Peptides And Proteins

from chapter(s) _____ in the recommended text

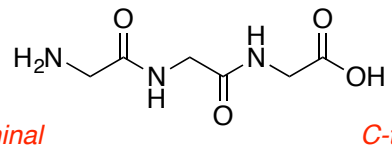
A. Introduction

B. Nomenclature And Conventions

by *amide* bonds.

on the *left*,

right.



N-terminal *C-terminal*

triglycine

amine,

acid.

ammonium and a *C*-terminal *carboxylate*.

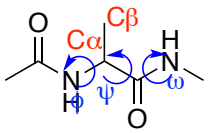
trans (based on the *peptide polyamide backbone*

alkenes.

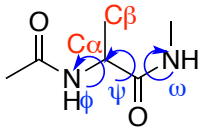
local conformations

like ϕ (the *N*-*C*α dihedral

ω because of amide



trans



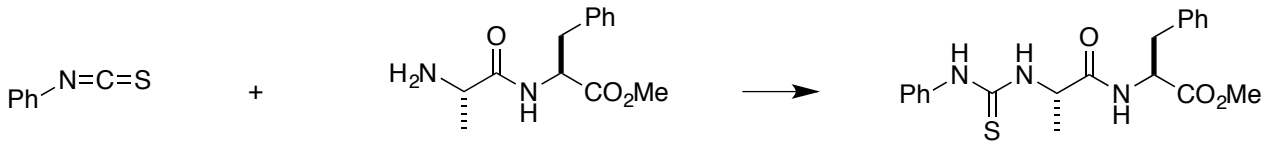
cis

C. Primary Structures

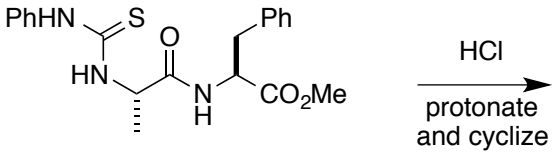
sequence of amino
sequence of
similarity
fold into similar shapes.

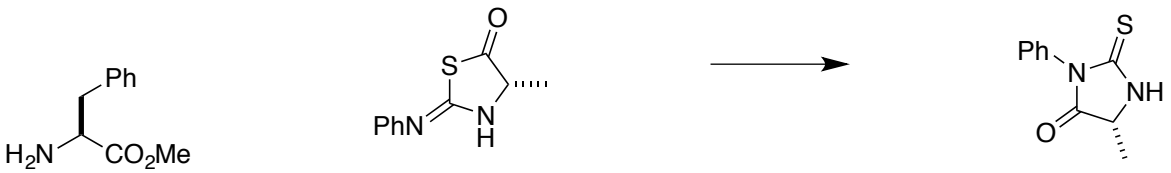
Elucidation Of Primary Peptide Structure Via The Edman Degradation

primary structure



PhNCS *H-Ala-Phe-OMe*

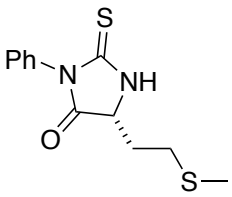




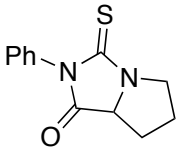
amino acid *_H-Phe-OMe_* *initial cyclization product* *rearranged cyclized product*

Chromatographic analysis
does require

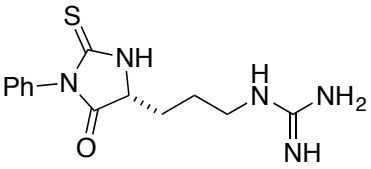
It *is* possible.
It *is not*



first thiohydantoin



second thiohydantion



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-OH

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

fragment 3: H-His-Lys-OH

fragment 4: H-Pro-Trp-Pro-Ser-Tyr-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

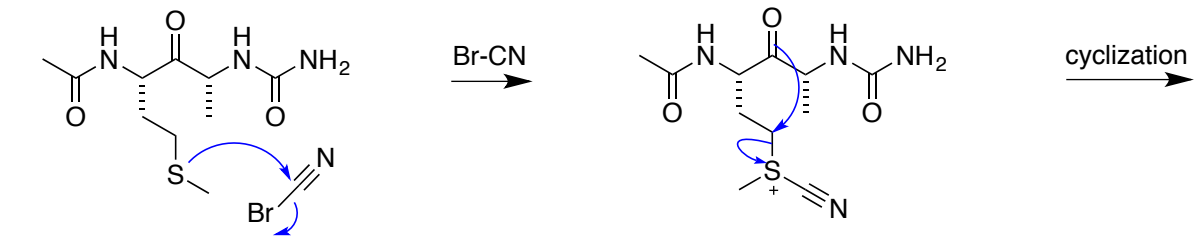
fragment 2: H-Pro-Gly-OH

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

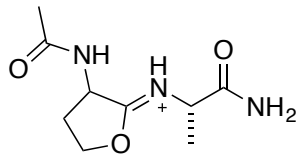
fragment 4: H-His-Gln-Met-Val-Lys-His-Lys-Pro-Trp-Pro-Ser-Tyr-Thr-Ala-OH

