

The Serine Project

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Introduction

An amino acid is an organic molecule that contains an amino group ($-\text{NH}_2$), an acidic carboxyl group ($-\text{COOH}$), and a unique side chain ($-\text{R}$) that is used to identify the different amino acids (See Figure 1). Amino acids are used for protein synthesis in all living organisms. They are joined by peptide bonds to form proteins, which are a necessity for cell life. (1)

Serine is one of the twenty common amino acids. In 1865 it was first obtained and then in 1902 its structure was found. Serine partakes in the biosynthesis of nucleotides, cysteine and tryptophan, two common amino acids, and many other metabolites. Many enzymes have serine in their structure, which is very important to their catalytic activity (2). Also, the serine residues of certain enzymes allow O-linked glycosylation, which is important for proteoglycan proteins. Serine residue is also very important for phosphorylation, which controls cell signaling for protein production and other processes in eukaryotes. (3)

The goal of the research performed during C-Term lab periods was to identify an unknown amino acid out of the twenty most common acids. The amino acid we were given was "Unknown #40." The research was done using a variety of techniques, including solubility, density, melting points, thin-layer chromatography, UV-visible spectrum tests, and an infrared spectrum test.

After performing these tests, the unknown amino acid was determined to be serine, containing an R-group of CH_2OH (See Figure 2).

Experimental

Quantitative Solubility. Using a 1.00-mL pipet, we put 1.00-mL of distilled water into a 1-dram vial. We weighed the vial containing the amino acid. We added small portions of the amino acid to the 1-dram vial, covered the vial, and shook it until the amino acid had dissolved into the water. We repeated the process until the amino acid ceased to dissolve. After letting the vial sit for a few minutes, we observed that the remaining solid amino acid in the vial had dissolved. We added more amino acid and repeated the process. We weighed the vial with the amino acid again to obtain the weight of the dissolved amino acid.

Density by Flotation. We put 1.00-mL of bromochloromethane (CH_2BrCl) using a 1.00-mL pipet into a 1-dram vial. We added amino acid to the vial and observed that the solid floated in the bromochloromethane; therefore, the amino acid was less dense. We chose chloroform (CHCl_3) and observed that the amino acid sank, showing that the amino acid was denser. As a third test, we used carbon tetrachloride (CCl_4); the unknown was suspended. We added chloroform (0.1 mL) to determine an upper bound of the density of the amino acid.

Determination of Melting Points. We ground up some amino acid in a watch glass using a stirring rod, placed it into a closed capillary tube, and carefully tapped it until the powder had a height of approximately 2.0 mm. We placed the capillary into a Mel-Temp apparatus with a temperature sensor attached. We turned the power level of the Mel-Temp to

4 and the amino acid was observed until the temperature stopped increasing. We increased the level to 5 and began observing changes in the amino acid. We recorded the temperature when the amino acid changed color and again as the bubbling was observed. We compared the unknown amino acid with serine, which fit the density and solubility of our unknown. We again observed changes of the amino acids and recorded the temperatures at which they occurred.

Thin Layer Chromatography. We added unknown amino acid to distilled water in a 1-dram vial using a ratio of 0.001 g amino acid to 0.2 mL water. We prepared a serine solution using the same ratio. We made light pencil lines 1 cm from each end of each of five TLC plates to mark the start and end points of the mobile phase and set two of the plates aside. TLC using ink: We transferred ink onto the TLC plates using capillaries. While doing this process, we also filled three developing bottles to a height of 0.5 cm: one with ethanol, one with dichloromethane, and the third with a 50/50 mix of ethanol and dichloromethane. Once ready, we placed one TLC plate in each of the three developing bottles. Once the mobile phase traveled to the second line, we took out the TLC plate and dried it. We could then view the marks created on the TLC plate.

TLC using amino acid: We transferred a small amount of the amino acid solutions to the prepared TLC plates on the bottom line using a capillary which had a diameter no greater than 1 mm. We placed a third spot on the plate using a mixture of both the unknown and serine. We filled two developing bottles to a height of 0.5 cm, one with a mixture of 30/70 concentrated ammonia (NH₃)/n-propanol, the other with 50/50 water/n-propanol, and placed the plates in the developing bottles, making sure to keep the TLC plate as vertical as possible. When we observed that the mobile phase had reached the second line on the plate, the plate was removed and placed on a watch glass, which was transferred to an oven heated to approximately 60°C. When the plate dried, we removed it from the oven and dipped the plate into a solution of 0.2% ninhydrin in ethanol to stain the amino acid spots produced. We dried the plate in the oven again. When completely dry, we removed the plate and outlined stains on the plate using a pencil. We measured the distance that the amino acid traveled from the starting line to the center of the spot and the distance between the two pencil lines. (See Figure 3.)

UV-Visible Spectroscopy. We prepared a 0.01 M solution of our unknown amino acid in a 10-mL volumetric flask. To do this, we assumed the amino acid was serine and calculated the molarity based on the molar mass of serine (105.09 g/mol). Once completely dissolved, we transferred the solution into to a quartz cuvet. We prepared a second cuvet containing pure distilled water. We dried the outside of the cuvetts and placed them into a UV-VIS spectrometer. Using a computer, we scanned the spectrum and it was determined that the concentration of the solution was too high. We diluted the solution to 1/5 of its original molarity and repeated the tests using the new solution. (See Figure 4.)

Infrared Spectroscopy. We ground the amino acid in an agate mortar using a pestle until the amino acid no longer looked crystalline. We added 1 drop of Nujol to the amino acid and the amino acid was mixed until a paste formed. We transferred the paste onto a sodium chloride plate using a flat spatula. We put a second plate on the first and gently rotated to spread the paste between the two plates. We then put the plates into a plate holder and

screwed them in securely. We placed the plates into an IR spectrometer and scanned them using a computer. We compared the results (See Figure 5) with charts of known amino acids.

Titration. In order to accurately measure the molarity of NaOH and HCl solutions that were provided, we needed to accurately know the molarity of each solution.

