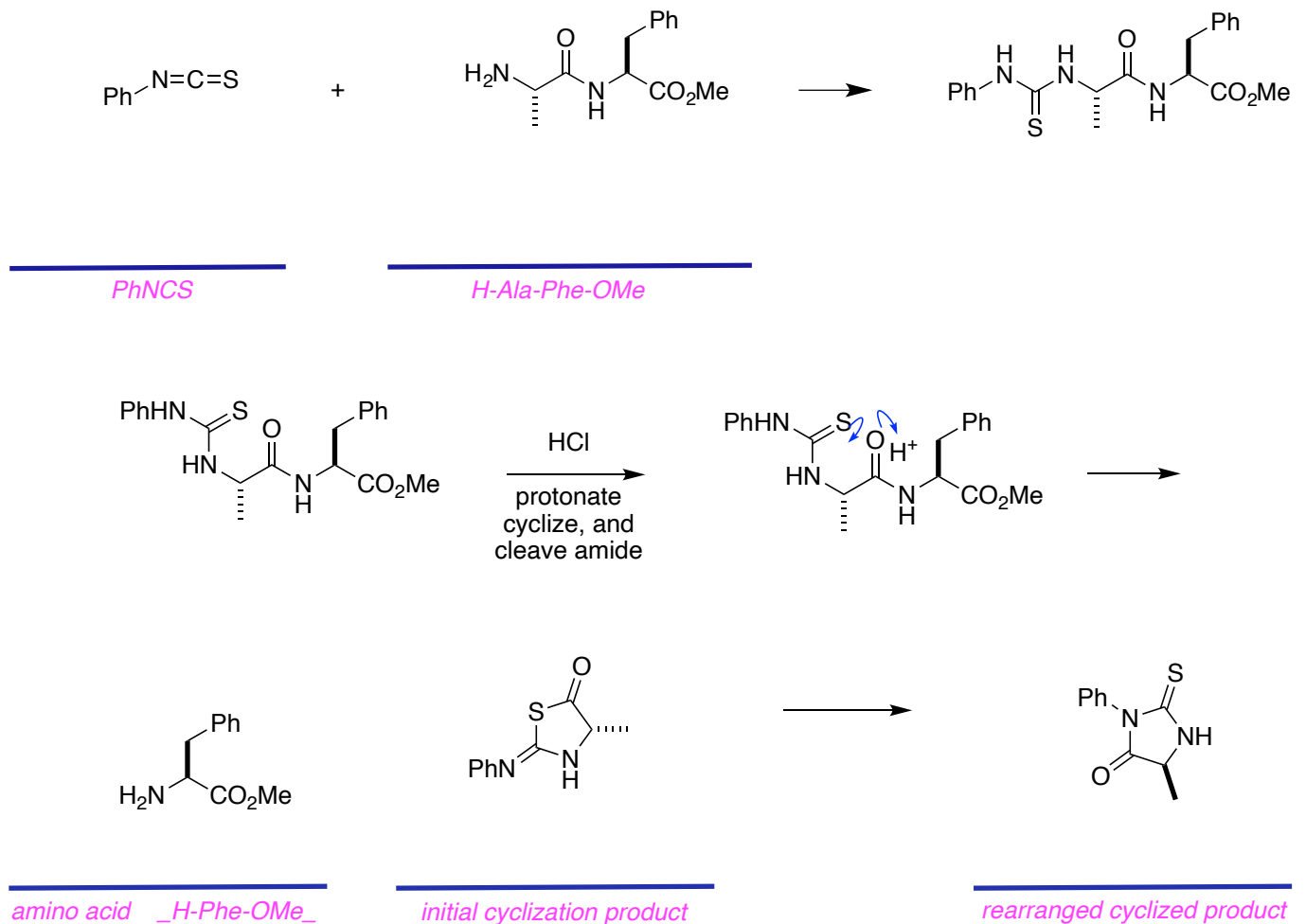
sequence of

similarity

fold into similar shapes.

Elucidation Of Primary Peptide Structure Via The Edman Degradation

primary structure

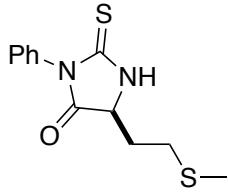


Chromatographic analysis

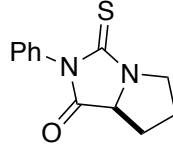
does require

It *is* possible.

