Supporting Information

Morphology-Dependent Nanoplasmonic Assay: A Powerful Signaling Platform for Multiplexed Total Antioxidant Capacity Analysis

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Table of Contents	
Content	Page
Chemicals and Materials	S4
Instrumentation	S4
Synthesis of AuNRs	S4
Statistical Analysis	85
LOD and LOQ Formulas	S6

Fig. S1 Assessing the stability of AuNRs in pH 7 B.R. buffer: UV-vis spectra within 15 minutes. S7

Table S1. Comparative redox potentials for key antioxidants in the human body.S8

Fig. S2 Effect of NBS concentrations on the multi-colorimetric responses of AuNRs, (A) the corresponding images of the probe, (B) the absorption spectra of the proposed probe, and (C) the corresponding bar plot as a function of NBS concentration (pH 7 B.R. buffer) at 15 min in both incubation time and analysis time. **S9**

Fig. S3 Effect of incubation time on the multi-colorimetric responses of AuNRs, spectral variations of 10 μ M of each antioxidant, pH 7 B.R buffer, and analysis time 15 min (A) AA, (B) CYS, (C) GSH, and (D) UA, (E-H) bar plots representing variations of AuNRs spectra as a function of incubation time in the presence of AA, CYS, GSH, and UA respectively. **S10**

Fig. S4 UV-vis absorption profile of the proposed probe after 10-minute incubation with 75 μ M NBS and 10 μ M of individual antioxidants in pH 7 B.R. buffer. S11

Fig. S5 Effect of time-course variation in absorption spectra of the AuNRs, (A) spectral variations, (B) bar plot representing variations of AuNRs spectra as a function of time-course variation in the presence of 75 μ M NBS. The incubation time was 10 min. S12

Fig. S6 Effect of time-course variation in absorption spectra of the AuNRs, spectral variations of (A) AA, (B) CYS, (C) GSH, and (D) UA, (E-H) bar plots AA variations of AuNRs spectra as a function of time-course variation in the presence of AA, CYS, GSH, and UA, respectively. The concentration of NBS and each antioxidant was 75 μ mol L⁻¹ and 10 μ mol L⁻¹, respectively. The incubation time was 10 minutes in pH 7 B.R. buffer. **S13**

Fig. S7 (A) Color variation images and variation responses of the probe to different concentrations of (B) AA, (C) CYS, (D) GSH, and (E) UA. **S14**

Fig. S8 3D LDA score plots for the discrimination of four classes of antioxidants (i.e., AA, CYS, GSH, and UA) and total antioxidants as a TAC-mixture. **S15**

Table S2. Jackknifed classification matrix for the discrimination of single-component samples(AA and CYS 1-60 μ mol L⁻¹; UA and GSH 0.05-20 μ mol L⁻¹) and TAC as a multi-component(0.05-14 μ mol L⁻¹) in their entire concentration range.**S16**

Table S3. Jackknifed classification matrix for the discrimination of AA in the entireconcentration range.S17

Table S4. Jackknifed classification matrix for the discrimination of CYS in the entireconcentration range.\$18

Table S5. Jackknifed classification matrix for the discrimination of GSH in the entireconcentration range.S19

Table S6. Jackknifed classification matrix for the discrimination of UA in the entireconcentration range.S20

Table S7. Jackknifed classification matrix for the discrimination of TAC in the entireconcentration range.S21

Fig. S9 Predicted vs measured concentration plots with PLSR for (A) AA, (B) CYS, (C) GSH, (D) and UA. **S22**

Table S8. Comparison of the proposed method with other reported methods for detection of
antioxidants.S23

Fig. S10 UV-vis spectra and corresponding color photographs of three different TAC unknown in total concentration of 5, 7, and 9 μ mol L⁻¹ in human saliva sample. **S24**

Table S9. LDA posterior probability outcomes for identifying TAC unknown samples inhuman saliva. All 9 samples were given as a test set to the pre-trained LDA model of AA, CYS,GSH, UA, and TAC-mixture.S25

Table S10. LDA posterior probability outcomes for identifying TAC unknown samples inhuman saliva. All 9 samples were given as a test set to the pre-trained LDA model of TAC-mixture within the total concentration range of $0.05-14 \ \mu mol \ L^{-1}$.S26

Fig. S11 3D LDA score plots for the discrimination of TAC unknown of real human saliva samples after combining the test set (real samples) with the pre-trained LDA model of AA, CYS, GSH, UA, and TAC-mixture. The saliva samples were spiked with three concentrations of total antioxidant.