Standardization of NaOH: We standardized NaOH by using a solution of 0.1000M potassium acid phthalate (KHP), which was previously standardized by the Chemistry Department staff. We filled a buret with approximately 50.0mL of the NaOH solution. We let the solution run out of the buret in order to assure no air bubbles were present in the buret to throw off readings. We measured the amount of NaOH in the buret before we began titrating. We added 5.00mL KHP solution using a pipet to a 25.0mL Erlenmeyer flask. Phenolphthalein (2 drops) was added into the flask. We began titrating by slowly adding amounts of NaOH from the buret into the flask while continuously swirling the flask. When a pink color started to appear for prolonged periods, we slowed down the rate at which NaOH was added. We continued to monitor the solution until a faint pink color became permanent. We took the final volume of NaOH in the buret. We repeated this process until we had three titrations with an error of less than 1.00% between them.

Standardization of HCl: We added 5.00mL HCl using a pipet into an Erlenmeyer flask and added 2 drops of phenolphthalein. We then read the initial value of NaOH in the buret. We began titrating using the same process as we used for standardizing the NaOH solution. When the solution turned faint pink, we took the final volume of the NaOH. We continued the process until we had three titrations with an error of less than 1.00% between them.

Amino Acid Titration: We weighed 0.2651g of the unknown amino acid into a 25.0mL volumetric flask. We added enough water to make a uniform 0.1009M solution of the amino acid. We transferred 5.00mL of the unknown amino acid solution to a 100mL beaker. We calculated the amount of the standardized HCl needed to provide a 1:1 ratio of moles amino acid to moles HCl and added it to the same beaker. We placed the beaker on a heating and stirring plate and placed a magnetic stirrer into the beaker. We placed a pH meter electrode into the solution and added distilled water to fully submerge the electrode. We turned on the stirring plate and read the initial pH. We began adding NaOH into the beaker, using an automatic pipette, 0.50mL at a time. After each addition of NaOH, we allowed the solution to become homogeneous, allowing the pH to stabilize. We then recorded the pH. Once the pH had passed 3.00, we added the NaOH 0.10mL at a time to obtain more data readings. We continued this until the pH reached about 8.00, and switched back to adding 0.50mL at a time. At a pH of 9.00, we titrated the protonated solution with 0.20mL NaOH until the pH reached 11.00. We repeated this procedure of titration again to obtain accurate data.

Synthesis of Copper Complex. We weighed 0.2066g of our amino acid into a 50mL beaker. We also weighed 0.1971g copper (II) acetate monohydrate into a separate 50mL beaker. We added 5mL of water (5mL) to each of the beakers and swirled them to create solutions. When the solutions were both uniform, we added the copper²⁺ solution drop-wise to the amino acid solution. After the addition of the copper²⁺ solution was complete, we swirled the new solution to allow the reaction to come to completion. We placed a few drops of the copper complex solution into a small test tube and added 1mL acetone. After finding that a precipitate formed using acetone as a solvent, we placed 10mL of acetone into a 50mL beaker and added the copper-amino acid complex solution drop-wise into the solvent. After

the copper-amino acid complex precipitated, we suctioned the liquid from the solid using a vacuum apparatus with a filter to contain the solid. We weighed an empty 1-dram vial. After storing the copper-amino acid complex in the vial, we weighed the vial again to obtain the weight of the copper-amino acid complex. We calculated the percent yield of the copper-amino acid complex.

Copper-Amino Acid Complex Tests. Using the methods above for the amino acid, we measured the density, melting point, and UV-visible and IR spectra of the copper-amino acid complex.

Determination of Stoichiometry of Copper Complex Using Job's Method. We measured out 10.0mL of a 0.1M copper (II) acetate monohydrate solution into a 25mL Erlenmeyer flask. We put 0.1057g of the copper-amino acid complex into a separate 25mL Erlenmeyer flask and added 10.0mL distilled water using a graduated pipet. We cleaned and labeled ten test-tube cuvetts. Using a 1.00mL graduated pipet, we added different volumes of the copper (II) acetate monohydrate and copper-amino acid solutions to the ten cuvetts (see Table 8 for amounts added). Distilled water (3.1mL) was added to each of the ten cuvetts. We used distilled water in a test-tube cuvet to zero out a Spectronic 20 Spectrometer. We used the Spectronic 20 Spectrometer to determine the absorbance of the solutions at a wavelength of 550nm.

Spectrometric Analysis of Copper. (See Figure 12.)

Preparation of solutions: We added a stock solution of copper (II) acetate hexahydrate (25mL of .050M) to a 25mL volumetric flask. We used a graduated pipet to transfer different volumes of the stock solution into five labeled 10mL volumetric flasks (see Table 9 for amounts added). We filled each 10mL flask to the mark with 7.5M ammonia solution. We sealed the 10mL flasks and shook them vigorously to create a homogeneous solution.

Preparation of copper-amino acid complex: We weighed .0236g of the copper-amino acid complex into a 50mL beaker. We added 1.0mL nitric acid to the copper-amino acid complex and swirled gently until the solid dissolved completely and the solution appeared light blue. We added 6 drops of 6M NaOH to the copper-amino acid complex solution to balance the pH of the solution. We carefully poured the solution into a 10.0mL volumetric flask and washed the beaker with 2mL distilled water, transferring the water into the flask. Concentrated ammonia was added to raise the liquid level to the mark on the volumetric flask. We sealed and shook the flask.

Generation of Standard Analysis Curve and Analysis of the Copper Complex: We added each of the prepared solutions to six separate labeled test-tube cuvetts. We zeroed out the Spectronic 20 Spectrometer using concentrated ammonia. We tested the absorbency of the six solutions with a wavelength of 600nm.

Results

Quantitative Determination of Solubility. Based on the trials of solubility performed, the solubility of the amino acid is 0.0429 g/mL. The amino acid was found to be insoluble in ethanol.

