



**Abgent Biotin Single-Shot
Antibody Labeling Kit**

(Cat. #KT1001a)

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I. Introduction

a. Product Description

The Abgent Biotin Single-Shot antibody labeling kit is specifically designed to biotinylate a single 100 microgram quantity of antibody resuspended in 100 μ l of buffer. The kit comes complete with all the necessary components to label and rapidly quantify biotin incorporation from a small quantity of antibody in about 90 minutes.

The labeling process is based on a patented UV-traceable linker, Sulfo-ChromaLink™ Biotin (Figure 1). This advanced protein biotinylation reagent contains an aromatic water-soluble N-hydroxy-sulfosuccinimidyl ester functional group **(a)**, which efficiently modifies protein lysine residues in a mild aqueous phosphate buffer system. The linker also possesses an embedded bis-aryl hydrazone structure **(b)**, which forms the compound's UV-traceable chromophore. This UV-traceable absorbance signature enables the non-destructive and sensitive quantification of biotin **(c)**, attached to the antibody. All these diverse chemical elements are then linked together through a long-chain PEG3 spacer **(d)**, which preserves streptavidin/biotin affinity while simultaneously enhancing antibody solubility.

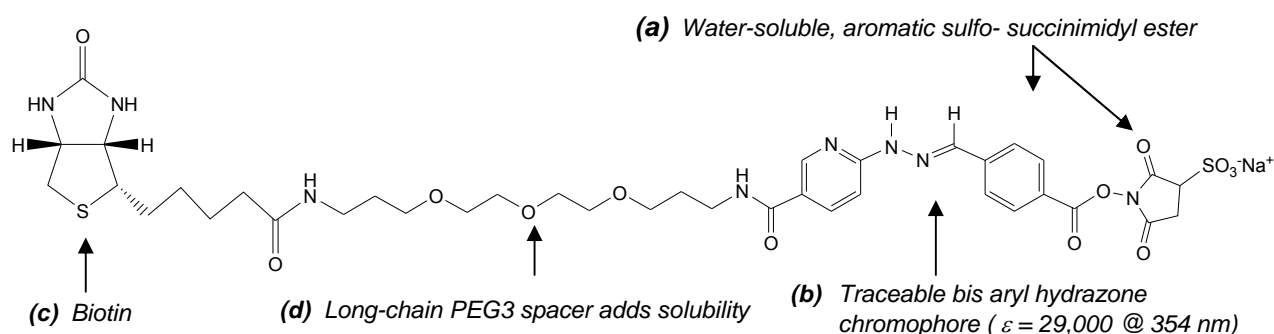


Figure 1. Structure of Sulfo-ChromaLink Biotin ($C_{38}H_{49}N_8NaO_{13}S_2$) (M.W. 912.96)

b. Benefits and Features

The Abgent Biotin Single-Shot kit is a convenient, cost-effective way of biotinylating a small quantity (100 μ g) of an antibody. Post-labeling biotin incorporation is rapidly quantified using a non-destructive UV-scan (220-400nm). The kit features high antibody recovery (70-80%) with consistent biotin incorporation. The degree of incorporation or molar substitution ratio (MSR) will generally range from 3-8 biotins per antibody when used as directed.

The kit can be used to label a diverse group of antibodies including all mammalian IgG, IgE, and avian IgY molecules. Abgent's Single-Shot kit offers a robust method of both labeling and quantifying biotin incorporation using small quantity of antibody. This "double-feature" now provides researchers with greater confidence, consistency and reproducibility in all downstream applications.

c. Procedure Overview

The Abgent Biotin Single-Shot antibody labeling procedure is illustrated in Figure 2.

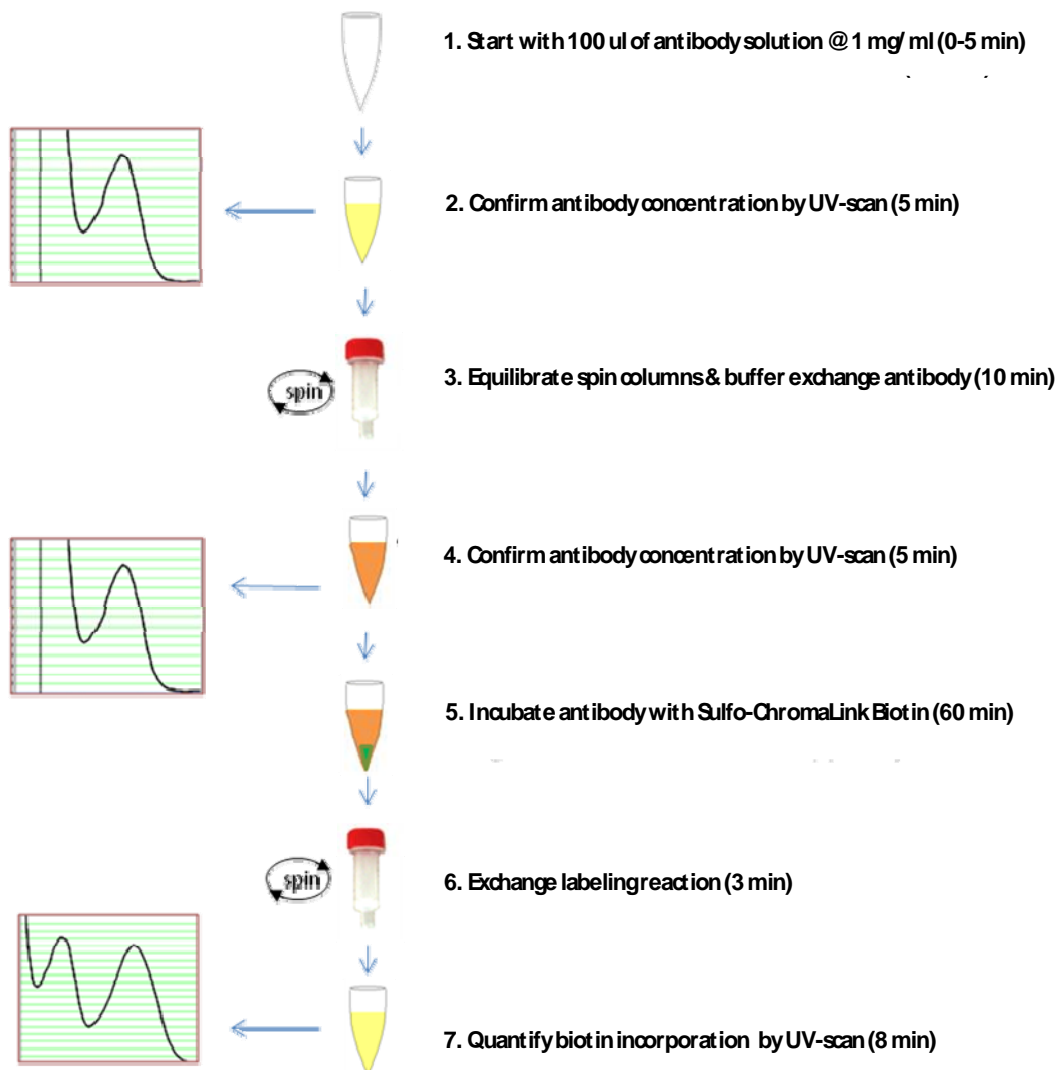


Figure 2. Abgent Biotin Single-Shot antibody labeling procedure.

d. Process Summary

1. *Sample Preparation:* adjust antibody to 1mg/ml in 100µl buffer
2. *Sample Analysis:* confirm antibody concentration using a spectrophotometer
3. *First Buffer Exchange:* equilibrate spin columns & buffer exchange antibody
4. *Sample Analysis:* reconfirm antibody concentration using a spectrophotometer
5. *Biotinylation:* label antibody with Sulfo-ChromaLink™ Biotin linker
6. *Second Buffer Exchange:* remove excess labeling reagent
7. *Biotin Incorporation:* quantify incorporation using a spectrophotometer

e. Important Labeling Parameters

The Abgent Biotin Single-Shot antibody labeling kit is specifically designed to biotinylate a single 100 microgram quantity of antibody resuspended in 100µl of a suitable buffer as indicated in Table 1.

Initial Antibody Concentration	Initial Mass of Antibody	Initial Antibody Volume
1.0 ± 0.1 mg/ml	100 ± 10 µg	100 µl

Table 1. Initial starting conditions required for the Abgent Biotin Single-Shot procedure.

