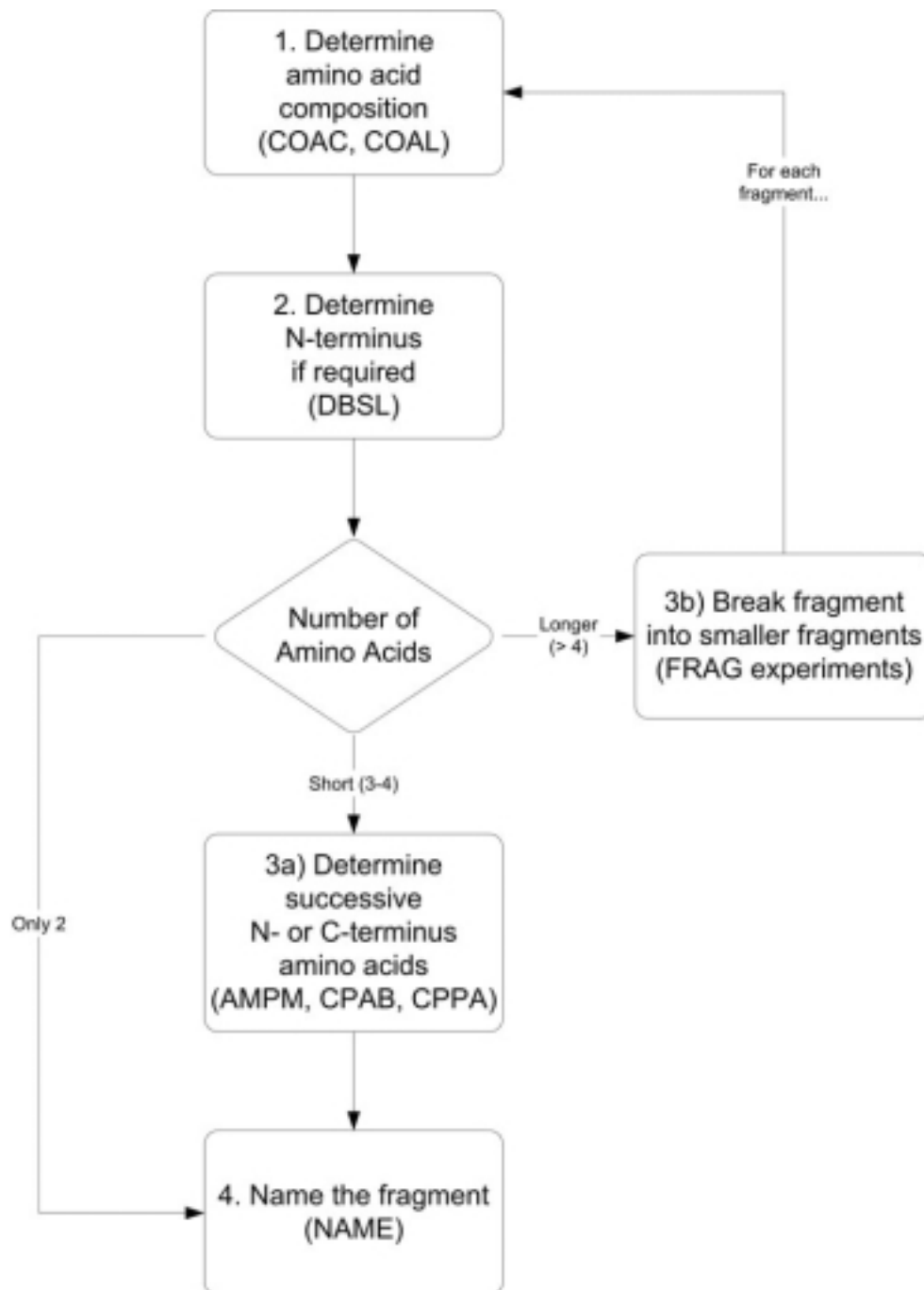


# Example Experiment

## *Suggested Strategy*



## Experiment Overview

Fragment	Experiment
F0	1. Amino acid composition
F0	2. Amino acid composition (cont...)
F0	3. N-terminus determination
F0 <i>F1</i> <i>F2</i>	4. Fragmentation
F2	5. Amino acid composition
F2	6. N-terminus determination
F2	7. Successive C-terminus determination
<b>F2</b>	8. Naming
F1	9. Amino acid composition
F1	10. N-terminus determination
F1 <i>F3</i> <i>F4</i>	11. Fragmentation
F4	12. Amino acid composition
F4	13. N-terminus determination
<b>F4</b>	14. Naming
F3	15. Composition
F3	16. Successive C-terminus determination
F3	17. Successive N-terminus determination
<b>F3</b>	18. Naming
<b>F1</b>	19. Naming
<b>F0</b>	20. Naming

## Introduction

After logging in, the student is presented with their first experiment. In this example, 10.2mg of a peptide fragment has been issued.

The aim of this process is to identify the amino acid sequence of the original fragment (F0), using N-terminus and C-terminus determination, composition identification and fragmentation reactions.

The screenshot shows a web browser window titled "PepSeq - Dodo Internet". The address bar displays "http://localhost/student/". The page content includes a navigation bar with "Back", "Search", "Favorites", and "Media" buttons. Below this is a header with the "PepSeq" logo (stylized letters P, E, P, S, E, Q) and the text "Welcome Sample Student - Experiment 1 in progress". There are links for "Report" and "Logoff".

The main interface is divided into several sections:

- Table:** A table with columns "#", "Qty", and "Fragment". It contains one row: "F0 10.2 mg".
- Notes:** A large text area on the right side with a "Save notes" button.
- Experiments:** A section at the bottom left with a "HELP" dropdown, an "AMPM" dropdown, and a "Go" button.