Density by Flotation. The density was found to be between 1.5839 g/mL and 1.5940 g/mL. The unknown was less dense than bromochloromethane and denser than chloroform. The unknown was suspended in carbon tetrachloride but floated in a mixture of carbon tetrachloride (1.0 mL) and chloroform (0.1 mL). A chart of amino acids with densities near the experimental value (1.5940 ± 0.1000 g/mL) was compiled containing 13 amino acids, which were further eliminated by comparing solubility and physical appearance, shrinking the list to 3.

Determination of Melting Point. A discoloration of the amino acid occurred at 235°C and bubbling occurred at 247°C. When the unknown was tested next to serine, both the unknown and serine were observed to discolor at 236°C and bubble at 239°C, which was quite different than 247°C originally observed.

Thin Layer Chromatography. Using 30/70 concentrated NH_3 /n-propanol, the R_f value for the unknown was 0.34, while serine's R_f value was 0.35; the mixture of both serine and the unknown had a value of 0.33. Using the 50/50 water/n-propanol mixture as a mobile phase, the unknown's R_f value was calculated to be 0.78; serine's in this solution was 0.74 and the mixture was 0.74. By having both serine and the unknown side-by-side, we were able to conclude that the unknown was serine. Although the given values for the R_f in the table of common amino acids was 0.28 for the 30/70 mixture, testing serine as well as the unknown allowed us to use the experimental data instead of given data for proof. (See Figure 3.)

UV-Visible Spectroscopy. Using the UV-Visible spectrum, it was concluded that the unknown amino acid absorbs light at wavelengths of less than 190 nm, which the spectrometer is unable to scan. (See Figure 4.)

Infrared Spectroscopy. Using infrared spectroscopy, a fingerprint of the unknown is found. The spectrometer measures vibration energy between atoms in the molecule. Using the results of the test, the unknown amino acid is serine. The broad range from 2000-3500 cm^{-1} is from N-H bonds and other bonds involving H^+ and electronegative ions, while 1400-1600 cm^{-1} has energy from C=O bonds. The fingerprint of the amino acid occurs from 500-1400 cm^{-1} . (See Figure 5.)

NMR Spectroscopy. The NMR spectrum should have four spikes on it; one for the reference compound, one for the solvent, H_2O , and two main signals from the amino acid. The hydrogen atoms bonded to an electronegative atom will end up creating a signal with the H_2O , leaving only C-H and H-C-H to create signals. The H-C-H has two hydrogen atoms

bonded to a carbon and therefore the strength of the absorption should be twice as large, which is seen in the spectrum. (See Figure 6.)

Titration. After performing numerous titrations of 0.1000M KHP and NaOH of an unknown molarity, the molarity of NaOH was found to be 0.0791M. Using this standardized NaOH, the molarity of HCL was found to be 0.0995M.

Synthesis of Copper Complex. The percent yield of the synthesis of a serine copper complex was 5.43%. This was due to difficulties in completing the lab, including a faulty vacuum apparatus, an inability to filter the solution a second time, a lack of adequate time to complete the experiment forcing the solid to be left to dry on filter paper for a week, and difficulties in transferring the solid into a 1-dram vial.

Copper Complex Properties. Density, melting point, and UV-visible and IR spectra were measured. The color of the copper-amino complex was found to be purple-blue.

Density: The density of the copper-amino acid complex was measured to be between 1.8323 g/mL and 1.8663 g/mL. The copper-amino acid complex was found to sink in a 0.300mL carbon tetrachloride and 0.700mL bromochloromethane while the complex floated in 0.200mL carbon tetrachloride and 0.800mL bromochloromethane.

Melting Point: The copper-amino acid complex began to change color at 191.5°C and completely changed color at 200.0°C. Bubbling was observed at 201.0°C.

IR Spectrum: The absorptions of the copper-amino acid complex (see Figure 10) were higher than that of the amino acid (see Figure 5). Also, at 1600cm⁻¹, the copper-amino acid complex absorbed the wavelengths, while the amino acid did not, resulting from the Cu-ser bond.

UV-Visible Spectrum: The copper-amino acid complex (0.01M) absorbed light with a wavelength of 622nm. This is due to the copper absorbing blue light, giving copper solutions their blue color. (See Figure 9.)

Determination of Stoichiometry of Copper Complex Using Job's Method. From the data collected using the Spectronic 20 Spectrometer, the stoichiometry of Cu(C₂H₃O₂)₂·H₂O to serine is 1:2, which agrees with the group's guess. This was determined by finding the greatest absorbency at a specified wavelength (550nm). Cu²⁺ ions bond with the amino acid's carboxyl group, which when in solution loses its H atom, becoming -COO⁻. (See Figure 11.)

Spectrometric Analysis of Copper. The purpose of spectrometric analysis was to determine the amount of copper present in the copper-amino acid complex. We were not able to determine the amount of copper present in the copper-amino acid complex using the curve. This was because if we used the graph with the molarity of Cu²⁺ in the solution that was calculated, the absorption does not fit the curve. However, if the absorption value for the copper-amino acid solution was used to determine molarity based on the standard curve, the molarity found was less than zero, although very close to zero (-6.079*10⁻⁵M), which is not possible for a solute in solution.

Summary

During C-Term 2005, we have learned various techniques to identify an unknown substance, which provided us with a background required for jobs within the chemistry field. In doing so, we successfully identified an unknown amino acid given to us at the start of the term. We also learned how to be more precise in observations and conclusions. We concluded as a group that the unknown amino acid (#40) was serine, which has an R-group of HOCH₂-. We then went further in discovering many properties of the amino acid that were not provided to us.

The most important experiment done to identify the amino acid was the infrared spectroscopy experiment; all molecules have a unique fingerprint which is easily found by performing this experiment. Thin layer chromatography was also helpful in identifying the amino acid. Many of the experiments performed in the lab were helpful in collecting background data for the amino acid serine which can be used in later labs.

In experiments that we performed with both the unknown amino acid and the copper-amino acid complex, we were able to explain key differences, such as extra absorptions in the infrared and UV-visible spectra.

This table contains characteristics of unknown amino acid #40 compared to serine values experimentally found in the laboratory.