The kit provides consistent and reliable biotinylation by controlling the following reaction variables:

- Initial antibody mass (100µg) and volume (100µl)
- Reaction buffer composition
- Reaction time (60min)
- Reaction stoichiometry (12x equivalents)

Critical to labeling success is the ability to accurately determine a sample's protein concentration in a non-destructive manner. The Single-Shot procedure employs a spectral scan (220-400nm) rather than a single wavelength measurement @ 280nm to accomplish this task. Commercial antibodies often contain preservatives or other additives that can mask or distort the intrinsic UV spectrum of a sample. As a consequence, additives often make it more difficult to **accurately** estimate protein concentration using a single wavelength (i.e. A280) measurement. A scan provides greater assurance that a sample's concentration is correct since a spectrum often reveals the tell-tale presence of A280 altering additives. Commonly used additives may include preservatives such as sodium azide, thimerosal, protein stabilizers such as BSA or gelatin, or small molecule additives such as glycine and trehalose. If a commercial antibody sample contains any of these additives, please refer to the Trouble-shooting Guide in the Appendix to determine which materials might interfere with the labeling procedure.

f. Materials Provided and Storage Conditions

Components	Size/Quantity	Storage Conditions
Sulfo-ChromaLink™ Biotin	8.0 µg /1	room temp
1x Modification Buffer (pH 7.4)	1.5 ml /1	room temp
1x PBS (pH 7.2)	1.5 ml /1	room temp
Collection tubes	1.5 ml /4	room temp
Zeba™ Spin Columns	0.5 ml /2	room temp
Biotinylated IgG Control	100 µg /1	room temp
1M Tris·HCL (pH 8.9)	100 µl /1	room temp

g. Additional Materials Required But Not Provided

UV-VIS Scanning or NanoDrop™ Spectrophotometer
 Semi-micro quartz cuvette (50-100µl capacity) (not required w/NanoDrop™)
 Variable speed microcentrifuge (e.g. Eppendorf 5415D, IEC MicroMax or similar)
 Standard 1.5ml microfuge tubes, molecular grade water
 Pipettes and tips for P-10, P-200, P-1000 (e.g. Rainin, Eppendorf or equivalent)

II. Abgent Biotin Single-Shot Antibody Labeling Protocol

a. Sample Preparation (0-5min)

Antibodies are packaged in a variety of different physical forms including solids and liquids. Individual antibody samples vary greatly from vendor to vendor and are often sold in a variety of different sizes (e.g. 0.05–1mg) or concentrations (e.g. mg/ml). Proceed as follows to prepare your sample.

Sample (Solid Form)

Initial Sample: 100 µg/vial (e.g. lyophilized solid)

Resuspend the sample in 100µl 1X Modification Buffer (pH 7.4) to yield a 1 ± 0.1 mg/ml solution and proceed directly to the Sample Analysis section (II-b).

Initial Sample: > 120 µg/vial (e.g. lyophilized solid)

Resuspend the sample in a sufficient volume of 1X Modification buffer (pH 7.4) to yield a 1 mg/ml solution. Transfer a 100µl volume to a new 1.5ml microfuge tube and refrigerate the unused portion of the sample. Proceed directly to the Sample Analysis section (II-b).

Initial Sample: < 90 µg/vial (e.g. lyophilized solid)

We do not recommend using the Abgent Biotin Single-Shot labeling kit to label sample quantities less than 90µg. Obtain additional material before proceeding to the Sample Analysis section (II-b).

Sample (Liquid Form)

Initial Sample: 1 mg/ml (e.g. liquid form)

If the antibody sample is already in liquid form @ 1 mg/ml (100µl) in a suitable buffer (e.g. PBS or TBS), proceed directly to the Sample Analysis section (II-b).

Initial Sample: > 1 mg/ml (e.g. liquid form)

Adjust the antibody concentration by diluting an aliquot to 1mg/ml and 100ul with 1X Modification buffer (pH 7.4). Transfer this volume (100µl) to a new 1.5ml microfuge tube and refrigerate the unused portion of the concentrated sample. Proceed directly to the Sample Analysis section (II-b).

Initial Sample: < 1 mg/ml (e.g. Liquid form)

Concentrate the antibody sample to 1mg/ml and 100µl before proceeding to the Sample Analysis section (II-b). Numerous commercial diafiltration spin filters are available for this purpose (Millipore-Amicon), Sartorius-VivaSpin). **Note**-a minimum volume equivalent to 100ug of total antibody is required.

b. Sample Analysis (5-10min)

After the sample is adjusted to 100µl and 1mg/ml, it is ready to be scanned on either a UV-VIS or NanoDrop™ spectrophotometer. A scan is used to confirm and validate sample concentration. Scan the sample as directed below for the corresponding instrument (UV-VIS or NanoDrop™ spectrophotometer). **Important**-Never attempt to label antibody samples

containing protein-based carriers such as BSA or gelatin. A small volume (50-100 μ l) quartz micro-cuvette (1-cm path length) is required when using a UV-VIS spectrophotometer.

b1. UV-VIS Spectrophotometer

1. Program the spectrophotometer to scan from 220-400nm.
2. Using a clean semi-micro quartz cuvette, blank the instrument using the appropriate sample buffer (e.g. PBS or 1x Modification buffer).
3. Discard the blank solution.
4. Transfer the antibody sample (100 μ l @ 1mg/ml) to the cuvette and scan.
5. Recover the sample from the cuvette by placing it into a clean 1.5ml microfuge tube.
6. Calculate the initial antibody concentration as illustrated for the example below.

Example: Bovine IgG (100 μ l @ 1mg/ml)

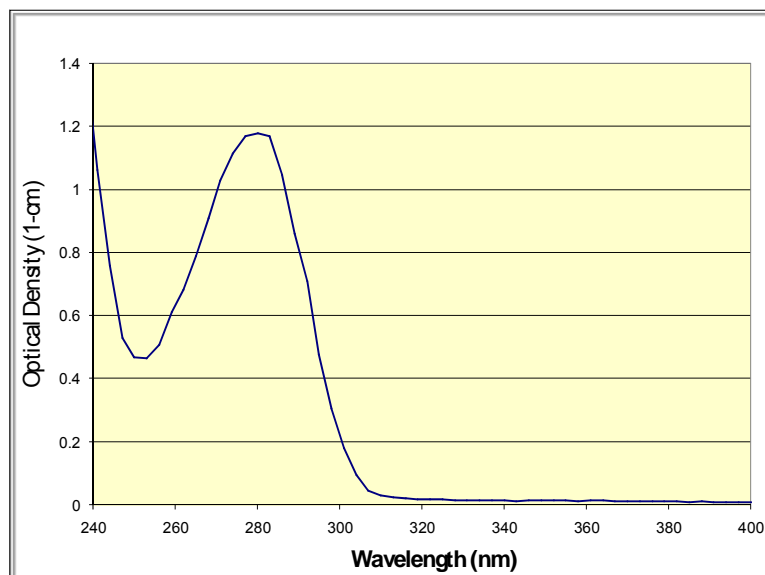


Figure 3. Scan of bovine IgG 100 μ l @ 1mg/ml in 1x Modification buffer (100mM sodium phosphate, 150mM NaCl, pH 7.4) using a quartz semi-micro cuvette (50-100 μ l).

Sample Calculation

Equation #1: $[A_{280} / *E_{1\%}] \times 10\text{mg/ml} = \text{protein concentration (mg/ml)}$

*E1% (antibody extinction coefficient, see Table 2)

Antibody Source	Antibody E1% (1-cm path)
Human IgG	13.60
Human IgE	15.30
Rabbit IgG	13.50
Donkey IgG	15.00
Horse IgG	15.00
Mouse IgG	14.00
Rat IgG	14.00
Bovine IgG	12.40
Goat IgG	13.60
Avian IgY	12.76

Table 2. Antibody extinction coefficients (E1%) used to calculate antibody concentration. The E1% is the A280 of a 10 mg/ml solution using a 1-cm path length.

Sample: Bovine IgG 100 μ l @ 1 mg/ml
 A280 (from scan in Figure 3) = 1.18
 Antibody E1% (Table 2) = 12.40

$$[A280 / E1\% \text{ bovine IgG}] \times 10 \text{ mg/ml} = \text{protein concentration (mg/ml)}$$

$$[1.18 / 12.40] \times 10 \text{ mg/ml} = 0.95 \text{ mg/ml}$$

- After calculating a sample's concentration, adjust it to 1 ± 0.1 mg/ml and 100 μ l by addition of 1x Modification buffer (if necessary).
- Once the sample's concentration is @ 1 ± 0.1 mg/ml and 100 μ l, proceed directly to the buffer exchange procedure (section II-c).

Note-sample volume is important because the sample mass represented should be as close as possible to 100 μ g. The accuracy of this mass is critical to maintaining the ratio of labeling reagent to antibody. The volume should also be as close as possible to 100 μ l (e.g. ± 5 μ l) for optimal results. **Important**-if a sample's spectrum does not appear similar to the example provided in Figure 3 or if the spectrum appears altered, distorted, or contains a large baseline offset error, please refer to the Troubleshooting Guide found in the Appendix. A proper antibody spectrum is required to confirm protein concentration.

b2. NanoDrop™ Spectrophotometer

- Turn on the NanoDrop™ spectrophotometer and click on the NanoDrop™ icon to launch the software.
- Place a 2 μ l drop of molecular grade water on the clean pedestal, click OK.