- Experiment Results:** A section at the bottom right with a "checkbox" and the labels "Experiment" and "Results".

# 1. Amino acid composition: F0

The first experiment chosen to determine amino acid composition of F0 was COAC (hydrolysis using 6M HCl at 105°C).

To perform this experiment:

- F0 (Fragment 0) was selected in the Fragment frame (top left)
- The COAC experiment was chosen in the Experiments frame (bottom left), revealing information about the experiment in the box below
- Experiment parameters were entered (0.5mg, 24 hrs)
- Go button was clicked to perform the experiment

Experiment results are given in the Results frame (bottom right), and the fragment quantity is reduced by 0.5mg to 9.7mg (Fragments frame).

#	Qty	Fragment	Notes
F0	9.7 mg		

Experiments	Experiment	Results
COAC: Hydrolysis of a peptide using 6M HCl at 105° C. The quantity required is 0.4 μ-mole for short chains (4 aa's), up to 0.8 μ-mole for longer chains (> 10-12 aa's). The quantity in mg can be estimated - for the original peptide from the knowledge that the issued quantity is about 10 μ-mole - for fragments from a calculation involving the FW of the parent peptide and the standard 80% (molar) recovery rate in fragmentations. The completeness of a hydrolysis increases with	F0 COAC 0.5mg, 24.0hr	Arg 0.75; Glu 0.45; Gly 0.43; His 0.41; Ile 0.27; Leu 0.42; Val 0.83 (μ-moles)

## 2. Amino acid composition: F0 (cont...)

The rapid decomposition of Trp with acid hydrolysis means it cannot be detected with COAL, so COAC (hydrolysis using barium hydroxide at 100°C) was also required.

Approximate proportions of amino acids are determined by a comparison of quantities returned ( $\mu$ -moles). According to COAC and COAL, F0 contains various proportions of Arg, Glu, Gly, His, Ile, Leu and Val, but the order is unknown (indicated below by square brackets in the Notes frame, bottom right).