Elucidation Of Primary Structure Via Cyanogen Bromide Cleavage And Mass Spectroscopy

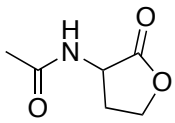
methionine
methionine
Cγ atom
iminolactone produced

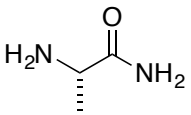


Ac-Met-Ala-NH_2 *sulfonium salt*



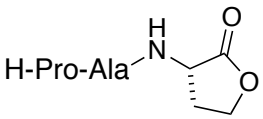
hydrolysis



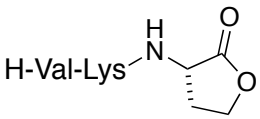


iminolactone *lactone* *Ala-NH$_2$*

H-Pro-Ala-Met-Val-Lys-Met-Lys-NH$_2$ BrCN

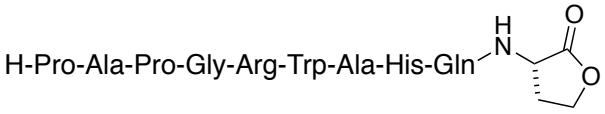


+



+ H-Lys-NH$_2$

H-Pro-Ala-Pro-Gly-Arg-Trp-Ala-His-Gln-Met-Val-Lys-His-Lys-Pro-Trp-Pro-Ser-Tyr-Thr-Ala-OH BrCN



+ 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 *CO* lone pairs with other *CO* π^* orbitals
increased temperature addition of high concentrations of guanidine hydrochloride

secondary structure.
primary structures.

are called *helices*.

right handed
the N-terminus.

most common
3.6 amino acid
Pro is rarely
in *collagen*.

in *the same* directions.

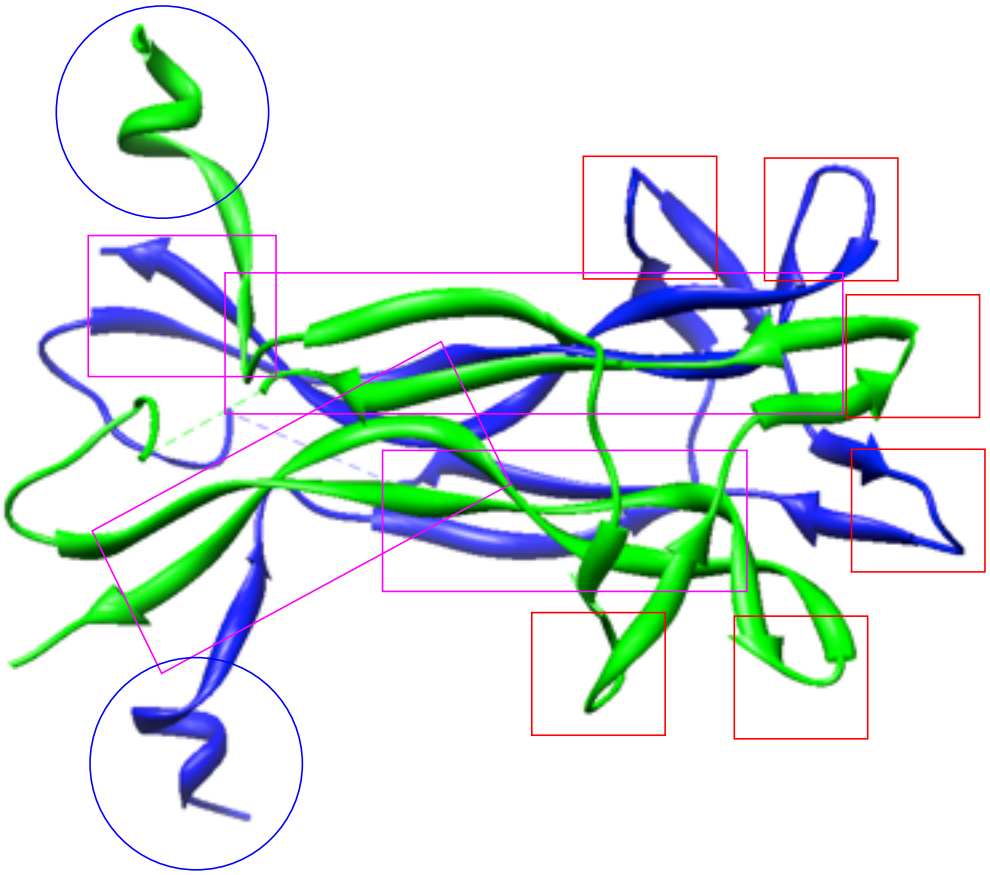
in *opposite* directions.

