

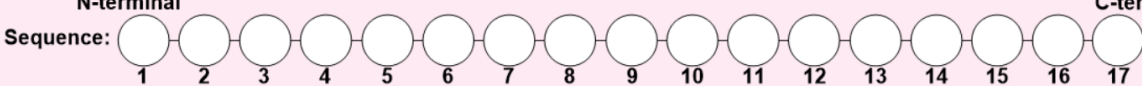
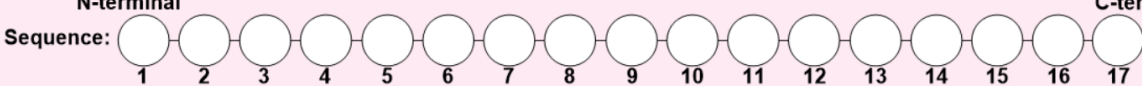
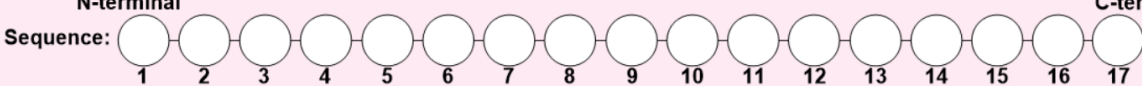
CONCEPT: STRATEGY FOR ORDERING CLEAVED FRAGMENTS

• There are multiple strategies to order cleaved fragments, but here's a solid strategy involving just ____ steps!

Step #1: Scan problem for helpful _____ that reveal composition/sequence info (ex. use of FDNB, hydrazine, etc.).

Step #2: Recall which specific peptide bonds the reagent _____.

EXAMPLE: A peptide with 17 amino acids is treated with trypsin to give three fragments and separately treated with chymotrypsin to give four fragments. Identify the sequence of the 17 amino acid residues in the original/starting peptide.

Step #1: Scan the problem for helpful _____.											
Step #2: Peptide bonds cleaved? ____-terminal of ____ & ____	<table border="1"><thead><tr><th>Trypsin Fragments</th><th>Chymotrypsin Fragments</th></tr></thead><tbody><tr><td>Ala-Ser-Ala-Gly-Phe-Lys</td><td>Ile-Trp</td></tr><tr><td>Val-Ala-Cys</td><td>Lys-Val-Ala-Cys</td></tr><tr><td>Ile-Trp-Met-His-Phe-Met-Cys-Arg</td><td>Met-His-Phe</td></tr><tr><td></td><td>Met-Cys-Arg-Ala-Ser-Ala-Gly-Phe</td></tr></tbody></table>	Trypsin Fragments	Chymotrypsin Fragments	Ala-Ser-Ala-Gly-Phe-Lys	Ile-Trp	Val-Ala-Cys	Lys-Val-Ala-Cys	Ile-Trp-Met-His-Phe-Met-Cys-Arg	Met-His-Phe		Met-Cys-Arg-Ala-Ser-Ala-Gly-Phe
Trypsin Fragments	Chymotrypsin Fragments										
Ala-Ser-Ala-Gly-Phe-Lys	Ile-Trp										
Val-Ala-Cys	Lys-Val-Ala-Cys										
Ile-Trp-Met-His-Phe-Met-Cys-Arg	Met-His-Phe										
	Met-Cys-Arg-Ala-Ser-Ala-Gly-Phe										
Step #3: Circle the ____-terminal fragment.	Step #3: Circle the ____-terminal fragment.										
Step #4: _____ terminal fragments like a puzzle to reveal the sequence.											
Step #5: If you get stuck, use the _____ peptide fragment for overlapping.											
<table border="1"><thead><tr><th>Trypsin Fragments</th><th>Chymotrypsin Fragments</th></tr></thead><tbody><tr><td colspan="2">Sequence: </td></tr></tbody></table>		Trypsin Fragments	Chymotrypsin Fragments	Sequence: 							
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Step #3: Identify ____-terminal or ____-terminal fragments.

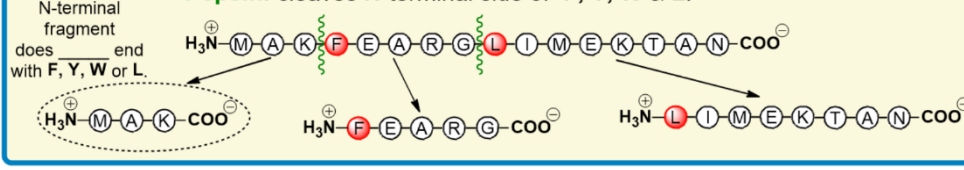
- ☐ These fragments usually do *NOT* have terminal amino acids that the reagent _____ for cleavage.
- ☐ Check if identified terminal fragments from different cleavage reagents _____.