#	Qty	Fragment	Notes
F0	9.2 mg		F0 = [2 Arg, Glu, Gly, His, Ile, Leu, 2 Val]

Experiments	Experiment	Results
COAL: Hydrolysis of a peptide using barium hydroxide at 100°C. For quantity to use, see COAC. As in COAC, a balance between hydrolysis and decomposition rates determines the reliability of analysis figures. In alkaline conditions, Trp is more stable; however Arg and Cys are decomposed so rapidly in alkaline conditions that they are detected very rarely.	F0 COAC 0.5mg, 24.0hr	Arg 0.75; Glu 0.45; Gly 0.43; His 0.41; Ile 0.27; Leu 0.42; Val 0.83 ( $\mu$ -moles)
	F0 COAL 0.5mg, 24.0hr	Glu 0.47; Gly 0.45; His 0.43; Ile 0.29; Leu 0.44; Val 0.85 ( $\mu$ -moles)

## 3. N-terminus determination: F0

Determination of N-terminus using dabsyl chloride (DBSL) was performed for F0.

When DBSL returns "No amino acid found in measurable quantity", it indicates that the N-terminus must be either Trp or acetylated. Since Trp was absent (COAC & COAL), the N-terminus must be acetylated (indicated as "Ace-" below in the Notes frame).

#	Qty	Fragment	Notes
F0	9.1 mg		F0 = Ace-[2 Arg, Glu, Gly, His, Ile, Leu, 2 Val]

Experiments	Experiment	Results
DBSL: Determination of N-terminus using dabsyl chloride. This extremely sensitive test requires the minimum quantity of sample, 0.1 mg (default quantity). Acidic conditions will cause the decomposition of acid-sensitive tryptophan; neither can they remove an acetylating group from the N-terminus. In these 2 cases (Trp or Ace), the test gives a null result. The result of the determination of the N-terminus with dabsyl chloride is a qualitative result only.	F0 COAC 0.5mg, 24.0hr	Arg 0.75; Glu 0.45; Gly 0.43; His 0.41; Ile 0.27; Leu 0.42; Val 0.83 ( $\mu$ -moles)
	F0 COAL 0.5mg, 24.0hr	Glu 0.47; Gly 0.45; His 0.43; Ile 0.29; Leu 0.44; Val 0.85 ( $\mu$ -moles)
	F0 DBSL 0.1mg	No amino acid found in measurable quantity

## 4. Fragmentation: F0

Fragmentation of F0 was required to create smaller fragments for further analysis. TRPS (treatment with trypsin) was chosen to cause fragmentation at the C-terminus of each Arg present in F0.

Two new fragments were produced (F1 and F2). TRPS cannot produce fragments shorter than two amino acids, which in this case prevented three fragments being produced.

The relative order of F1 and F2 is unknown (indicated by square brackets below).

#	Qty	Fragment	Notes
F0	0.0 mg		F0 = Ace-[2 Arg, Glu, Gly, His, Ile, Leu, 2 Val]
F1	4.2 mg		F0 = [F1, F2]
F2	2.7 mg		

Experiments	Experiment	Results
TRPS: Treatment with trypsin. Catalyses hydrolysis at the C-terminal of arginine and lysine (Arg and Lys), these being basic aminoacids.	F0 COAC 0.5mg, 24.0hr	Arg 0.75; Glu 0.45; Gly 0.43; His 0.41; Ile 0.27; Leu 0.42; Val 0.83 ( $\mu$ -moles)
	F0 COAL 0.5mg, 24.0hr	Glu 0.47; Gly 0.45; His 0.43; Ile 0.29; Leu 0.44; Val 0.85 ( $\mu$ -moles)
	F0 DBSL 0.1mg	No amino acid found in measurable quantity
	F0 TRPS 9.1mg	Fragment 1: 4.2mg; Fragment 2: 2.7mg

## 5. Composition: F2

The amino acid composition of either new fragment (F1 or F2) can be determined with COAC, since this revealed all amino acids present in F0 (Step 1). COAC was run on the shorter fragment (F2) since it is generally easier to determine the amino acid sequence for shorter fragments.