	Unknown	Serine
Solubility (g/mL)	0.0429	0.05
Density (g/mL)	1.59	1.60
Melting Point (°C)	236	236
R _f in 30/70 NH ₃ /n-prop	0.34	0.35

Discussion

A purpose of this lab was to understand how dynamic equilibrium is tied into lab experiments. In connection with dynamic equilibrium and solubility, solute dissolved in a solvent experiences equilibrium of solute particles coming in and out of solution. Full solubility occurs when the rate into solution is equal to the rate out of solution. Titration measures dynamic equilibrium of an acid and a base using pH, a measure of the concentration of hydronium ions in a solution. The equivalence point of a titration curve (Figures 7,8) is the point at which the concentration of H₃O⁺ ions equals that of OH⁻, forming the most product possible by the reaction. By finding the amount of OH⁻ added at the equivalence point, it is possible to find the pK_a by finding the pH at the half-equivalence point, when half the total amount of OH⁻ needed to equal the amount of H₃O⁺ is present in the solution. The pH at this point is equal to the pK_a, which then can be used to find the K_a of the amino acid solution. By using the formula $K_{eq} = K_a(\text{reactant acid})/K_a(\text{product acid})$, and knowing that the acid present as a product is H₂O with a K_a value of $1 \cdot 10^{-14}$, the K_{eq} value can be solved for.

In the formation of a copper-amino acid complex, there is equilibrium between reactants (Cu²⁺ and AA⁻) and its product (Cu(AA)₂). Based on data collected in the lab, the K_{eq} value of this reaction favors the reactants, providing very little product to work with in later experiments. The copper-amino acid complex was soluble in distilled water, as the copper-amino acid complex did not precipitate out of solution; therefore the solution was slowly

added to acetone, a solvent which the complex was insoluble in, which allowed the complex to precipitate.

Using Job's method of determining a reaction's stoichiometric ratio, there needs to be an equal amount of reactants in the correct stoichiometric ratio to produce the most product. By finding the amount of absorbance of the product at a certain wavelength, a graph can be produced. When there is the most absorbance on the graph (a relative maximum), the greatest amount of product is produced; therefore the reactants in solution have been used as much as possible. It is not possible to say that all the reactants were used because there is no way to determine the equilibrium constant, not allowing speculation about relative amounts of any substance in the solution. (See Figure 11.)

References

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2. "Serine." Columbia Encyclopedia, Sixth Edition, Copyright (c) 2005. <http://encyclopedia.com/html/s1/serine.asp>
3. "Serine." <http://en.wikipedia.org/wiki/Serine>

Data Tables

Table 1: Quantitative Determination of Solubility

	Trial 1	Trial 2
Weight Before (g)	8.1042	8.0379
Weight After (g)	8.0613	7.9716
Amino Acid Used (g)	0.0429	0.0663
Amount of Water (mL)	1.00	1.00
Solubility (g/mL)	0.0429	0.0663

Table 2: Density by Flotation

Chloroform (g/mL)	1.4832
1.0mL CCl ₄ + 0.1mL Chloroform (g/mL)	1.5839
CCl ₄ (g/mL)	1.5940
CH ₂ BrCl (g/mL)	1.9344

Table 3: Thin Layer Chromatography

	30/70	50/50	30/70
	Trial 1	Trial 1	Trial 2
Mobile Phase Length (cm)	4.00	3.90	3.90
Unknown Movement (cm)	1.35	3.05	1.30
R _f Unknown	0.3375	0.7821	0.3333
Serine Movement (cm)	1.40	2.90	1.35
R _f Serine	0.3500	0.7436	0.3462
Mixture Movement (cm)	1.30	2.90	1.30
R _f Mixture	0.3250	0.7436	0.3333

Table 4: UV-Visible Spectroscopy

Weight Before (g)	7.9146
Weight After (g)	7.9033
Amino Acid Used (g)	0.0113
Amount of Water (mL)	10.00
Molarity (M)	1.0753×10^{-2}
Dilution	0.2
Molarity (M)	2.1505×10^{-3}

Table 5: Standardization of Solutions

mL KHP Used	mL NaOH Added	mL HCl Used	mL NaOH Added
5.00	6.32	5.00	6.28
5.00	6.40	5.00	2.29
5.00	6.30	5.00	6.29
6.00	7.09		
5.00	6.25		
5.00	6.35		

Table 6: Titration of Unknown Amino Acid

NaOH Added (mL)	pH Trial 1	pH Trial 2	NaOH Added (mL)	pH Trial 1	pH Trial 2	NaOH Added (mL)	pH Trial 1	pH Trial 2
0.00	2.25	2.22	6.20	4.72	4.19			
0.50	2.29	2.29	6.30	6.64	5.09	11.40	9.61	
1.00	2.33	2.33	6.40	7.34	6.00	11.50		9.46
1.50	2.39	2.39	6.50	7.63	6.57	11.60	9.68	
2.00	2.44	2.46	6.60	7.80	7.12	11.80	9.75	
2.50	2.51	2.52	6.70	7.93	7.49	12.00	9.84	9.60
3.00	2.58	2.60	6.80	8.04	7.71	12.20	9.93	9.65
3.50	2.66	2.68	6.90	8.11	7.86	12.40	10.02	9.72
4.00	2.75	2.77	7.00	8.19	7.97	12.60	10.15	9.78
4.50	2.87	2.88	7.50	8.45	8.32	12.80	10.26	9.85
5.00	3.03	3.02	8.00	8.64	8.54	13.00	10.37	9.92
5.10		3.06	8.50	8.79	8.71	13.20	10.48	10.00
5.20		3.11	9.00	8.93	8.85	13.40	10.58	10.07
5.30		3.14	9.50	9.05	8.98	13.60	10.67	10.15
5.40		3.20	10.00	9.19	9.10	13.80	10.74	10.24
5.50	3.26	3.25	10.50	9.32	9.21	14.00	10.82	10.33
5.60	3.32	3.31	10.60	9.35		14.20	10.89	
5.70	3.40	3.39	10.70	9.39		14.40	10.94	
5.80	3.49	3.46	10.80	9.43		14.60	10.99	
5.90	3.61	3.56	10.90	9.45		14.80	11.02	
6.00	3.77	3.70	11.00	9.48	9.34	15.00	11.05	
6.10	4.03	3.88	11.20	9.55				