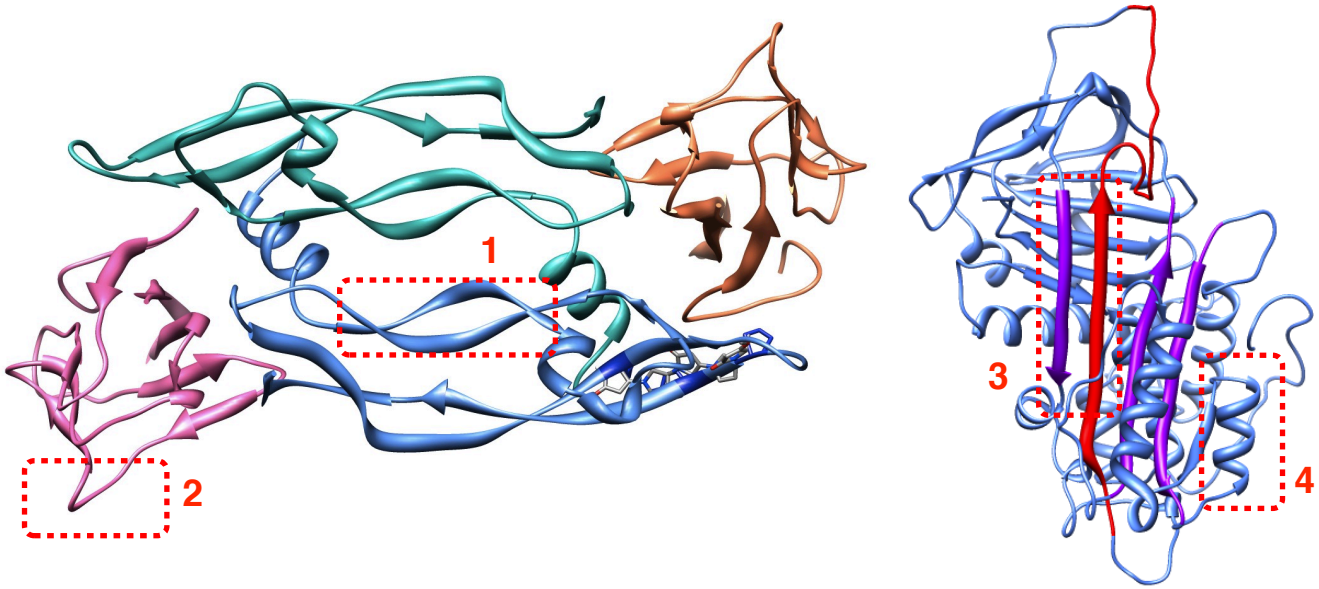
the strand loops back on itself.

β-turns, while *γ-turns*
antiparallel β-sheets.