3. When the main menu appears, select the A280 menu option. **Note**-do not use the UV-VIS menu option on the NanoDrop™ to read the sample.
 4. After the A280 menu appears, **click-off the 340nm normalization option** using the mouse.
 5. In the window labeled Sample Type, select 'Other protein E1%' option from the pull-down menu. Enter the appropriate E1% value (from Table 2) corresponding to your particular antibody sample type. For example, 14.00 for mouse IgG.
 6. Blank the NanoDrop™ spectrophotometer by placing a 2µl drop of the appropriate sample buffer (e.g. PBS or 1x Modification) and with the mouse click on the 'Blank' icon.
 7. Immediately re-click the 'Measure' icon to validate a flat baseline. Clean the pedestal and repeat (if necessary) until a flat baseline is obtained.
- Note**-sometimes air bubbles can become trapped on the pedestal during pipetting and cause baseline offsets. Remove air bubbles and rescan to insure a proper baseline.
8. Transfer a 2µl volume of antibody solution @ 1mg/ml to the pedestal, with the mouse click in the 'Measure' icon. Wait until the spectrum (220-350nm) appears in the window.
 9. Record the antibody concentration directly from the NanoDrop™ display window [mg/ml]. Alternately, calculate the antibody concentration (manually) as illustrated for the following example.

Example: Mouse IgG (100 µl @ 1 mg/ml)

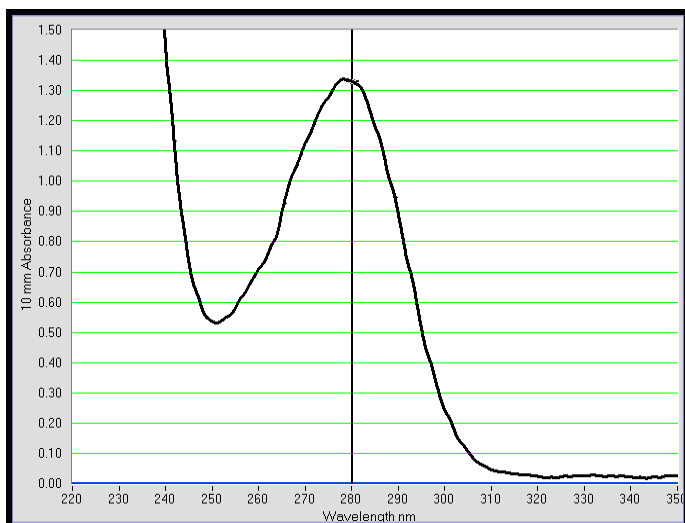


Figure 4. Mouse IgG 100µl @ 1mg/ml in 1x modification buffer (100mM sodium phosphate, 150mM NaCl, pH 7.4) scanned on a NanoDrop™ (220-350nm).

Sample Calculation

Equation #1: $[A_{280} / *E_{1\%} \text{ value}] \times 10 \text{ mg/ml} = \text{protein concentration (mg/ml)}$

*E1% (antibody extinction coefficient, see Table 2)

Sample: Mouse IgG @ 1mg/ml

A_{280} (from scan in Figure 3) = 1.34

Antibody E1% value (Table 2) = 14.00

$[A_{280} / E_{1\%} \text{ bovine IgG}] \times 10 \text{ mg/ml} = \text{protein concentration (mg/ml)}$

$[1.34 / 14.00] \times 10 \text{ mg/ml} = 0.96 \text{ mg/ml}$

10. After calculating the sample's concentration, adjust it to $1 \pm 0.1 \text{ mg/ml}$ and $100 \mu\text{l}$ by small additions of 1x Modification buffer (if necessary). Proceed directly to the buffer exchange procedure section (II-c).

Note-sample volume is important because the sample mass represented should be as close as possible to $100 \mu\text{g}$. The accuracy of this mass is critical to maintaining the ratio of labeling reagent to antibody. The volume should also be as close as possible to $100 \mu\text{l}$ (e.g. $\pm 5 \mu\text{l}$) for optimal results. **Important**-if a sample's spectrum does not appear similar to the example provided in Figure 4 or if the spectrum appears altered, distorted, or contains a large baseline offset error, please refer to the Troubleshooting Guide found in the Appendix. A proper antibody spectrum is required to confirm protein concentration.

c. First Buffer Exchange Procedure (10min)

After adjusting the sample to $1 \pm 0.1 \text{ mg/ml}$ and $100 \mu\text{l}$, buffer exchange the antibody with the following procedure.

1. Prepare the two spin columns provided by twisting off the bottom closures and loosening the red caps (do not remove caps).
2. Place each spin column into separate 1.5 ml microcentrifuge collection tubes (provided).
3. Place the spin columns opposite each other in the microcentrifuge and spin @ $1,500 \times g$ for 1 minute to remove the storage solution from the resin. After centrifugation the column matrix will appear dry and white in color.
4. Remove the columns from the centrifuge and discard the solutions from the bottom of the collection tubes. **Note**-do not discard the collection tube.
5. Using a marker pen, place a mark on the side of each spin column where the compacted resin is slanted upward.
6. Using the same marker pen, mark one cap with the letter **A** and the other spin column cap **B**.
7. Add $300 \mu\text{l}$ 1x Modification buffer (pH 7.4) to the top of the resin bed labeled **A** and $300 \mu\text{l}$ 1x PBS to the top of the resin bed labeled **B**. Loosely recap the lids. **Note**-when loading the buffer or sample, do not disturb the resin bed with the pipette tip.

8. Place the spin columns back into their used collection tubes, centrifuge at 1,500 x g for 1 minute to remove the buffer. **Important**-always orient the spin column with the pen mark aiming outward and away from the center of the rotor.
9. Repeat steps 7 and 8 two additional times, discarding the flow-through buffer each time.
10. After this last spin, transfer the now equilibrated spin column labeled **A** into a new 1.5ml collection tube (provided). **Note**-do not transfer the spin column labeled **B** into a new 1.5ml collection tube at this time.
11. Buffer exchange the antibody sample (100µl @ 1mg/ml) by loading the contents to the top of the equilibrated spin column labeled **A**.
12. Add 100µl 1x PBS buffer to the top of the equilibrated spin column labeled **B**. Recap the lid loosely. **Note**-this column will serve as a balance tube.
13. Centrifuge the columns @ **1500 x g for 2 minutes** to collect the eluate at the bottom of the collection tubes.
14. Remove the spin column/collection tube assembly labeled **A** containing the antibody sample from the centrifuge and set aside. **Important**-Do not discard the eluate!
15. Now remove the spin column/collection tube assembly labeled **B** from the centrifuge and discard the bottom eluate. Add an additional 300ul 1x PBS to the top of the resin bed to rehydrate and set this **B** assembly aside for later use.
Note-the 300ul 1xPBS keeps the resin hydrated for later use.

d. Sample Analysis (5min)

1. Using a spectrophotometer or NanoDrop™ scan the buffer exchanged antibody sample from the bottom of the collection tube **A** to confirm the amount of recovered antibody. Refer to the previous Sample Analysis section (IIb-1 or IIb-2) to calculate the recovered antibody concentration.
2. If the recovered antibody concentration is confirmed to be @ **1 ± 0.2mg/ml** in a volume of 100 ± 5ul, proceed directly to the biotinylation procedure below (II-e).

Note-a small loss of antibody mass is sometimes seen after buffer exchange. This loss is generally ~10% or less.

Note-If the antibody concentration at this juncture is higher than the required range (e.g. 1±0.2mg/ml), adjust the sample to 100µl and 1mg/ml with additional 1x modification buffer before proceeding. If the antibody concentration is less than 1 ± 0.2mg/ml, do not attempt to label the sample. Refer to the Trouble Shooting Guide in the Appendix.

e. Biotinylation Procedure (60min)

1. Transfer the antibody solution from the bottom of the collection tube labeled **A** (100µl @ 1mg/ml) directly to a vial of Sulfo-ChromaLink™ Biotin labeling reagent (vial with yellow cap). Do not discard the collection tube.

2. Mix the solution thoroughly by pipetting the solution up and down ~10 times, vortex for a few seconds. Briefly centrifuge the contents of the tube (e.g. 5 seconds) to collect the entire reaction mixture at the bottom of the tube.
3. Allow the reaction to proceed for 60min at room temperature.
4. After the reaction is complete, quench the reaction by addition of 10ul 1M Tris (pH 8.9), mix well. Set this reaction aside. **Important**-do not skip addition of 1M Tris.
5. Place the previously set aside (hydrated with 300ul 1x PBS) spin column assembly labeled **B** into the centrifuge. Loosely recap the lid and properly orient in the centrifuge.
6. Now add 300ul molecular grade water to the spin column labeled **A**, and place the properly oriented assembly opposite **B** in the centrifuge. **Note**-The **A** assembly now serves as the balance tube.
7. Centrifuge at 1,500 x g for 1 minute. Discard the flow through from each spin column assembly.
8. Transfer (only) the spin column labeled **B** to a new 1.5ml collection tube (provided). Proceed immediately to the second buffer exchange procedure (see below).

f. Second Buffer Exchange Procedure (3min)

1. Add the entire contents of the quenched biotinylation reaction to the center of the compacted resin of the spin column labeled **B**. Recap the column loosely.
2. Apply 100µl of 1x Modification buffer to the center of the spin column labeled **A**. Recap loosely. **Note**-once again this column's purpose at this stage is to serve as a balance tube.
3. Orient the columns in the microcentrifuge and spin at 1,500 x g for **2 minutes**. **Note**-approximately 100µl will be recovered at the bottom of each collection tube.
4. Transfer the biotinylated antibody from the bottom of the collection tube labeled **B** to a new 1.5ml microfuge tube. Proceed to determine biotin incorporation as directed below.

g. Determining Biotin Incorporation (10 min)

Biotin incorporation is determined by scanning the final biotinylated antibody sample on either a UV-VIS or NanoDrop™ spectrophotometer. Proceed as directed below for the corresponding instrument.

g1. UV-VIS Spectrophotometer

1. Program the spectrophotometer to scan from 220-400nm.
2. Using a clean semi-micro quartz cuvette (50-100µl), blank the instrument with 1x PBS buffer.
3. Discard the blank solution.
4. Transfer the biotinylated antibody sample to the cuvette and scan.
5. Record the A280 and A354 from the spectrum.