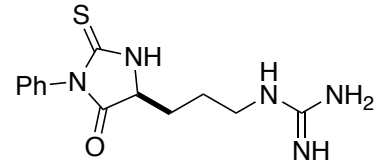
It *is not*



first thiohydantoin



second thiohydantoin



third thiohydantoin

Elucidation Of Primary Structure Via *Enzymatic* Cleavage And Mass Spectroscopy

mass spectrometry

so *proteases*

at predictable sites

within of a chain.

Positions of cleavage *vary*

fragment 1: H-Pro-Ala-Pro-Gly-Arg-Trp-OH

fragment 2: H-Ala-His-Gln-Met-Val-Lys-His-Lys-Ala-Trp-OH

fragment 3: H-Pro-Ser-Tyr-OH

fragment 4: H-Thr-Ala-OH

Chymotrypsin

fragment 1: H-Pro-Ala-Pro-Gly-Arg-Trp-OH

fragment 2: H-Ala-His-Gln-Met-Val-Lys-His-Lys-Pro-Trp-OH

fragment 3: H-Pro-Ser-Tyr-OH

fragment 4: H-Thr-Ala-OH

Elastase

fragment 1: H-Pro-Ala-OH

fragment 2: H-Pro-Gly-OH

fragment 3: H-Arg-Trp-Ala-OH

fragment 4: H-His-Gln-Met-Val-Lys-His-Lys-Pro-Trp-Pro-Ser-Tyr-Thr-Ala-OH

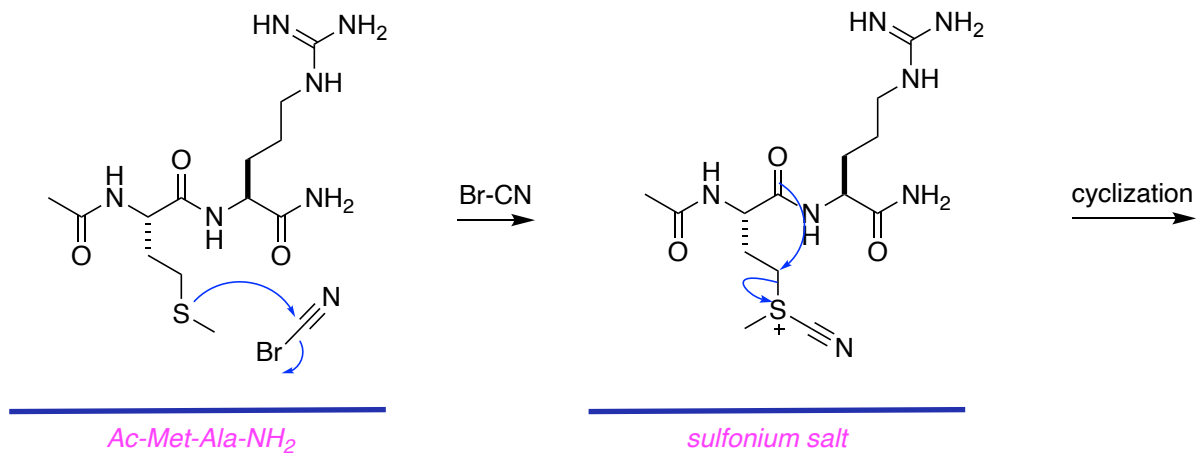
Elucidation Of Primary Structure Via Cyanogen Bromide Cleavage And Mass Spectroscopy

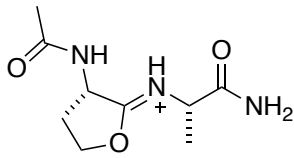
methionine

methionine

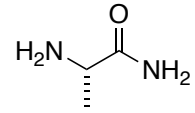
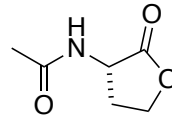
C_γ atom

iminolactone produced





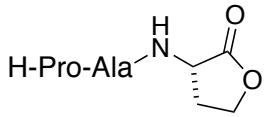
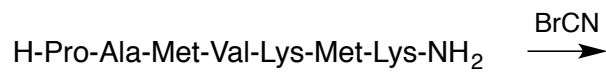
hydrolysis
→