#	Qty	Fragment	Notes
F0	0.0 mg		F2 = [Arg, Ile, Leu]
F1	4.2 mg		
F2	2.4 mg		

Experiments	Experiment	Results
COAC: Hydrolysis of a peptide using 6M HCl at 105 $\circ$ C. The quantity required is 0.4 $\mu$ -mole for short chains (4 aa's), up to 0.8 $\mu$ -mole for longer chains (> 10-12 aa's). The quantity in mg can be estimated - for the original peptide from the knowledge that the issued quantity is about 10 $\mu$ -mole - for fragments from a calculation involving the FW of the parent peptide and the standard 80% (molar) recovery rate in fragmentations. The completeness of a hydrolysis increases with	F2 COAC 0.3mg, 24.0hr	Arg 0.60; Ile 0.50; Leu 0.49 ( $\mu$ -moles)

## 6. N-terminus determination: F2

DBSL indicates that the N-terminus of F2 is acetylated.

Since the N-termini of F0 and F2 were both acetylated, the relative position of F1 and F2 is now known.

#	Qty	Fragment	Notes
F0	0.0 mg		F2 = Ace-[Arg, Ile, Leu] F0 = F2-F1
F1	4.2 mg		
F2	2.3 mg		

Experiment	Results
F2 COAC 0.3mg, 24.0hr	Arg 0.60; Ile 0.50; Leu 0.49 ( $\mu$ -moles)
F2 DBSL 0.1mg	No amino acid found in measurable quantity

**Experiments** DBSL 0.1 mg Go

DBSL: Determination of N-terminus using dabsyl chloride.

This extremely sensitive test requires the minimum quantity of sample, 0.1 mg (default quantity). Acidic conditions will cause the decomposition of acid-sensitive tryptophan; neither can they remove an acetylating group from the N-terminus. In these 2 cases (Trp or Ace), the test gives a null result.

The result of the determination of the N-terminus with dabsyl chloride is a qualitative result only.

## 7. Successive C-terminus determination: F2

As F2 contains only three amino acids, successive C-terminus determination was used to find the amino acid sequence. CPPA (Carboxypeptidase A digestion) is unable to hydrolyse bonds next to Arg (present in F2), so CPAB (digestion with a mixture of carboxypeptidases A+B) was chosen.

CPAB indicates that the C-terminus amino acids are -Ile-Arg. The only other amino acid in F2 is Leu, which must be the acetylated amino acid on the N-terminus.

#	Qty	Fragment	Notes
F0	0.0 mg		F2 = Ace-Leu-Ile-Arg
F1	4.2 mg		
F2	1.6 mg		

Experiment	Results
F2 COAC 0.3mg, 24.0hr	Arg 0.60; Ile 0.50; Leu 0.49 ( $\mu$ -moles)
F2 DBSL 0.1mg	No amino acid found in measurable quantity
F2 CPAB 0.7mg, 0.8hr	Arg 1.12; Ile 0.45 ( $\mu$ -moles)

**Experiments** CPAB 0.7 mg, 0.8 hrs Go

CPAB: Digestion with a mixture of carboxypeptidases A+B.

Carboxypeptidases release aminoacids in succession from the C-terminal of a peptide. If the digestion is interrupted before it is complete, those aminoacids nearest to the C-terminal of the peptide will be present in higher analytical concentrations. When an aminoacid is released only slowly by an exopeptidase, the faster released aminoacids which follow it will be present in similar concentrations.

Arginine and proline (Arg and Pro) are not released by carboxypeptidase A. aspartic acid, cysteine

## 8. Naming: F2

NAME was conducted on F2, and the correctly named amino acid sequence was shown beside F2 in the Fragments frame.