6. Recover the biotinylated sample from the cuvette by transferring the solution back to a clean 1.5ml microfuge tube. Label the sample and store refrigerated.
7. Input the A280 and A354 values along with the corresponding E1% into the Biotin MSR calculator (located on the flash drive) to automatically calculate the biotin molar substitution ratio (MSR). **Note**-typical MSR values generally range from 3-8 biotins per antibody. The amount of biotinylated antibody (mass) recovered can range from 50 to 100µg depending on the exact starting mass and type of antibody being labeled.

g2. NanoDrop™ Spectrophotometer

1. Turn on the NanoDrop™ spectrophotometer and click on the NanoDrop™ icon to launch the software.
2. Place a 2µl drop of molecular grade water on the clean pedestal, click 'OK'.
3. When the main menu appears, select the A280 menu option. **Note**-do not use the UV-VIS menu option on the NanoDrop™ to read the sample.
4. After the A280 menu appears, **click-off the 340nm normalization** option using the mouse.
5. In the window labeled Sample Type, select 'Other protein E1%' option from the pull-down menu. Enter the appropriate E1% value (from Table 2) corresponding to your particular antibody sample type.
6. Blank the NanoDrop™ spectrophotometer by placing a 2µl drop of 1x PBS on the pedestal and using the mouse click 'Blank'.
7. Re-click the 'Measure' icon to validate that the baseline is flat and near zero. Clean the pedestal and repeat the procedure if necessary until a flat baseline is observed.
8. Transfer a 2µl volume of the antibody solution @ 1mg/ml to the pedestal, and click 'Measure'. Wait until the spectrum (220-350nm) appears in the window.
9. Record the absorbance @ 280nm from the λ absorbance window.
10. Record the absorbance @ 354nm by typing the numeric value '354' into the λ window.
11. Input the A280 and A354 and the corresponding E1% value into the Biotin MSR calculator (located on the flash drive) to automatically calculate the biotin molar substitution ratio (MSR). **Note**-typical MSR values range from 3-8 biotins per antibody. The amount of biotinylated antibody (mass) recovered can range from 50 to 100µg depending on the exact starting mass and type of antibody being labeled.

III. Biotinylating Antibodies: Some Examples

Single-Shot Biotinylation of Goat Anti-Mouse IgG (Example 1)

A goat anti-mouse IgG (100µg lyophilized solid) was dissolved in 100µl 1x Modification buffer (100mM sodium phosphate, 150 mM NaCl, pH 7.4) to yield a 1mg/ml solution. The sample was scanned using a NanoDrop™ spectrophotometer (Figure 5). The shape of the spectrum appears ideal with a flat baseline at 350nm. The initial concentration was calculated to be 0.93mg/ml (E1% value of 13.60). After the 1st spin column buffer exchange the sample was scanned to yield a 0.87mg/ml solution (Figure 6). The sample was then labeled with Sulfo-ChromaLink Biotin reagent for 60 minutes, quenched and excess reagent removed with a

second spin column (1x PBS). The labeled sample was then rescanned (220-350nm) as shown in Figure 7. The calculated molar substitution ratio was 7.0 with 62 μ g of recovered antibody.

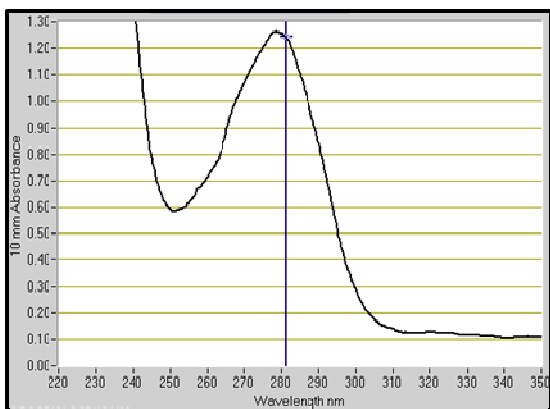


Figure 5. Antibody before buffer exchange

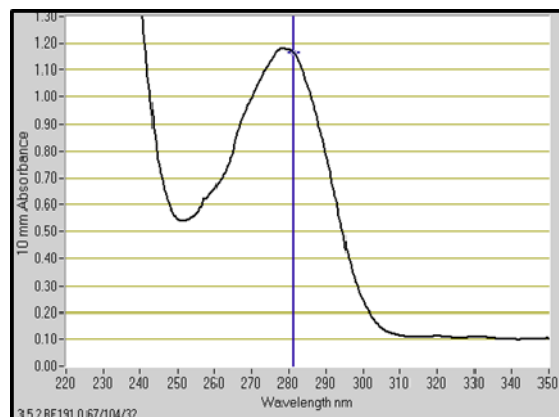


Figure 6. Antibody after buffer exchange

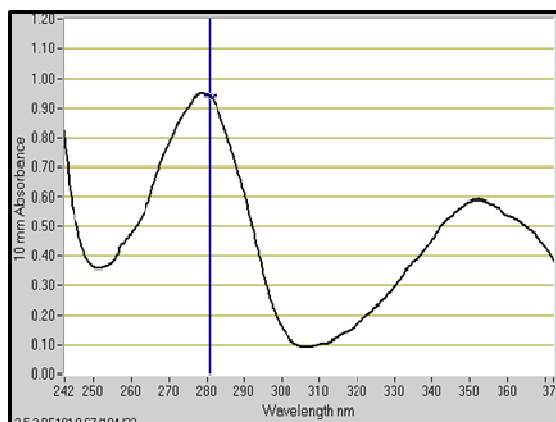


Figure 7. Antibody after biotinylation

Single-Shot Biotinylation of *Rat Anti-Mouse IgG (Example 2)*

A commercial rat anti-mouse IgG₁ (500 μ g lyophilized solid) was dissolved in 500 μ l PBS to obtain a 1mg/ml solution. An aliquot (2 μ l) of the sample was scanned on a NanoDropTM spectrophotometer (Figure 8). The shape of the spectrum appeared ideal with a flat baseline at 350nm. The initial concentration was determined to be 0.80mg/ml (E1% value of 14.00). After the 1st spin column the sample was rescanned to yield a sample concentration of 0.99mg/ml solution (Figure 9). The sample was then labeled with Sulfo-ChromaLink Biotin reagent for 60 minutes, quenched and excess reagent removed with a second spin column (1x PBS). The labeled sample was then rescanned (220-350nm) as shown in Figure 10. The calculated molar substitution ratio was 6.4 with 89 μ g of recovered antibody.

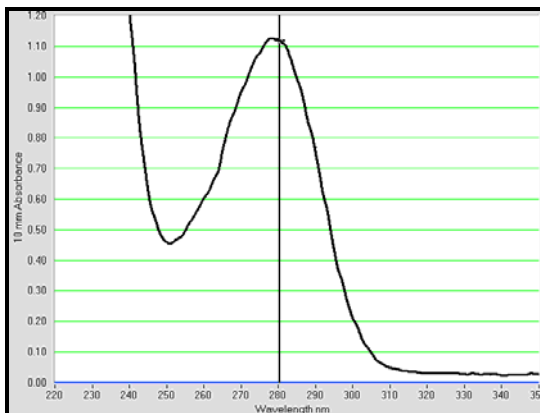


Figure 8. Antibody before buffer exchange

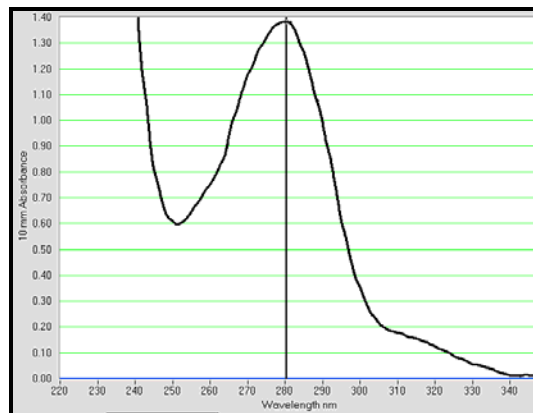


Figure 9. Antibody after buffer exchange

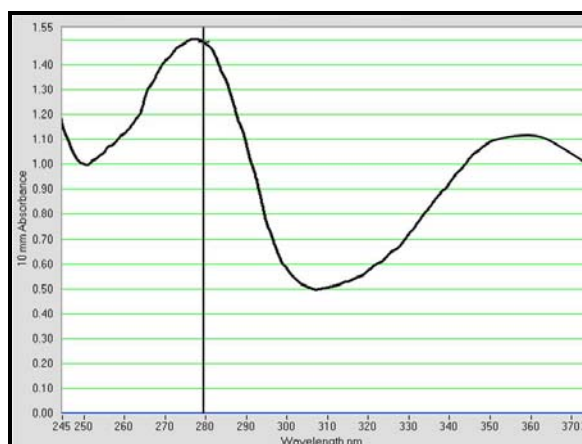


Figure 10. Antibody after biotinylation

Single-Shot Biotinylation of *Rabbit anti-Bovine IgG₁* (Example 3)