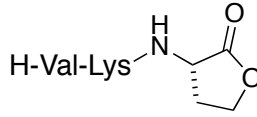
iminolactone

lactone

Ala-NH₂

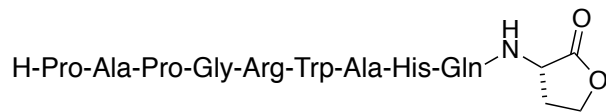
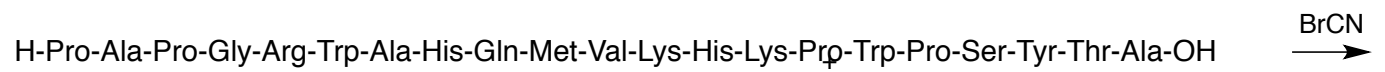


+



+

H-Lys-NH₂



+

H-Val-Lys-His-Lys-Pro-Trp-Pro-Ser-Tyr-Thr-Ala-OH

D. Secondary Structures

hydrogen bonding between residues shielding of hydrophobic residues from aqueous surroundings
 entropy gains placing hydrophilic residues at the core placing hydrophilic residues at the periphery
 ionic interactions between charged side-chains stacking of aromatic rings
 packing of one chain against another overlap of orbitals containing C=O lone pairs with other C=O π^* orbitals
 increased temperature addition of high concentrations of guanidine hydrochloride

secondary structure.

primary structures.

are called *helices*.

right handed

does not matter (right helical in both directions)

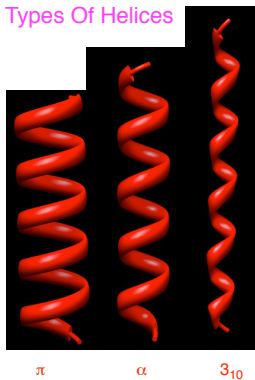
most common

3.6 amino acid

Pro is rarely

in *collagen*.

Types Of Helices



Amino acid blocks that coil into spring-like arrangements are called *helices*.

right handed corkscrew when viewed from *does not matter*.

most common, α -helices, have *3.6* amino acid residues per coil of the helix.

Pro is rarely found in α , π , or 3_{10} helices because..... found in *collagen* /.

in *the same* directions.

in *opposite* directions.