Table 7: Density of Copper-Amino Acid Complex

1.00mL CCl ₄ (g/mL)	1.5940
1.00mL CH ₂ Br ₂ (g/mL)	2.4970
1.00mL CH ₂ BrCl (g/mL)	1.9344
.50mL CCl ₄ + .50mL CH ₂ BrCl (g/mL)	1.7642
.40mL CCl ₄ + .60mL CH ₂ BrCl (g/mL)	1.7982
.30mL CCl ₄ + .70mL CH ₂ BrCl (g/mL)	1.8323
.20mL CCl ₄ + .80mL CH ₂ BrCl (g/mL)	1.8663

Table 8: Stoichiometry of Copper Complex Using Job's Method

Trial #	mL 0.1M Cu (C ₂ H ₃ O ₂) ₂ ·H ₂ O Added (A)	mL 0.10M Serine Added (B)	mL H ₂ O Added	[B]/[A]	UV-vis Spectrum at 550nm
1	0	0.9	3.1	---	0.009
2	0.1	0.8	3.1	8.0000	0.063
3	0.2	0.7	3.1	3.5000	0.095
4	0.3	0.6	3.1	2.0000	0.125
5	0.4	0.5	3.1	1.2500	0.115
6	0.5	0.4	3.1	0.8000	0.088
7	0.6	0.3	3.1	0.5000	0.077
8	0.7	0.2	3.1	0.2857	0.055
9	0.8	0.1	3.1	0.1250	0.045
10	0.9	0	3.1	0.0000	0.025

Table 9: Spectrometric Analysis of Copper

Solution #	mL 0.05M Stock	M Cu ²⁺	Absorbtion at 600nm
1	0.5	0.005	0.289
2	1.0	0.010	0.560
3	1.5	0.015	0.835
4	2.0	0.020	1.090
5	2.5	0.025	1.340
Complex		0.009	0.030

Figures

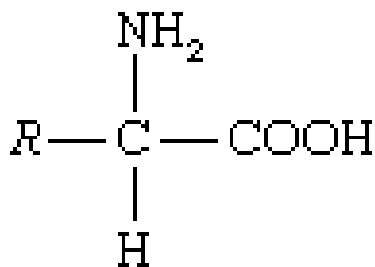


Figure 1. The basic structure of an amino acid, containing the amino group (-NH₂), the carboxyl group (-COOH), and the R-group. (1)

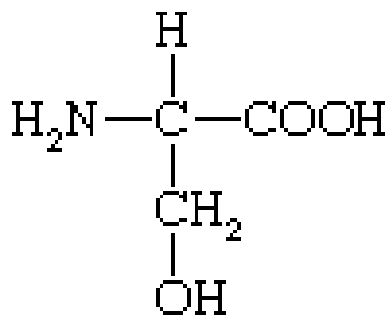


Figure 2. The structure of serine, containing an R-group CH₂OH. (1)



Figure 3. From left to right: Ethanol ink TLC plate, dichloromethane ink TLC plate, 50/50 ethanol/dichloromethane ink TLC plate, 30/70 ammonia/n-propanol TLC plate with amino acid, 50/50 water/n-propanol TLC plate with amino acid. On the amino acid TLC plates, from left to right: Unknown, serine, 50/50 unknown/serine.

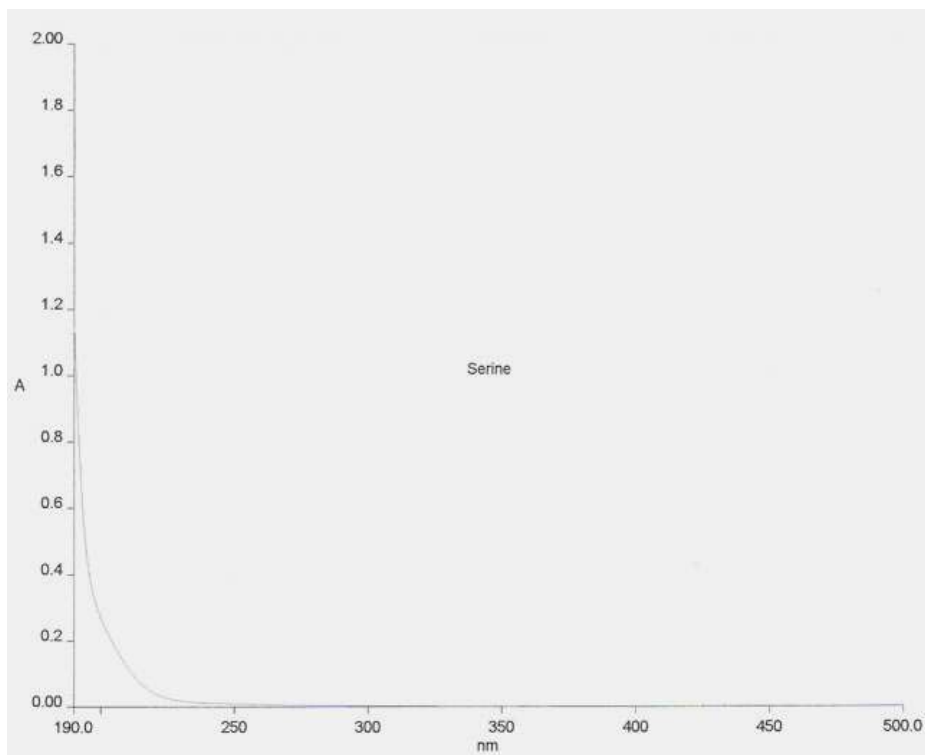


Figure 4. The UV-Visible spectrum of the unknown amino acid.