A commercial rabbit anti-bovine IgG₁ @ 1mg/ml in 100 μ l PBS was scanned using a NanoDropTM spectrophotometer to confirm the initial protein concentration (scan not shown). After the 1st spin column the concentration was determined to be 0.95mg/ml (E1% value of 13.5) Figure 11. The sample was then labeled with Sulfo-ChromaLink Biotin reagent for 60 minutes, quenched and excess reagent removed with a second spin column (1x PBS). The labeled sample was then rescanned (220-350nm) as shown in Figure 12. The final biotinylated rabbit IgG sample had a calculated molar substitution ratio of 6.6 with 82 μ g of recovered antibody.

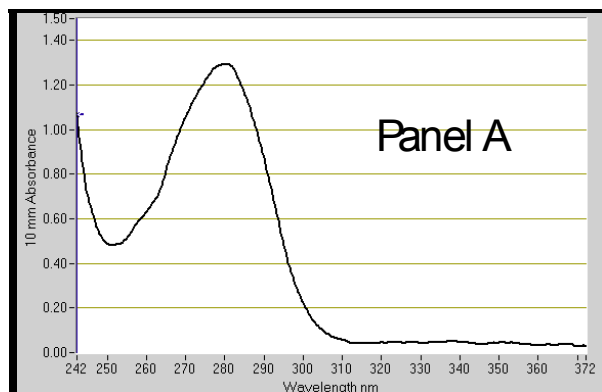


Figure 11. Antibody after buffer exchange

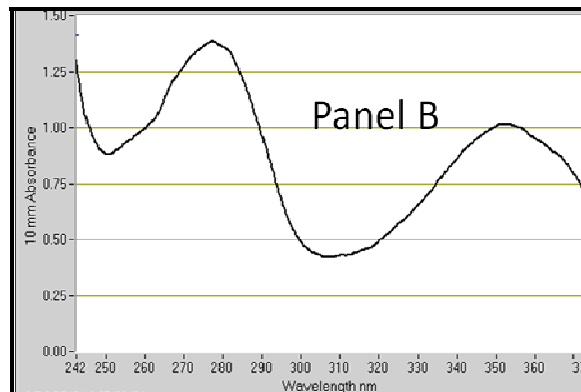


Figure 12. Antibody after biotinylation

IV. Appendix

a. Biotinylated IgG Control

The Abgent Biotin Single-Shot Antibody Labeling Kit comes complete with a biotinylated antibody control. This control consists of a lyophilized biotinylated bovine IgG at a precisely known biotin molar substitution ratio (refer to the lot specific product data sheet on the flash drive). This control is used to validate the accuracy of a given spectrophotometer and to practice MSR calculations. To use the control proceed as follows:

1. In a semi-micro quartz cuvette (50-100 μ l) record a “blank” buffer spectrum using 1x modification buffer (220-400nm). Discard the blank buffer solution from the cuvette.

Note-when using the NanoDrop™ refer to instructions on page 9.

2. Resuspend the control (lyophilized solid, 100 μ g) using 100 μ l molecular grade water @ 1 mg/ml.
3. Scan the biotinylated antibody.
4. Record the A280 and A354 values generated from the spectrum.
5. Input these values along with an E1% (12.40) and M.W. (e.g. 150kD) into the Biotin MSR Calculator located on the flash drive to determine the biotin molar substitution ratio.
6. Confirm the value obtained with the lot specific MSR found on the product data sheet.

b. HABA Assay vs. ChromaLink™ Spectrophotometric Assay (CSA)

Comparisons between the HABA assay (2-4'-hydroxyazobenzene-2-carboxylic acid dye-binding assay) and the ChromaLink™ spectrophotometric assay (CSA) are summarized in Table 3. These results reveal significant differences between the two biotin assays.

For example, the biotin molar substitution ratio using the HABA dye-binding assay is generally 1/3 the value obtained using the ChromaLink method. As seen in the table,

ChromaLink Biotin (mole-equivalents)	Biotin/IgG HABA	Biotin/IgG A ₃₅₄
5X	1.03	2.45
10X	1.60	4.71
15X	2.22	6.25

Table 3. Comparison of HABA and ChromaLink assays for determination of biotin molar substitution ratios (MSRs). Bovine IgG samples were biotinylated at different reaction equivalents and results tabulated.

the HABA dye-binding assay generally underestimates the true biotin molar substitution ratio because that assay measures the number of moles of biotin available for binding to streptavidin and not the absolute number of biotin molecules attached to the antibody surface. For example, two biotin molecules in proximity to each other are likely only to bind to one streptavidin molecule.

Additionally, the ChromaLink assay is a non-destructive assay whereas the HABA assay is destructive. HABA consumes a minimum of 75 micrograms of biotinylated antibody per assay whereas the ChromaLink method requires as little as 25µg and the labeled sample is fully recoverable. Finally, the HABA assay requires an external spectrophotometric calibration curve whereas the ChromaLink method requires no such external calibration and measures incorporation directly from the sample's spectrum.

c. Troubleshooting Guide

This section of the manual is intended to be used as a technical troubleshooting guide. Most of the problems associated with labeling antibodies using the Single-Shot procedure arise from inaccuracies in measuring initial antibody concentration. For this reason, the Single-Shot protocol employs a scan (220-400nm) to estimate antibody concentration rather than a single wavelength measurement @ 280nm. A scan provides greater assurance that a sample's concentration is correct since a spectrum often reveals the tell-tale presence of A280 altering additives. Spectrum altering effects of preservatives and other additives can be revealed from a sample's spectrum but not from a single A280 measurement. Distortions to an antibody's intrinsic spectrum or other spectral aberrations such as baseline offset errors create inaccuracies when estimating antibody concentration. Errors of this type are likely to lead to poor labeling results because the Single-Shot protocol requires precise control of the stoichiometry between antibody mass and labeling reagent (Sulfo-ChromaLink Biotin). Spectral errors are often associated with antibody preparations containing additives or preservatives. However, other factors can affect the accuracy of a sample's measured concentration when using a spectrophotometer including:

- Antibody sample contains preservatives (e.g. sodium azide, or thimerosal)
- Antibody sample contains protein-based additives (e.g. BSA or gelatin)
- Antibody sample contains an unknown concentration of some additive
- Antibody (protein) is degraded during storage
- Buffer blank is unknown or cannot be reproduced (baseline offset errors)
- Antibody sample was under-filled by vendor
- Antibody sample was over-filled by vendor
- Improperly calibrated spectrophotometer

In the examples that follow, we provide various spectra for reference and comparison purposes. These are intended to aid the troubleshooting process. Suggested corrective actions are also included for each type of sample spectrum problem.

Example #1: High purity mouse IgG (lyophilized solid, no additives or preservatives)

A commercial mouse IgG (100 μ g solid) was resuspended in 100 μ l 1x modification buffer @ 1 mg/ml solution and the sample scanned as illustrated in Figure 13. This sample was free of all preservatives, protein-stabilizers, and any other interfering additives. Note the ideal shape of the spectrum confirming both purity and concentration of this 'ideal' sample.

Corrective action: None. The theoretically expected A280 value for this mouse IgG is 1.35 vs. the experimentally measured value of 1.34 (see Table 4). The measured value is well within the acceptable labeling range (1 \pm 0.1mg/ml).

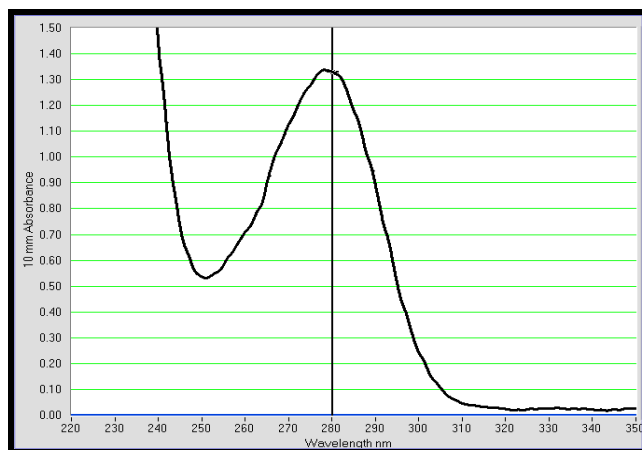


Figure 13. UV-spectrum (220-350nm) of a highly purified mouse IgG antibody @ 1mg/ml without any additives or preservatives. Note the uniform shape and flat baseline @ 350nm.