#	Qty	Fragment	Notes
F0	0.0 mg		F2 = Ace-Leu-Ile-Arg
F1	4.2 mg		
F2	1.6 mg	Ace-Leu-Ile-Arg	

Experiment	Results
F2 COAC 0.3mg, 24.0hr	Arg 0.60; Ile 0.50; Leu 0.49 (μ-moles)
F2 DBSL 0.1mg	No amino acid found in measurable quantity
F2 CPAB 0.7mg, 0.8hr	Arg 1.12; Ile 0.45 (μ-moles)
F2 NAME	Fragment 2 correctly named as Ace-Leu-Ile-Arg

**Experiments**

**NAME:** Any of the fragments present in memory can be named by entering:  
 - sequences of aminoacid codes (see topic AMAC) separated by hyphens (-), starting from the N-terminus;  
 - the identity numbers of previously identified fragments separated by -;  
 - combinations of the above.

After a fragment is named correctly, it is deleted as being of no further use. After you name correctly the original peptide, you can exit the program or

## 9. Composition: F1

Since F1 is the difference between F0 and F2, the amino acid composition of F1 can be deduced.

#	Qty	Fragment	Notes
F0	0.0 mg		F1 = F0 minus F2 F1 = Ace-[2 Arg, Glu, Gly, His, Ile, Leu, 2 Val] minus Ace-Leu-Ile-Arg F1 = [Arg, Glu, Gly, His, 2 Val]
F1	4.2 mg		
F2	1.6 mg	Ace-Leu-Ile-Arg	

Experiment	Results
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**Experiments**

## 10. N-terminus determination: F1

The N-terminus of F1 was determined with DBSL.

#	Qty	Fragment	Notes
F0	0.0 mg		F1 = His-[Arg, Glu, Gly, 2 Val]
F1	4.1 mg		
F2	1.6 mg	Ace-Leu-Ile-Arg	

Experiments	DBSL	0.1 mg	Go
DBSL: Determination of N-terminus using dabsyl chloride.  This extremely sensitive test requires the minimum quantity of sample, 0.1 mg (default quantity). Acidic conditions will cause the decomposition of acid-sensitive tryptophan; neither can they remove an acetylating group from the N-terminus. In these 2 cases (Trp or Ace), the test gives a null result.  The result of the determination of the N-terminus with dabsyl chloride is a qualitative result only.			

Experiment	Results
F1 DBSL 0.1mg	N-terminus identified: His

## 11. Fragmentation: F1

Fragmentation of F1 was required to create smaller fragments for further analysis. THML (treatment with thermolysin) was chosen to cleave the N-terminus of each Val. Cleavage only occurs where resulting fragments are 2 amino acids or more in length.

Two new fragments were produced (F3 and F4), one of which must have an N-terminus of Val. THML cannot produce fragments shorter than two amino acids, which prevented three fragments being produced.

#	Qty	Fragment	Notes
F0	0.0 mg		F1 = His-[Arg, Glu, Gly, 2 Val]
F1	0.0 mg		
F2	1.6 mg	Ace-Leu-Ile-Arg	
F3	2.2 mg		
F4	1.4 mg		

Experiments	THML	4.1 mg	Go
THML: Treatment with thermolysin.  Catalyses hydrolysis at the N-terminal of alanine, isoleucine, leucine, methionine, phenylalanine, tyrosine and valine (Ala, Ile, Leu, Met, Phe, Tyr and Val).			

Experiment	Results
F1 DBSL 0.1mg	N-terminus identified: His
F1 THML 4.1mg	Fragment 3: 2.2mg; Fragment 4: 1.4mg

## 12. Composition: F4

According to COAC, F4 contains His and Glu.

The only His in F0 was found to be in F1 on the N-terminus, and since F4 contains this His it must also be on the N-terminus.

#	Qty	Fragment	Notes
F0	0.0 mg		F1 = His-Glu
F1	0.0 mg		
F2	1.6 mg	Ace-Leu-Ile-Arg	
F3	2.2 mg		
F4	1.2 mg		

Experiments	Experiment	Results
COAC: Hydrolysis of a peptide using 6M HCl at 105° C. The quantity required is 0.4 μ-mole for short chains (4 aa's), up to 0.8 μ-mole for longer chains (> 10-12 aa's). The quantity in mg can be estimated - for the original peptide from the knowledge that the issued quantity is about 10 μ-mole - for fragments from a calculation involving the FW of the parent peptide and the standard 80% (molar) recovery rate in fragmentations. The completeness of a hydrolysis increases with	F4 COAC 0.2mg, 24.0hr	Glu 0.74; His 0.72 (μ-moles)

## 13. N-terminus determination: F4

Since enough sample was available, the amino acid sequence was confirmed with DBSL.