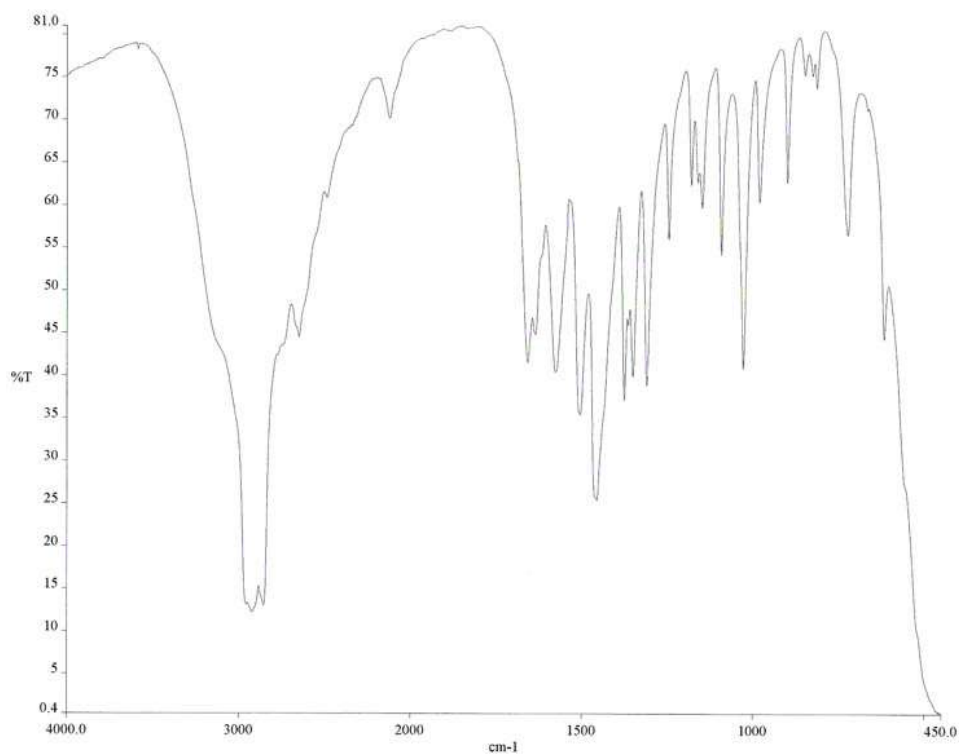


Figure 5. The IR spectrum of the unknown amino acid.

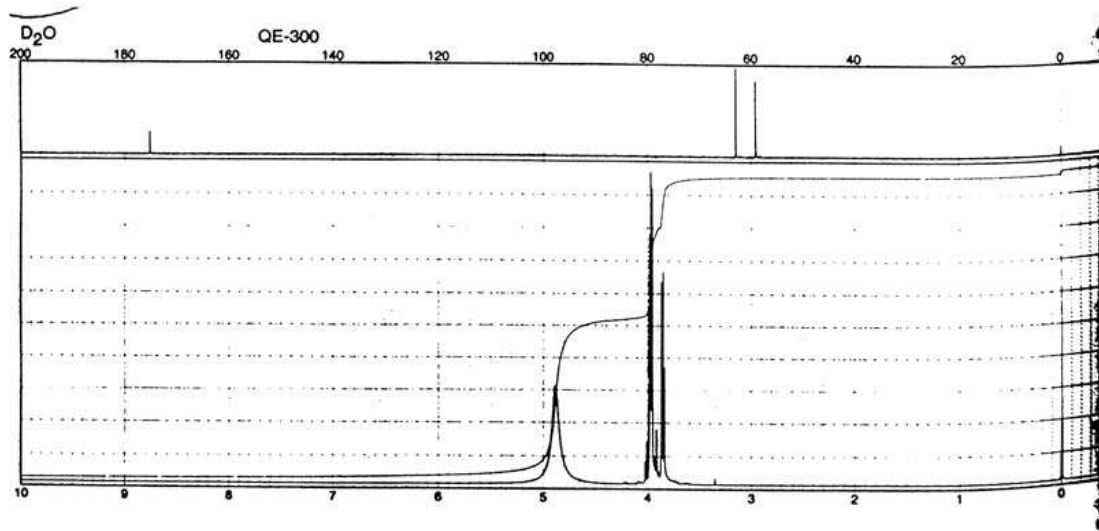


Figure 6. The NMR spectrum of the unknown amino acid.

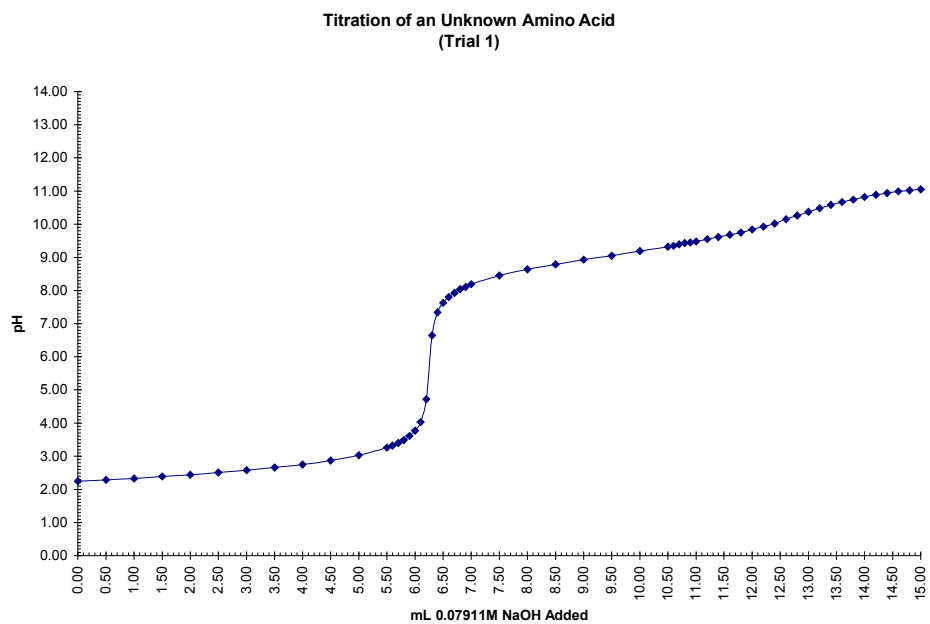


Figure 7. Titration of an Unknown Amino Acid (Trial 1).

