

Supporting Information

Nanomolar detection of Glucose using SERS substrates fabricated with Albumin coated gold nanoparticles.

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Calculation of total error for the parameters in table 1 (Column I).

The balance Sartorius, the Poseidon beta micropipette and the Labmate Soft LM100 micropipette were used to weigh and to prepare our solutions with glucose and albumin, the specifications for those instruments are:

Poseidon beta micropipette: volume range from 100µl to 1000µl, ISO 8655 validation and controls; V (100µL) accuracy (%): +0.152, precision (%): 0.01; V (1000µL) accuracy (%): +0.319, precision (%): +0.031.

Labmate Soft LM100 micropipette: volume range from 10µl to 100µl, ISO 8655 validation and controls; V (10µl) accuracy (%): +1.600, precision (%): +0.8; V (100µL) accuracy (%): +0.800, precision (%): +0.2.

Balance Sartorius CPA224S: Readability 0.1 mg, maximum weigh 200 gr.

Pyrex volumetric flask: 20 ml volume, precision: 0.04 ml (+0.2%)

In order to determine the error for the amount of molecules and moles distributed on our SERS substrates (see column J in table 2 of manuscript), the following procedure was achieved:

Calculation of the error for weighing: We weighed 0.3604 gr (0.0020 moles) of glucose 10 times and we calculated the standard deviation (SD), the value for SD was ±0.4802%

1. **Calculation of the error for volume:** We measured 10 times 1000 µl, 500 µl, 100 µl and 50 µl of tri-distilled water utilizing these micropipettes, and we weighed 10 times each one of these volumes of liquids. The values of SD were obtained using the differences of weight for these volumes of liquids taking into account that 1000 µl should weight 1 gr, 500 µl should weigh 0.5 gr, 100 µl should weight 0.1 gr and 50 µl should weigh 0.05 gr. Thus, the SD were ±0.012%, ±0.0008%, ±0.014% and ±0.0278% for the volumes of 1000 µl, 500 µl, 100 µl and 50 µl respectively.

2. The 0.0020 moles of dextrose were dissolved in 20 ml of water (this is named “main solution”) and we diluted that solution in water successively in order to get the final molar solution for each sample M1-M6, see table 2 in manuscript.
3. The total error for each sequential dilution was obtained with the formula: $[(0.012+0,0278) * N + 0.2]=$ Volume error, where N corresponds to the number of times for which we used the micropipette to get each dilution from the “main solution”.
4. The total error was obtained by adding the error corresponding to the volume to the error of weight for the preparation of the “main solution”. The total error corresponding to each number of moles on the substrate is summarized in column D of table S1:

Table S1: Total error for each sample used for Raman detection

M1	2	1.00E-05	0.76
M2	5	1.00E-08	0.88
M3	7	1.00E-10	0.96
M4	9	1.00E-12	1.04
M5	11	1.00E-14	1.12
M6	13	1.00E-16	1.20