#	Qty	Fragment	Notes
F0	0.0 mg		F1 = His-Glu
F1	0.0 mg		
F2	1.6 mg	Ace-Leu-Ile-Arg	
F3	2.2 mg		
F4	1.1 mg		

Experiments	Experiment	Results
DBSL: Determination of N-terminus using dabsyl chloride. This extremely sensitive test requires the minimum quantity of sample, 0.1 mg (default quantity). Acidic conditions will cause the decomposition of acid-sensitive tryptophan; neither can they remove an acetylating group from the N-terminus. In these 2 cases (Trp or Ace), the test gives a null result. The result of the determination of the N-terminus with dabsyl chloride is a qualitative result only.	F4 COAC 0.2mg, 24.0hr	Glu 0.74; His 0.72 (μ-moles)
	F4 DBSL 0.1mg	N-terminus identified: His

## 14. Naming: F4

F4 was named.

The relative position of F3 and F4 are now known, since the N-terminus of F1 and F3 don't match.

#	Qty	Fragment	Notes
F0	0.0 mg		F1 = His-Glu
F1	0.0 mg		F1 = F4-F3
F2	1.6 mg	Ace-Leu-Ile-Arg	
F3	2.2 mg		
F4	1.1 mg	His-Glu	

Experiment	Results
F4 COAC 0.2mg, 24.0hr	Glu 0.74; His 0.72 (μ-moles)
F4 DBSL 0.1mg	N-terminus identified: His
F4 NAME	Fragment 4 correctly named as His-Glu

Experiments:  NAME

NAME: Any of the fragments present in memory can be named by entering:  
 - sequences of aminoacid codes (see topic AMAC) separated by hyphens (-), starting from the N-terminus;  
 - the identity numbers of previously identified fragments separated by -;  
 - combinations of the above.

After a fragment is named correctly, it is deleted as being of no further use. After you name correctly the original peptide, you can exit the program or

## 15. Composition: F3

F3 is the difference between F1 and F4.

Since THML catalysed hydrolysis at the N-terminus of Val in F1, and F4 had His on the N-terminus, the N-terminus of F3 must be Val:

#	Qty	Fragment	Notes
F0	0.0 mg		F3 = F1 minus F4
F1	0.0 mg		= His-[Arg, Glu, Gly, 2 Val] minus His-Glu
F2	1.6 mg	Ace-Leu-Ile-Arg	= [Arg, Gly, 2 Val]
F3	2.2 mg		= Val-[Arg, Gly, Val]
F4	1.1 mg	His-Glu	

Experiment	Results

Experiments:  HELP  AMPM

## 16. Successive C-terminus determination: F3

If the two C-terminus amino acids of F3 are determined, then the whole fragment sequence can be determined. CPPA does not digest Arg, so CPAB was used.

CPAB indicates the C-terminus amino acids for F4 are -Gly-Arg-Val.

#	Qty	Fragment	Notes
F0	0.0 mg		F3 = Val-Gly-Arg-Val
F1	0.0 mg		
F2	1.6 mg	Ace-Leu-Ile-Arg	
F3	1.4 mg		
F4	1.1 mg	His-Glu	

Experiments	Experiment	Results
CPAB: Digestion with a mixture of carboxypeptidases A+B. Carboxypeptidases release aminoacids in succession from the C-terminal of a peptide. If the digestion is interrupted before it is complete, those aminoacids nearest to the C-terminal of the peptide will be present in higher analytical concentrations. When an aminoacid is released only slowly by an exopeptidase, the faster released aminoacids which follow it will be present in similar concentrations. Arginine and proline (Arg and Pro) are not released by carboxypeptidase A. aspartic acid, cysteine	F3 CPAB 0.8mg, 1.2hr	Arg 0.61; Gly 0.22; Val 1.64 (μ-moles)

## 17. Successive N-terminus determination: F3

To verify the amino acid sequence of F3, successive N-terminus determination was conducted.