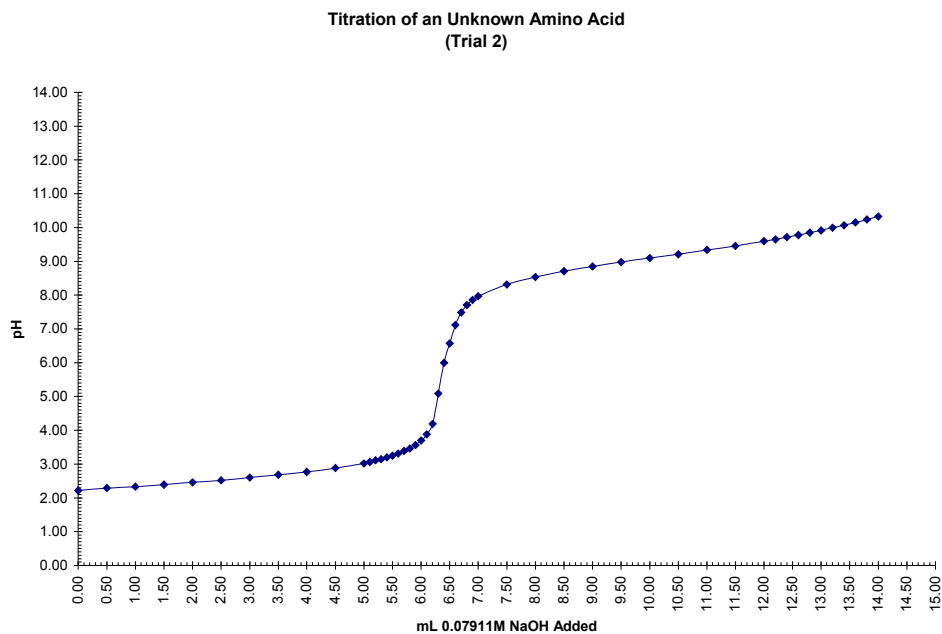


Figure 8. Titration of an Unknown Amino Acid (Trial 2).

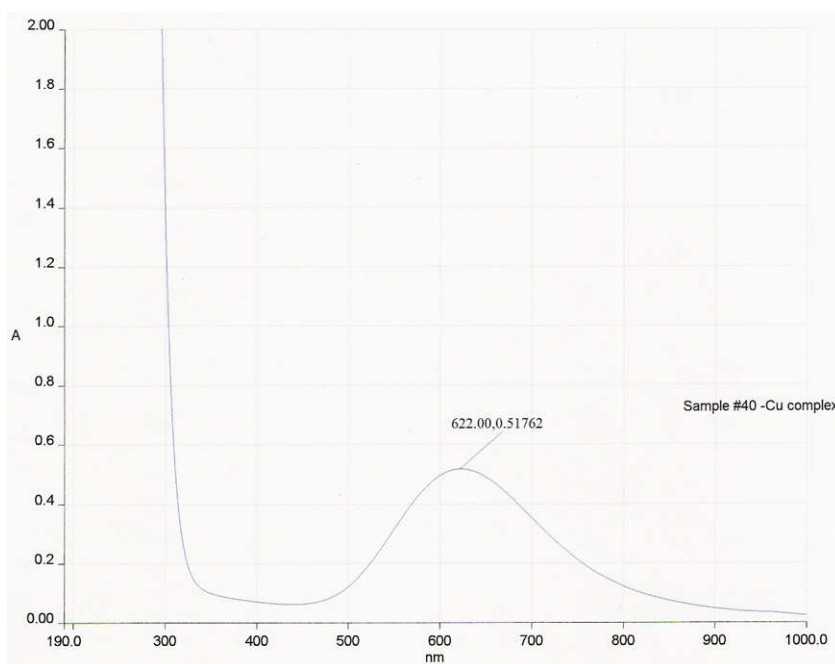


Figure 9. The UV-Visible spectrum of our amino acid copper complex, $\text{Cu}(\text{ser})_2$.

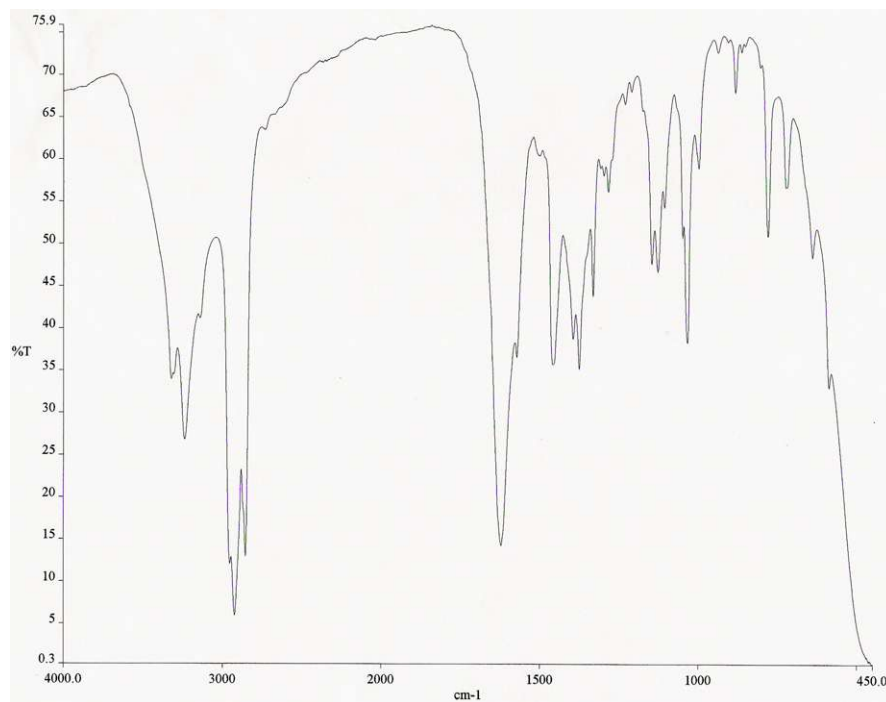


Figure 10. The IR spectrum of our amino acid copper complex, $\text{Cu}(\text{ser})_2$.