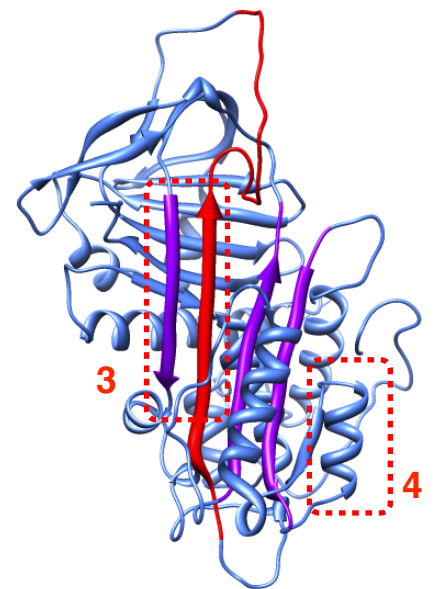
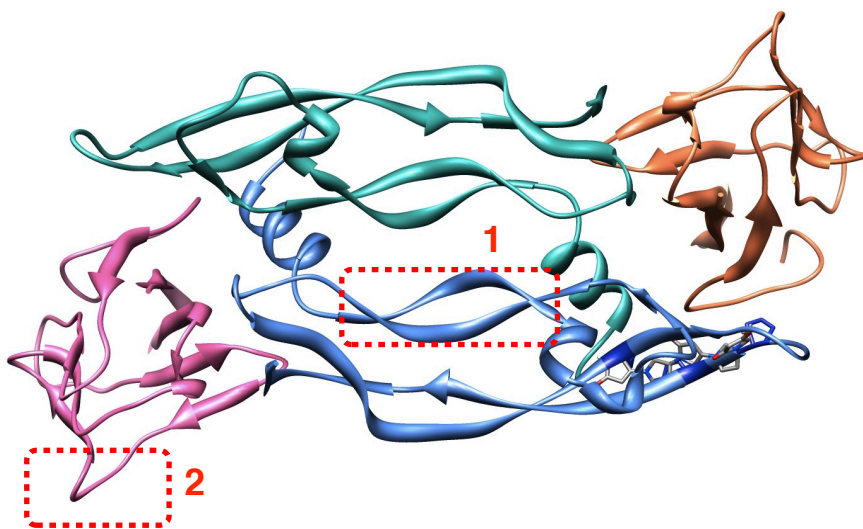
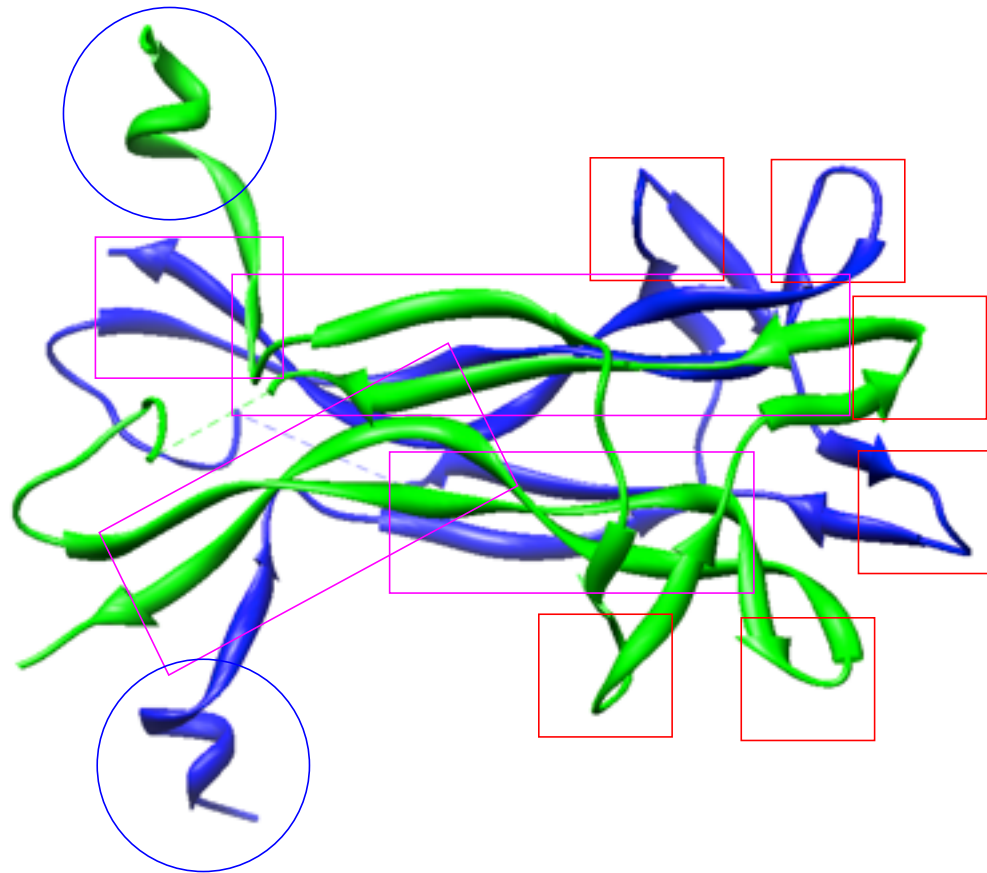
the strand loops back on itself.