AMPM (Aminopeptidase M digestion) indicates the N-terminus amino acids are: Val-Gly-Arg-

#	Qty	Fragment	Notes
F0	0.0 mg		F3 = Val-Gly-Arg-Val
F1	0.0 mg		
F2	1.6 mg	Ace-Leu-Ile-Arg	
F3	0.6 mg		
F4	1.1 mg	His-Glu	

Experiments	Experiment	Results
AMPM: Aminopeptidase M digestion. Aminoacids are released successively from the N-terminal of the peptide. Acetylated N-terminals block release completely. Proline (Pro) is released only very slowly (see topics CPAB and TAB2). Refer to topic EXOP for mass to use, and topic TAB2 for time to use.	F3 CPAB 0.8mg, 1.2hr	Arg 0.61; Gly 0.22; Val 1.64 (μ-moles)
	F3 AMPM 0.8mg, 1.5hr	Arg 0.21; Gly 0.61; Val 1.47 (μ-moles)

## 18. Naming: F4

NAME was conducted on F4.

#	Qty	Fragment
F0	0.0 mg	
F1	0.0 mg	
F2	1.6 mg	Ace-Leu-Ile-Arg
F3	0.6 mg	Val-Gly-Arg-val
F4	1.1 mg	His-Glu

**Notes** Save notes

F3 = Val-Gly-Arg-Val

---

**Experiments** NAME Go

Val-Gly-Arg-Val

- the identity numbers of previously identified fragments separated by -;  
 - combinations of the above.

After a fragment is named correctly, it is deleted as being of no further use. After you name correctly the original peptide, you can exit the program or continue with the next sample.

Both correct and incorrect namings are recorded by the program and may be used to evaluate your performance.

Experiment	Results
F3 CPAB 0.8mg, 1.2hr	Arg 0.61; Gly 0.22; val 1.64 (μ-moles)
F3 AMPM 0.8mg, 1.5hr	Arg 0.21; Gly 0.61; val 1.47 (μ-moles)
F3 NAME	Fragment 3 correctly named as Val-Gly-Arg-val

## 19. Naming: F1

Since F1 = F4-F3 (Step 14), F1 can also be named as F4-F3 (short-hand for His-Glu-Val-Gly-Arg-Val).

#	Qty	Fragment
F0	0.0 mg	
F1	0.0 mg	His-Glu-Val-Gly-Arg-Val
F2	1.6 mg	Ace-Leu-Ile-Arg
F3	0.6 mg	Val-Gly-Arg-val
F4	1.1 mg	His-Glu

**Notes** Save notes

F1 = F4-F3

---

**Experiments** NAME Go

F4-F3

NAME: Any of the fragments present in memory can be named by entering:  
 - sequences of aminoacid codes (see topic AMAC) separated by hyphens (-), starting from the N-terminus;  
 - the identity numbers of previously identified fragments separated by -;  
 - combinations of the above.

After a fragment is named correctly, it is deleted as being of no further use. After you name correctly the original peptide, you can exit the program or

Experiment	Results
F1 DBSL 0.1mg	N-terminus identified: His
F1 THML 4.1mg	Fragment 3: 2.2mg; Fragment 4: 1.4mg
F1 NAME	Fragment 1 correctly named as F4-F3 (His-Glu-Val-Gly-Arg-Val)

## 20. Naming: F0

Finally, given that  $F0 = F2-F1$  (Step 6), F0 can be named as F2-F1 (Ace-Leu-Ile-Arg-His-Glu-Val-Gly-Arg-Val)

#	Qty	Fragment
F0	0.0 mg	Ace-Leu-Ile-Arg-His-Glu-Val-Gly-Arg-Val
F1	0.0 mg	His-Glu-Val-Gly-Arg-Val
F2	1.6 mg	Ace-Leu-Ile-Arg
F3	0.6 mg	Val-Gly-Arg-Val
F4	1.1 mg	His-Glu