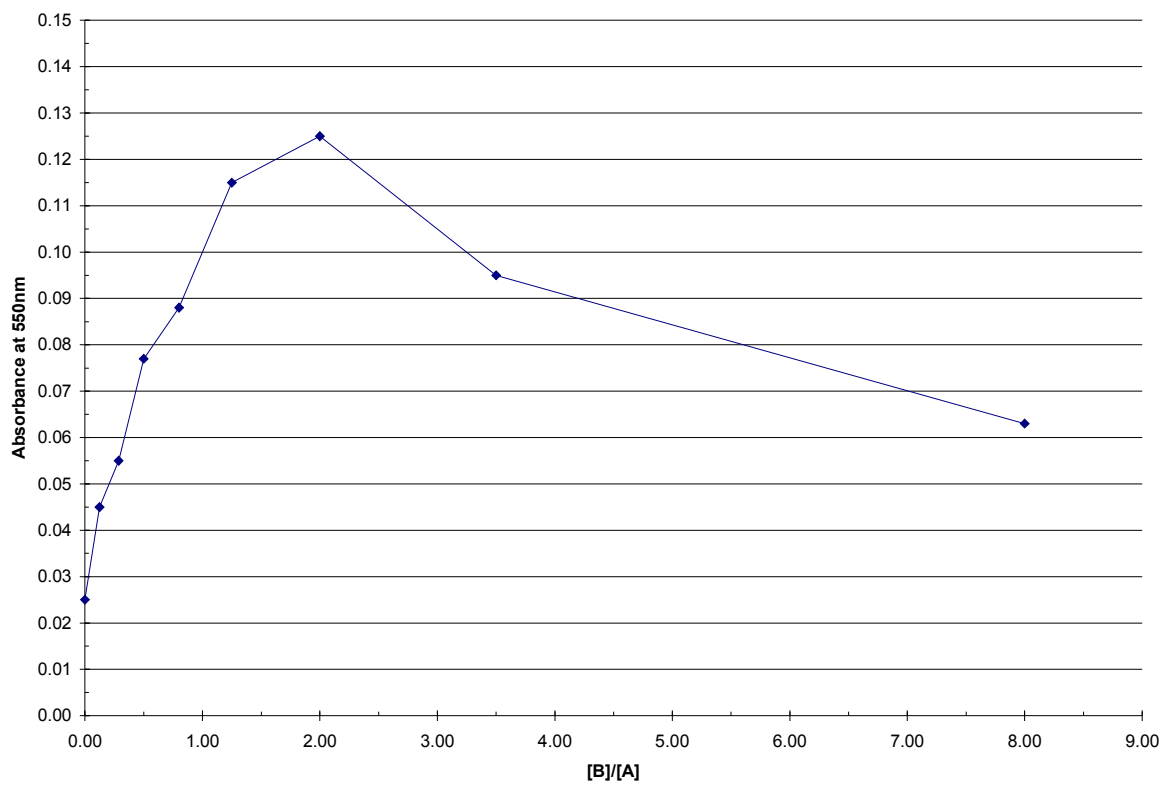


Figure 11. Determination of Stoichiometry using Job's Method

Spectrometric Analysis of Copper

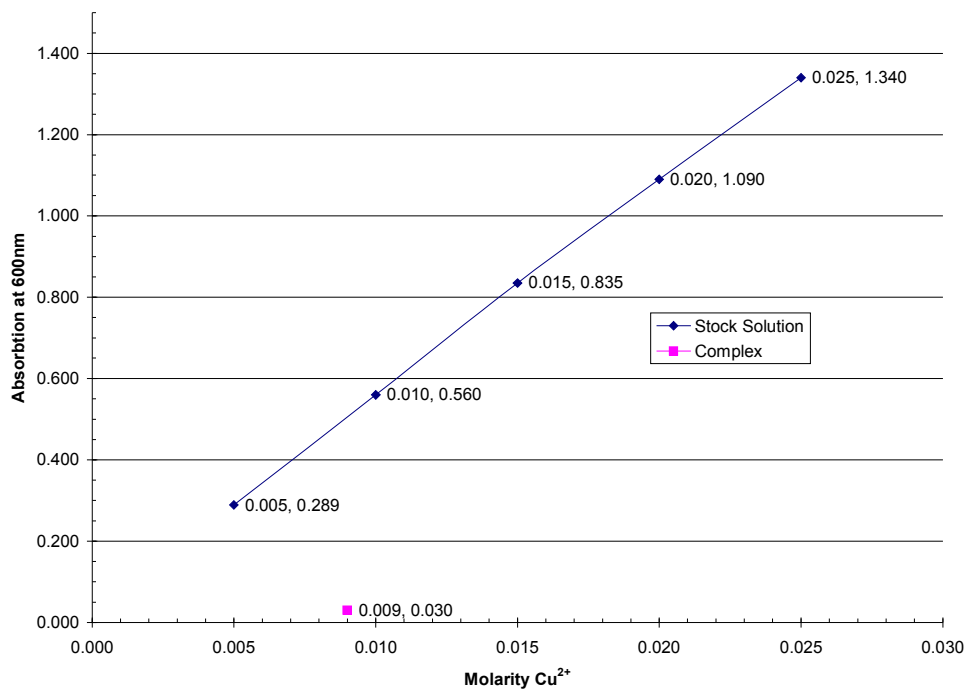


Figure 11. Spectrometric Analysis of Copper and Copper-Amino Acid Complex.