Antibody Source	Antibody A280 (1-cm path)
Human IgG	1.36 ± 0.136
Human IgE	1.53 ± 0.153
Rabbit IgG	1.35 ± 0.135
Donkey IgG	1.50 ± 0.150
Horse IgG	1.50 ± 0.150
Mouse IgG	1.40 ± 0.140
Rat IgG	1.40 ± 0.140
Bovine IgG	1.24 ± 0.124
Goat IgG	1.36 ± 0.136
Avian IgY	1.27 ± 0.127

Table 4. Expected A280 value of a 1 ± 0.1 mg/ml (1-cm path length) solutions for various types of antibodies.

Example #2: Bovine IgG containing sodium azide preservative

The presence of sodium azide @ 0.05 or 0.1% in a sample of bovine IgG @ 0.9mg/ml is illustrated in Figure 14. The presence of this additive primarily alters the shape of the antibody's spectrum. As seen in the figure, the presence of this additive does not alter the measurement of the sample's true protein concentration. However, this is not always the case at high or unknown concentrations of additive. Uncertainties in the concentration of this additive may sometimes lead to large baseline offset errors when blanking the spectrophotometer making it difficult to estimate protein concentration.

Corrective action: None if sample spectra are similar to those in Figure 14. These samples contain no significant baseline offset errors or other spectral distortions other than attenuation of the spectrum's valley and a general shift from 250 to 260nm.

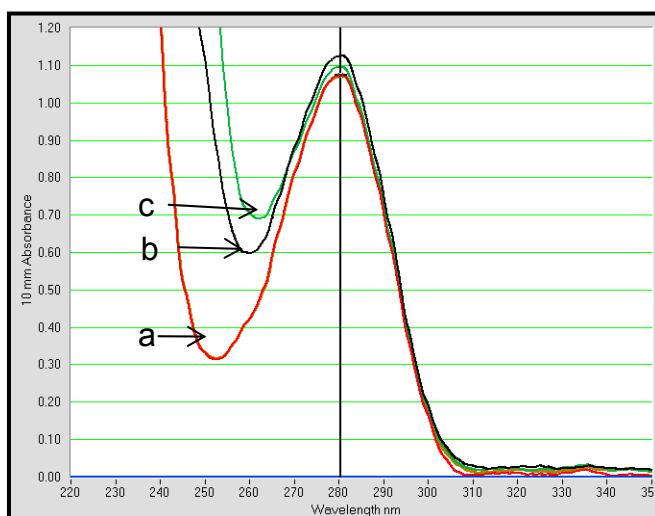


Figure 14. Superimposed spectra of purified bovine IgG @ 0.90mg/ml with a) no sodium azide, b) spiked with 0.05% sodium azide, or c) spiked with 0.1% sodium azide.

Example #3: Rat IgG containing an unknown concentration of sodium azide.

Sometimes antibody samples contain high or unknown amounts of sodium azide. If the quantity of azide is not precisely known it becomes difficult to properly blank a sample on the spectrophotometer. Unknown or high concentrations of this additive often contribute to large baseline offset errors that preclude accurate estimates of initial protein concentration. Two examples are illustrated in Figure 15.

Panel A illustrates the presence of high concentrations of sodium azide leading to both a positive baseline offset error and a distorted antibody spectrum. Panel B illustrates a severe negative baseline offset error caused by the presence of an unknown quantity of the preservative. Both examples make an accurate estimate of initial protein concentration impossible.

Corrective Action: In both Panel A and Panel B, we recommend passing each sample through the 1st spin column and rescanning to confirm antibody concentration. After the spin column exchanges the sample into 1x modification buffer, rescan the sample and recalculate the resultant protein concentration. If the resultant sample spectrum confirms a concentration of $1 \pm 0.1\text{mg/ml}$, proceed to the biotinylation procedure (II-e). If the sample contains significantly less or more than 1mg/ml than we recommend contacting the antibody vendor and requesting additional information on how product concentration was determined.

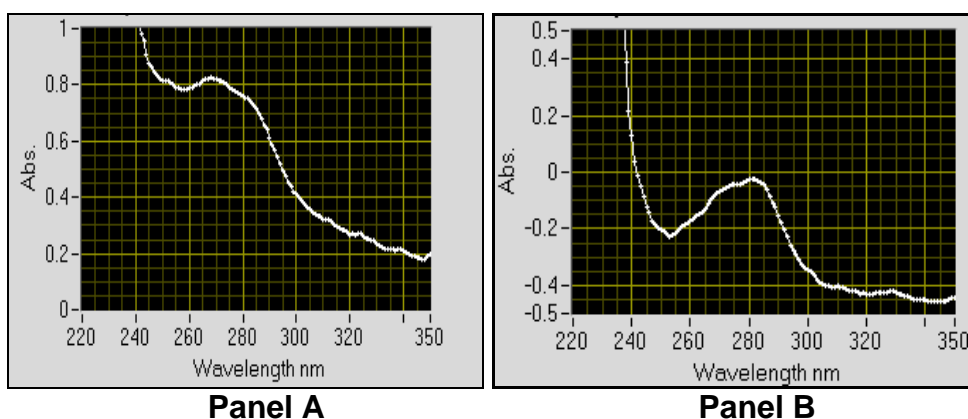


Figure 15. Two commercial rat monoclonal antibody preparations are illustrated in Panel A&B. The sample illustrated in Panel A contains a high concentration of sodium azide. The sample in Panel B contains an unknown quantity of sodium azide. Note the baseline offset errors and distortions to the spectra.

Example #4: Rabbit polyclonal IgG @ 1.0mg/ml (improper blank solution)

At times, a scan of a commercial antibody preparation can generate a large baseline offset error. These offset errors generally occur when an improper buffer solution is used to blank the spectrophotometer. Figure 16 is a scan of one such commercial preparation where the buffer blank could not be accurately matched. Although the spectrum may be normal in shape, it nonetheless contains a rather large 0.6 abs. unit offset @ 350nm. Acceptable offsets typically range from 0 to 0.1A units @ 350nm. As a consequence, the estimated protein concentration from such a preparation is significantly higher (1.4mg/ml) than the actual concentration (1.0mg/ml) based on A280. When using a NanoDrop™, offsets can also occur when air bubbles get trapped on the pedestal.

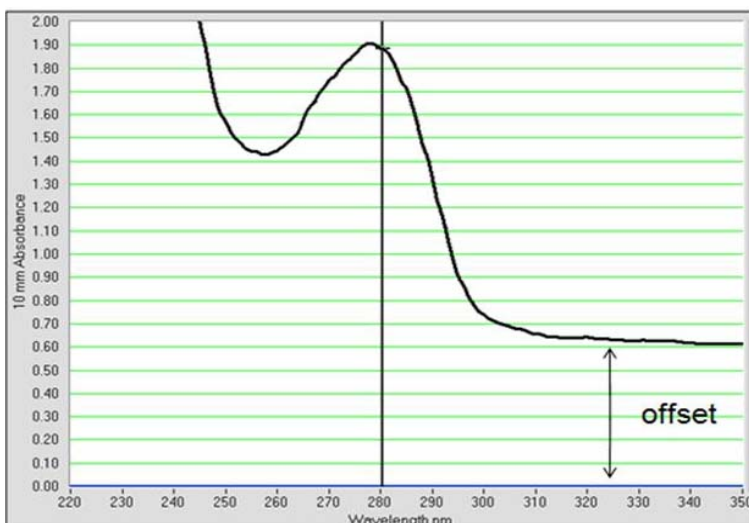


Figure 16. Baseline offset in a commercial rabbit polyclonal antibody preparation (5mg/ml) diluted to 1mg/ml in 1x modification buffer. Based on the A280 value the estimated concentration was 1.40mg/ml. The actual protein concentration after desalting the sample on a spin column to remove the buffer blank offset was 1mg/ml.

Corrective Action: For samples containing large baseline offset errors, we recommend passing the sample through the 1st spin column and rescanning to obtain a properly blanked sample spectrum. Since the spin column exchanges the antibody into a known buffer solution (1x modification buffer) it should readily remove any offset error originating from the buffer blank. After confirming sample concentration proceed to the biotinylation procedure (II-e). If after buffer exchange, it is determined that a sample contains significantly less or more than 1mg/ml than we recommend contacting the antibody vendor and requesting additional information on how protein and package concentration/quality was determined. Always adjust sample concentration to 1mg/ml and 100ul before proceeding.