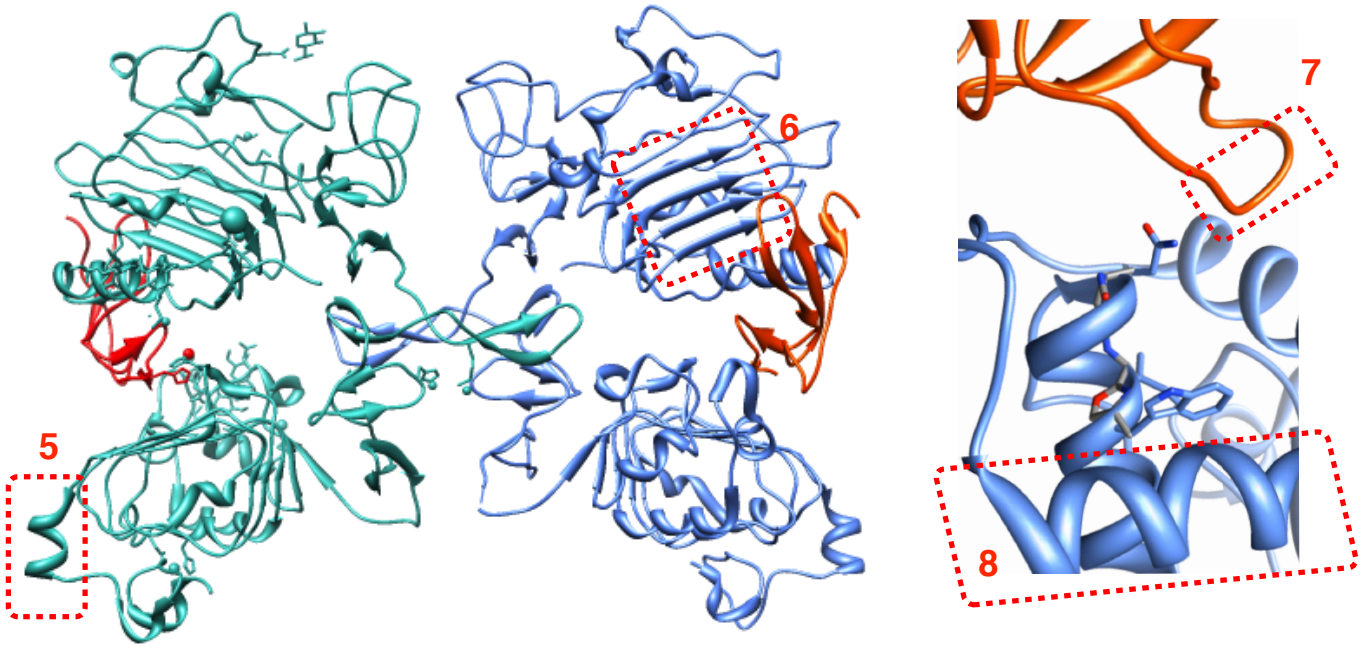
Different protein, Ha!

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





sheet	*turn*	*sheet*	*helix*
1	2	3	4



E. Tertiary And Quaternary Structures

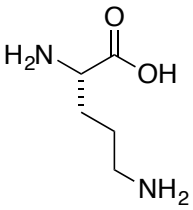
these protein units usually *are not* covalently

F. Constraints On Peptide And Protein Structures

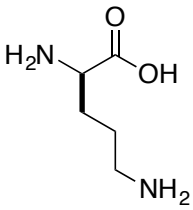
do not fold

cyclo(-Val-Orn-Leu-D-Phe-Pro-)$_2$

gramicidin S



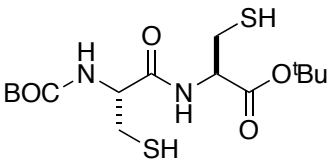
L-Orn



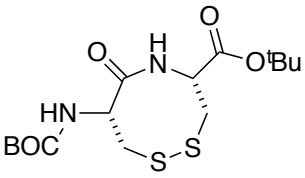
D-Orn

Cys residues.

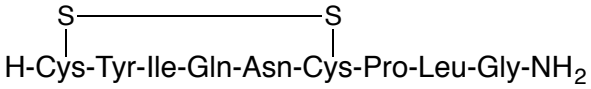
oxidizing agents.

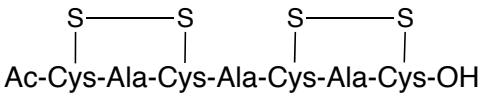


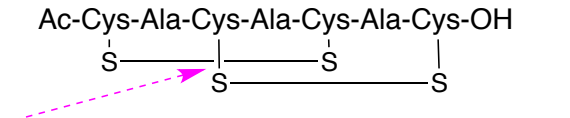
BOC-Cys-Cys-O^{t}Bu

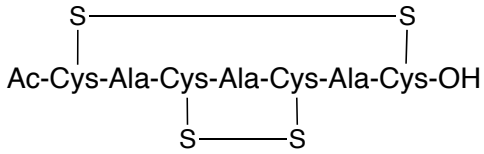


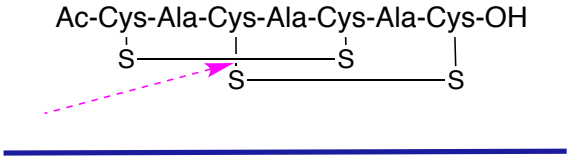
BOC-Cys-Cys-O^{t}Bu











It *is* necessary

could be done