β -turns, while *γ -turns*

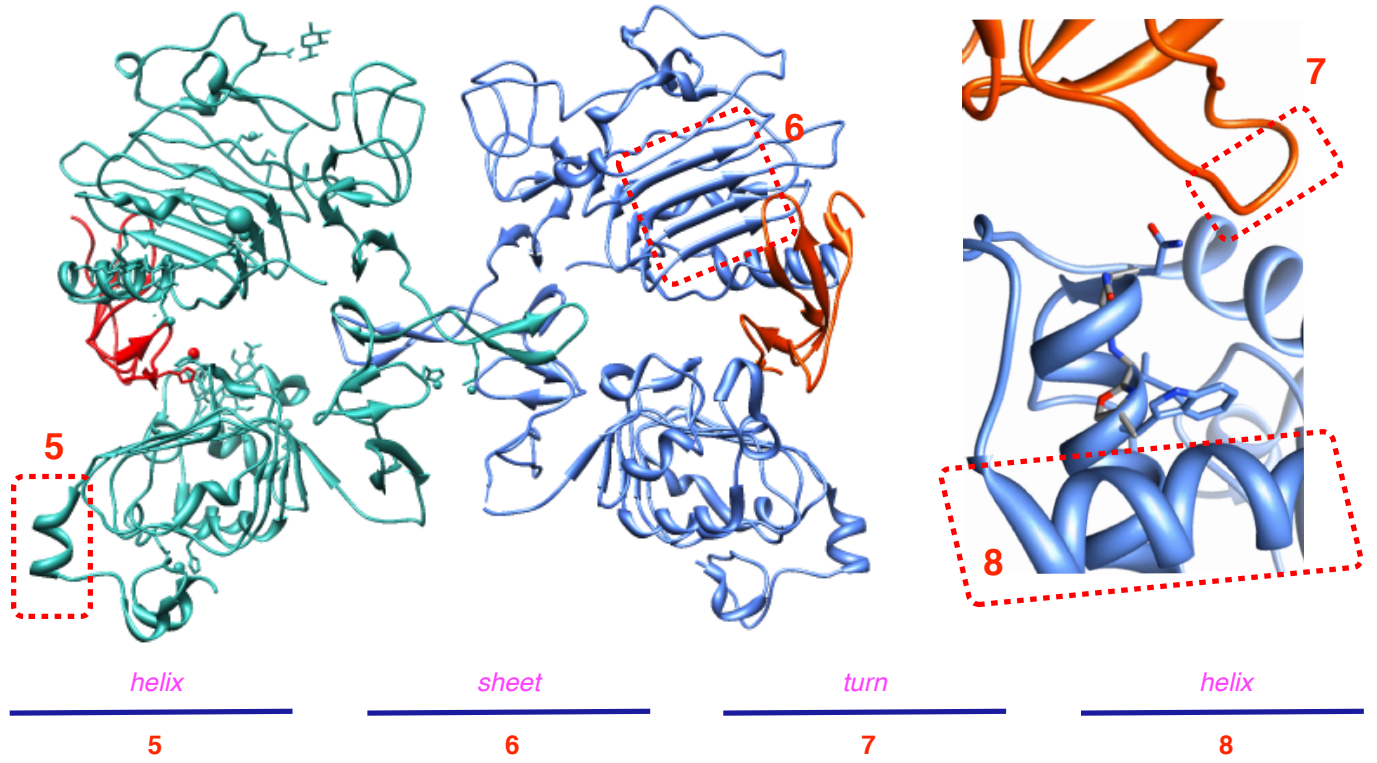
antiparallel β -sheets.

Different protein, Ha!

a *β -strand* b *sheet-turn-sheet* c *parallel β -sheet* d *antiparallel β -sheet*



sheet 1
turn 2
sheet 3
helix 4



E. Tertiary And Quaternary Structures

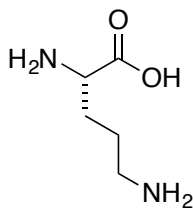
these protein units usually *are not* covalently

F. Constraints On Peptide And Protein Structures

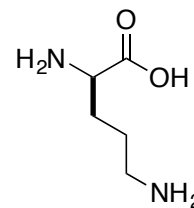
do not fold

cyclo(-Val-Orn-Leu-D-Phe-Pro-)₂

gramicidin S



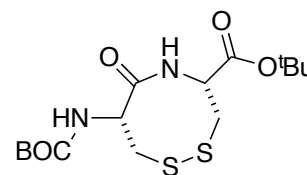
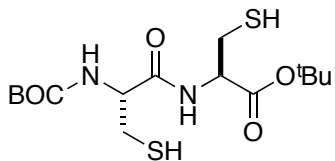
L-Orn



D-Orn

Cys residues.

oxidizing agents.



BOC-Cys-Cys-OtBu

BOC-Cys-Cys-OtBu

S—S