Example #5: Bovine IgG containing Thimerosal preservative

A bovine IgG sample was spiked with thimerosal preservative as illustrated in Figure 17 (Panel A). In this example, thimerosal was introduced @ 0.01% into 100ul of highly purified bovine IgG sample @ 0.9mg/ml. Note the dramatic masking influence of this preservative over the intrinsic antibody spectrum. This preservative makes it impossible to properly blank a sample on the spectrophotometer. Small errors in this preservative's concentration create large baseline offset errors. A second thimerosal containing sample is illustrated in Panel B. This sample contains a commercial monoclonal IgG solution @ 1mg/ml in PBS with an undetermined quantity of thimerosal. Note the large masking effect and baseline offset error created by this preservative.

Corrective action: We recommend passing the sample through the 1st spin column, and rescanning to confirm concentration. If the resultant sample spectrum confirms a concentration of 1 ± 0.1 mg/ml, proceed to the biotinylation procedure (II-e). If the sample concentration is greater than 1 mg/ml, the sample must be adjusted with 1x modification buffer to 1mg/ml and 100ul before proceeding. If the sample contains significantly less or more than 1mg/ml than we recommend that you contact your antibody vendor and request additional information on how product concentration was determined.

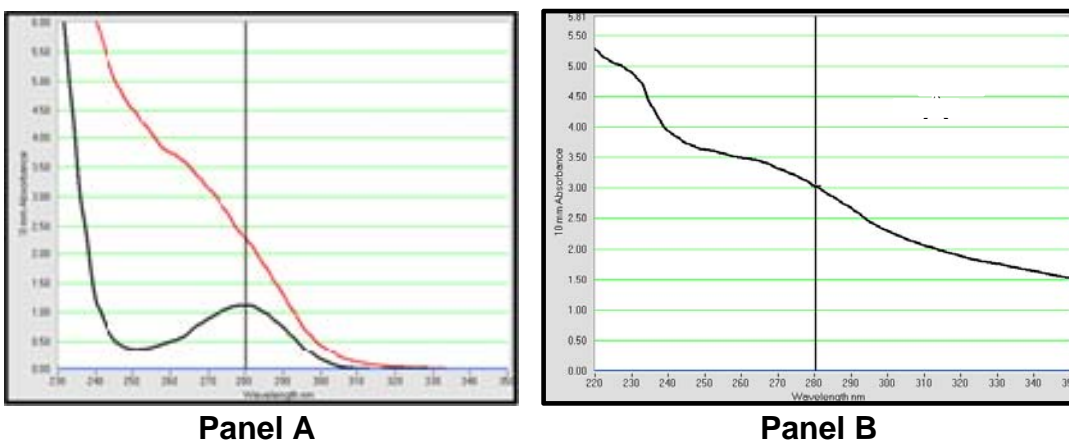


Figure 17. Superimposed spectra (Panel A) of purified bovine IgG @ 0.9 mg/ml spiked with a) no thimerosal or b) 0.01% Thimerosal. Note the masking effect of the preservative. Panel B is a commercial antibody preparation at 1 mg/ml with an unknown concentration of the preservative.

Example #6: Low Initial Antibody Concentration (Bovine IgG).

In rare cases, the amount of antibody packaged by the vendor may be lower than expected. Figure 18 illustrates an example of a commercial preparation of bovine IgG (100 μ g solid) that was dissolved in 100 μ l 1x Modification buffer. The sample spectrum indicated a concentration of 0.68mg/ml (A₂₈₀ = 0.84, E1% = 12.40) which is significantly less than the expected concentration (1mg/ml.).

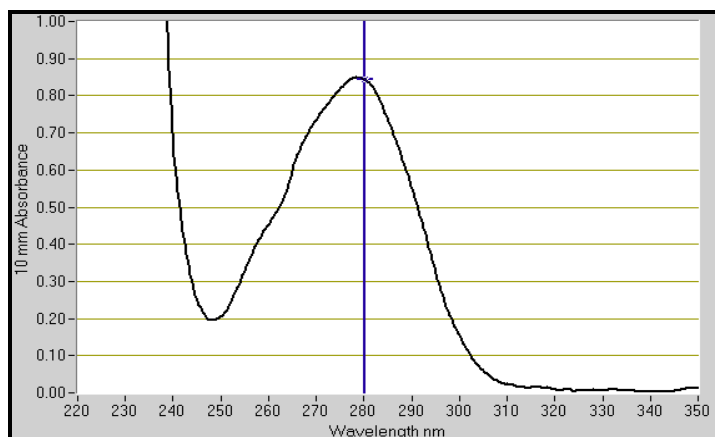


Figure 18. A commercial bovine IgG sample containing significantly less antibody (68 μ g) than expected from the original package label.

Corrective action: If a commercial antibody sample contains significantly less mass or concentration than expected, we recommend you contact the vendor and request additional product information. Do not attempt to label less than 80 μ g of buffer exchanged antibody using this procedure.

Example #7: Protein-Based Carriers or Additives (BSA or Gelatin)

The Abgent Biotin Single-Shot antibody labeling procedure is not compatible with the presence of protein-based carriers such as BSA or gelatin. Their presence is generally

detected when the A280 is much higher than anticipated while the sample retains its normal protein spectrum or profile.

Corrective Action: Contact the vendor to confirm the presence or absence of a protein additive. Do not attempt to label any product containing protein-based additives. Additives can be removed using affinity chromatography (e.g. Pierce's NAb™ Spin Columns) or other suitable methods. After affinity purification, insure that the final protein-free antibody is desalted to remove any excess glycine buffer used for elution of the antibody from the affinity column.

Example #8: Saccharide-based Carriers (5%Trehalose)

The Abgent Biotin Single-Shot antibody labeling procedure is fully compatible with the presence of 5% trehalose. This additive does not interfere in any way with either a sample's spectrum or its concentration.

Corrective Action: None. Proceed as directed in the procedure.

Example #9: Glycine-based buffers

The Abgent Biotin Single-Shot antibody labeling procedure is not compatible with high concentrations of glycine buffer. This amino acid additive is sometimes found in high concentrations (e.g.100mM). Although its presence does not interfere with a sample's spectrum, it can overwhelm the exchange capacity of the spin column. Glycine is an amine contaminant that competes with the labeling reaction and must be removed.

Corrective Action: Remove all traces of glycine and/or other amine-containing buffers by exhaustive dialysis or properly desalting the sample into a phosphate-based buffer.

Problem	Possible Cause	Recommended Action
Poor biotin modification of the antibody	-initial protein concentration was incorrect.	-follow the recommended procedures only -concentrate or dilute the antibody sample into the required range (i.e. 1mg/ml and 100µl)
	-a large excess of non-protein amine contaminants are present in the antibody preparation (e.g. Tris or glycine buffer).	-before labeling remove all amine contaminants. Some samples are so overly contaminated that exhaustive dialysis or two desalting steps may be required.
	-presence protein carrier (e.g. BSA or gelatin) contaminated the sample.	-remove and purify away all protein carriers such as BSA or gelatin by affinity or other chromatographic methods, re-adjust the initial antibody concentration to 1mg/ml
	-presence of preservative or other additive may be interfering with an accurate determination of the starting protein concentration.	-do not attempt to label an antibody containing any Thimerosal. First remove the preservative then re-measure and adjust the antibody

		concentration to 1mg/ml and 100µl.
	-presence of residual sodium azide interferes with the labeling reaction	-refer to recommended actions in the Trouble-shooting Guide
Complete failure of biotin labeling reaction	<p>-improper mixing of reaction components</p> <p>-improper operation of the spectrophotometer</p> <p>-presences of amine contaminants</p> <p>-improper storage of the ChromaLink Biotin reagent may have caused it to hydrolyze</p> <p>-failure to follow the recommended protocol</p>	<p>-make sure to mix the antibody-ChromaLink reaction mixture completely</p> <p>-use the biotinylated IgG positive control provided to validate the spectro-photometer</p> <p>-remove all amine contaminants such as glycine before labeling</p> <p>-store ChromaLink Biotin dessicated at room temp</p> <p>-follow the recommended labeling protocol</p>
Molar substitution ration was out of recommended range (3-8 biotins/antibody)	<p>-initial antibody concentration used was too low or too high.</p> <p>-antibody may have precipitated due to over-modification of available lysine residues</p>	<p>-make sure to properly estimate the initial antibody concentration</p> <p>-concentrate or dilute the antibody sample into the recommend range (1mg/ml in 100µl) before proceeding</p> <p>-follow the recommended protocol</p>
Low antibody recovery and/or sample precipitation	<p>-antibody may have aggregated/precipitated during labeling</p> <p>-incorrect antibody concentration</p> <p>-antibody was over-modified</p> <p>-Zeba column recovery problem</p>	<p>-make sure to add 1M Tris quench buffer to the labeled sample before final desalting</p> <p>-follow the recommended guidelines</p> <p>-always use a calibrated variable-speed centrifuge and spin at exactly 1.5xg for the indicated time, spins at lower or higher speeds can compromise recovery</p>

d. Relationship between Molar Substitution Ratio & ELISA Sensitivity

The Abgent Biotin Single-Shot antibody labeling kit was optimized to incorporate between 3 and 8 biotins per antibody molecule. This level of incorporation was evaluated in both direct and sandwich ELISA assays.