EXAMPLE:

If reagents cleave **N-terminal** peptide bonds, look to identify the ____-terminal fragment.

Pepsin: cleaves **N-terminal** side of **F, Y, W & L**.

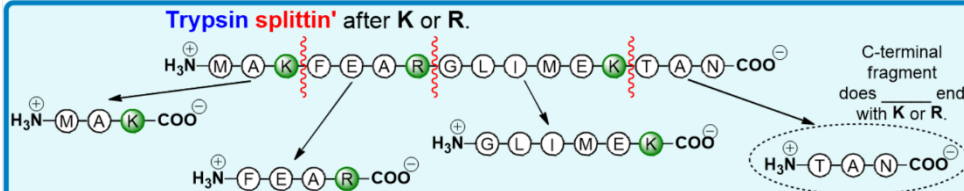
N-terminal fragment does ____ end with F, Y, W or L.



If reagent cleaves **C-terminal** peptide bonds, look to identify the ____-terminal fragment.

Trypsin splittin' after **K** or **R**.

C-terminal fragment does ____ end with K or R.



Step #4: Overlap terminal fragments from step #3 with other fragments from _____ cleavage techniques.

Step #5: If you get stuck, use the longest peptide fragment for overlapping. If there's a tie, pick one & continue to overlap.

- ☐ If you get stuck again, use the next largest fragment & overlap until the original sequence is revealed.

CONCEPT: STRATEGY FOR ORDERING CLEAVED FRAGMENTS

PRACTICE: A sample of an unknown peptide was divided into two aliquots. One aliquot was treated with trypsin; the other was treated with cyanogen bromide. Given the following sequences of the resulting peptide fragments, deduce the sequence of the original peptide.

Trypsin treatment:

Asn—Thr—Trp—Met—Ile—Lys

Gly—Tyr—Met—Gln—Phe

Val—Leu—Gly—Met—Ser—Arg

Cyanogen bromide treatment:

Gln—Phe

Val—Leu—Gly—Met

Ile—Lys—Gly—Tyr—Met

Ser—Arg—Asn—Thr—Trp—Met

Sequence: _____

PRACTICE: A peptide with 31 amino acid residues is independently treated with trypsin to give four fragments and separately treated with chymotrypsin to give six fragments (see chart below). FDNB treatment followed by amino acid hydrolysis resulted in DNP-Met and free amino acids. Identify the sequence of the 31 amino acid residues in the original unfragmented protein using one-letter amino acid codes.

Trypsin Fragments	Chymotrypsin Fragments
W-H-I-F-M-A-C-R	K-C-V-A-I-L-V-R-W
M-A-F-V-I-A-V-Y-K	V-I-A-V-Y
C-V-A-I-L-V-R	M-A-C-R-G-I-P-F
G-I-P-F-A-I-V	H-I-F
	A-I-V
	M-A-F

Sequence:

CONCEPT: STRATEGY FOR ORDERING CLEAVED FRAGMENTS

PRACTICE: The sequence of kassinin, a tachykinin dodecapeptide from the African frog *Kassina senegalensis*, was determined. A single round of Edman degradation identifies Asp as the N-terminus. A 2nd sample of the peptide is treated with chymotrypsin, releasing two fragments with the following amino acid compositions: fragment 1 (G, T, M, V) and fragment 2 (D₂, Q, K, F, P, S, V). Next, a 3rd sample of peptide is treated with trypsin, which results in two fragments with the following amino acid compositions: fragment 3 (D, P, K, V) and fragment 4 (D, Q, G, T, M, F, S, V). A 4th sample was treated with CNBr, but the dodecapeptide was not cleaved. A 5th sample treated with elastase yields a single Gly residue & three fragments—fragment 5 (T, M), fragment 6 (D, K, P, S, V), and fragment 7, which was sequenced as: D—Q—F—V. What is the sequence of the dodecapeptide?

Hint: Elastase cleaves C-terminal side of small neutral residues: G, A, V, L, I & S.

Sequence: _____