Experiment	Results
F0 COAC 0.5mg, 24.0hr	Arg 0.75; Glu 0.45; Gly 0.43; His 0.41; Ile 0.27; Leu 0.42; Val 0.83 (μ-moles)
F0 COAL 0.5mg, 24.0hr	Glu 0.47; Gly 0.45; His 0.43; Ile 0.29; Leu 0.44; Val 0.85 (μ-moles)
F0 DBSL 0.1mg	No amino acid found in measurable quantity
F0 TRPS 9.1mg	Fragment 1: 4.2mg; Fragment 2: 2.7mg
F0 NAME	Fragment 0 correctly named as F2-F1 (Ace-Leu-Ile-Arg-His-Glu-Val-Gly-Arg-Val)

**Experiments**

NAME: Any of the fragments present in memory can be named by entering:  
 - sequences of aminoacid codes (see topic AMAC) separated by hyphens (-), starting from the N-terminus;  
 - the identity numbers of previously identified fragments separated by -;  
 - combinations of the above.

After a fragment is named correctly, it is deleted as being of no further use. After you name correctly the original peptide, you can exit the program or

## Student Report

The "Report" link (top right of student screen) may be clicked throughout the experiment to reveal current progress:

<b>Experiment 1</b>				Show Date & Time: <input type="checkbox"/>		
<b>F0</b>	<b>F1</b>	<b>F2</b>	<b>F3</b>	<b>F4</b>	<b>Experiment (Mg &amp; Hrs used)</b>	<b>Results</b>
F0					COAC 0.5mg, 24.0hr	Arg 0.75; Glu 0.45; Gly 0.43; His 0.41; Ile 0.27; Leu 0.42; Val 0.83 (μ-moles)
F0					COAL 0.5mg, 24.0hr	Glu 0.47; Gly 0.45; His 0.43; Ile 0.29; Leu 0.44; Val 0.85 (μ-moles)
F0					DBSL 0.1mg	No amino acid found in measurable quantity
F0	F1	F2			TRPS 9.1mg	Fragment 1: 4.2mg; Fragment 2: 2.7mg
		F2			COAC 0.3mg, 24.0hr	Arg 0.60; Ile 0.50; Leu 0.49 (μ-moles)
		F2			DBSL 0.1mg	No amino acid found in measurable quantity
		F2			CPAB 0.7mg, 0.8hr	Arg 1.12; Ile 0.45 (μ-moles)
		F2			NAME	Fragment 2 correctly named as Ace-Leu-Ile-Arg
	F1				DBSL 0.1mg	N-terminus identified: His
	F1	F3	F4		THML 4.1mg	Fragment 3: 2.2mg; Fragment 4: 1.4mg
		F4			COAC 0.2mg, 24.0hr	Glu 0.74; His 0.72 (μ-moles)
		F4			DBSL 0.1mg	N-terminus identified: His
		F4			NAME	Fragment 4 correctly named as His-Glu
		F3			CPAB 0.8mg, 1.2hr	Arg 0.61; Gly 0.22; Val 1.64 (μ-moles)
		F3			AMPM 0.8mg, 1.5hr	Arg 0.21; Gly 0.61; Val 1.47 (μ-moles)
		F3			NAME	Fragment 3 correctly named as Val-Gly-Arg-Val
	F1				NAME	Fragment 1 correctly named as F4-F3 (His-Glu-Val-Gly-Arg-Val)
F0					NAME	Fragment 0 correctly named as F2-F1 (Ace-Leu-Ile-Arg-His-Glu-Val-Gly-Arg-Val)
<b>F0</b>	<b>F1</b>	<b>F2</b>	<b>F3</b>	<b>F4</b>	<b>5 3 4 3 3 &lt;- Experiments per fragment</b>	

When an experiment is finished, the next experiment is presented until all experiments are completed.