Direct ELISA

A goat anti-bovine IgG antibody was biotinylated using Sulfo-ChromaLink Biotin across a multitude of different molar substitution ratios. The biotinylated antibodies were then used to detect immobilized antigen (bovine IgG) using a standard ELISA procedure. Purified bovine IgG was immobilized (2-fold dilution series) (0.5 - 5,000ng/ml). After immobilization (4hr @ RT), the wells were blocked with 1% casein/PBS and subsequently washed. The immobilized antigen was then incubated with streptavidin-HRP @ 1µg/ml for 60 minutes. After washes, TMB substrate (3,3',5,5'- tetramethylbenzidine) was added for 20 minutes. Signals were measured on a Molecular Devices SpectraMax Plus plate reader @ 650nm. Direct ELISA dose response curves were plotted as illustrated in Figure 19.

Results: Signal/noise increased approximately 2.5-fold (linear portion of the curve) as the MSR increased from 1.3 to 6.1. Background controls were constant across the various MSRs (data not shown).

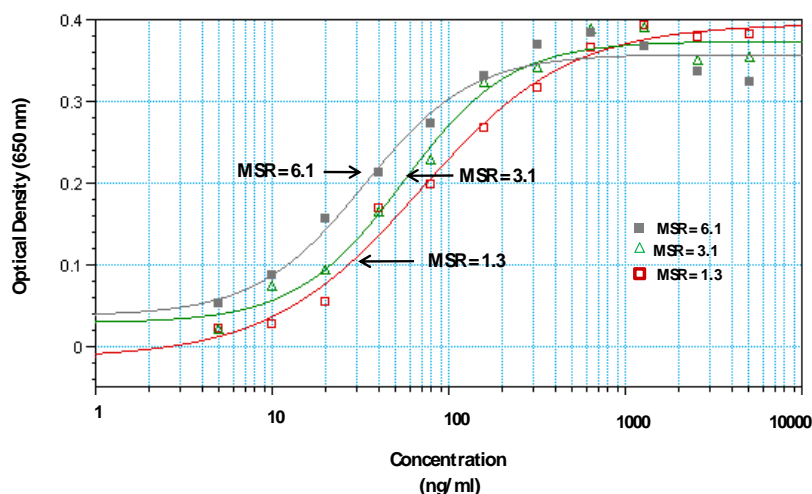


Figure 19. Direct ELISA response curves illustrating the relationship between biotin molar substitution ratio and direct ELISA signals @ 650nm.

To further illustrate the Signal vs. MSR relationship, plots were generated at a single fixed antigen concentration (e.g.2ng/well) across a range of molar substitution ratios (Figure 20).

Results: Measured signal/noise increases almost 2.9-fold as the MSR goes from 1.3 to 6.1. Note the slight reduction in signal as the MSR goes beyond 6.1 probably due to over-modification of the antibody.

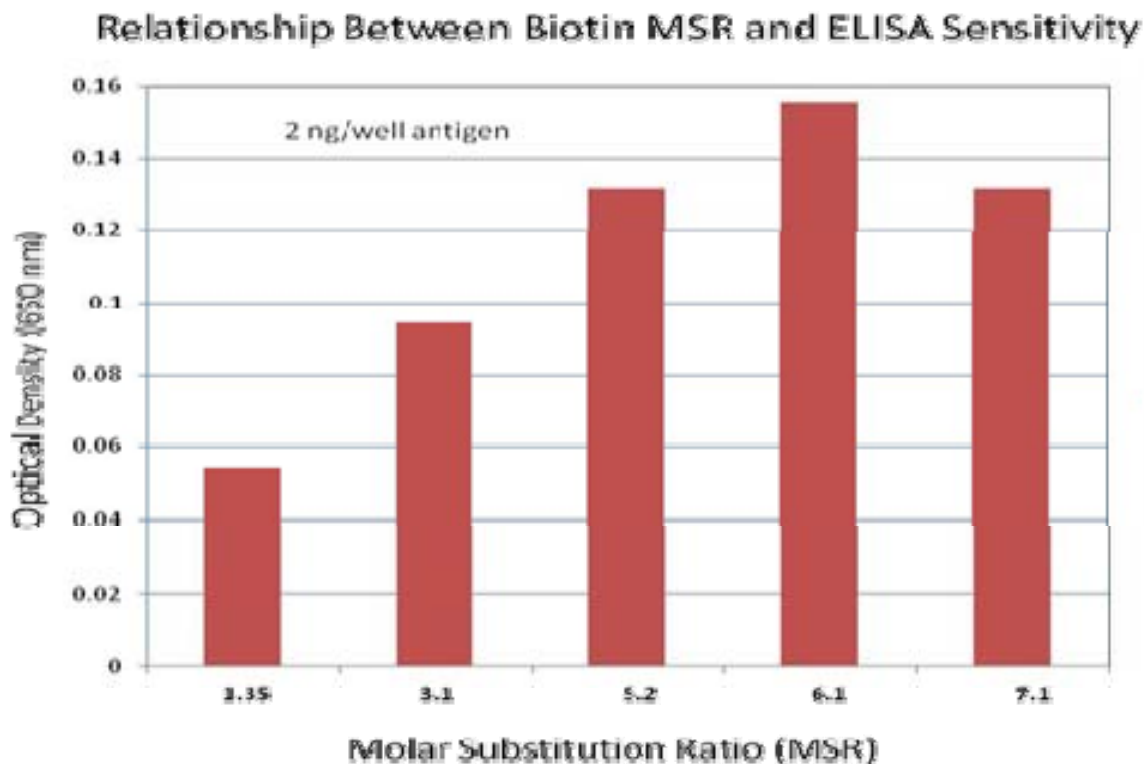


Figure 20. Background corrected direct ELISA signals at a fixed quantity of immobilized antigen (i.e. 2ng per well) vs. MSR. Note the gradual increase in S/N (~ 2.9-fold) as the MSR increases from 1.3 to 6.1.

Sandwich ELISA

Sandwich ELISA assays were performed by immobilizing IL-2 capture antibody in a 96-well plate. After blocking and wash steps, each well was incubated with a 2-fold dilution of analyte for 1 hour along with negative controls. After washes, a second monoclonal antibody (biotinylated at the indicated MSRs) was incubated @ 1 μ g/ml for 1 hour. After washes, wells were incubated with streptavidin alkaline phosphatase for 30 minutes. Substrate (pNPP) signals were read @ 405nm after 20 minutes. Sandwich ELISA response curve for IL-2 is summarized in Figure 21.

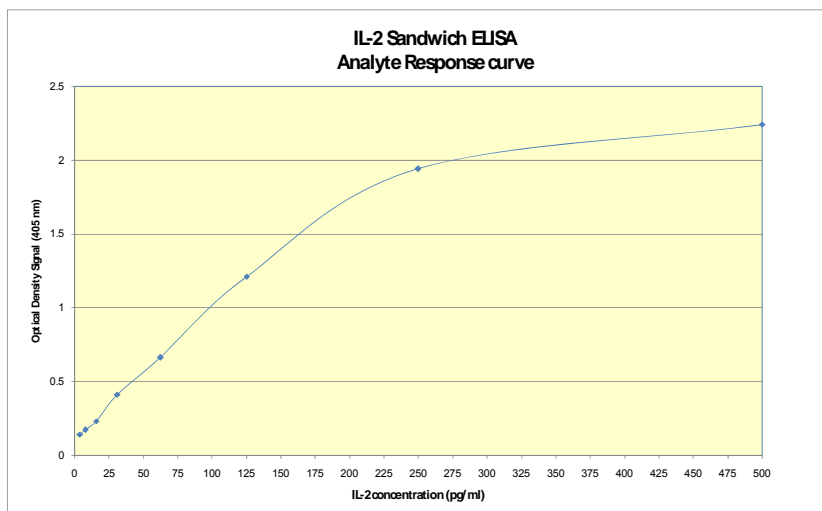


Figure 21. IL-2 specific sandwich ELISA response curve at an MSR = 6.35

e. Spin Column Antibody Recovery Yields

Table 5 summarizes typical antibody recovery yields using the Abgent Biotin Single-Shot procedure. Highly purified goat anti-mouse IgG samples (80-100 μ g) were resuspended in 100 μ l 1x Modification buffer at \sim 1mg/ml. Each sample was processed as described in the Single-Shot procedure using the NanoDropTM spectrophotometer (220-350nm). Recovery yields averaged 86.7%.

	Initial	After 1st Spin Column	After 2nd Spin Column	% Recovery
	Concentration (mg/ml) NanoDrop TM	Concentration (mg/ml) NanoDrop TM	Concentration (mg/ml) NanoDrop TM	
Goat IgG #1	0.80	0.75	0.65	81.25
Goat IgG #2	0.82	0.89	0.74	90.20
Goat IgG #3	0.98	0.95	0.87	88.78

Table 5. Spin column protein recovery yields.