Fig. S12 2D LDA score plots for the discrimination of TAC unknown of real human saliva samples after combining the test set (real samples) with the pre-trained LDA model of TAC-mixture within the total concentration range of $0.05-14 \mu mol L^{-1}$. The saliva samples were spiked with three concentrations of total antioxidants. **S28**

Fig. S13 Interference effect on the responses of the proposed probe $([AA] = [CYS] = [GSH] = [UA] = [TAC] = 10 \ \mu\text{M}, [Urea] = 475 \ \mu\text{M}, ([Na^+] = 1000 \ \mu\text{M}, [Ca^{2+}] = [K^+] = 500 \ \mu\text{M}, [Mg^{2+}] = 650 \ \mu\text{M}) ([Cl^-] = 650 \ \mu\text{M}, [PO_4^{3-}] = 375 \ \mu\text{M}).$

References

S30

Chemicals and Materials

Hydrogen tetrachloroaurate (HAuCl₄.3H₂O) (99.5% w/w), sodium borohydride (NaBH₄), cetyltrimethylammonium bromide (CTAB), ascorbic acid (AA), silver nitrate (AgNO₃), sodium hydroxide (NaOH), ortho-phosphoric acid (85%), acetic acid (glacial) (100%), boric acid, sodium borohydride, sodium hydroxide, and N-bromosuccinimide (NBS), cysteine (C₃H₇NO₂S), glutathione (C₁₀H₁₇N₃O₆S), and uric acid (C₅H₄N₄O₃) were acquired from Sigma-Aldrich at analytical grade and used without further purification. Milli-Q grade water with a resistivity of 18.2 M Ω was used throughout all experimental procedures in this research.

Instrumentation

Spectrophotometric absorbance measurements were conducted using an Agilent Cary 60 spectrophotometer with 1.0 cm glass cuvettes. Images capturing color variations were taken with a Samsung A71 smartphone. Transmission electron microscopy (TEM) analysis was performed on a Zeiss EM900 microscope, operating at an acceleration voltage of 200 kV. The pH measurements and adjustments to the solutions were carried out using a Denver Instrument Model 270 pH meter equipped with a glass electrode.

Synthesis of AuNRs

AuNRs were synthesized via a seed-mediated growth method, following previously reported protocols ¹. The synthesis process involved two main steps: preparing the seed and growth solutions. For the seed solution, 0.125 mL of HAuCl₄ (0.01 mol L⁻¹) and 5.0 mL of CTAB (0.1 mol L⁻¹) were combined, followed by the addition of 0.3 mL of freshly prepared ice-cold NaBH₄ (0.01 mol L⁻¹). This resulted in a brownish-yellow solution, which was allowed to stand at room temperature for 2–5 hours. The growth solution was prepared by mixing 50.0 mL of CTAB (0.1 mol L⁻¹), 2.5 mL of HAuCl₄ (0.01 mol L⁻¹), and 0.3 mL of AgNO₃ (0.01 mol L⁻¹), followed by the addition of 0.3 mL of Aa (0.1 mol L⁻¹). The color change from yellow to colorless indicated the reduction of Au³⁺ to Au⁺. Finally, the 0.25 mL seed solution was gently added to the growth mixture, and then left overnight at room temperature. Excess CTAB was eliminated through centrifugation at 8000 rpm for 15 minutes, and the AuNRs were isolated in deionized water. The resultant AuNRs were utilized without further purification for subsequent experiments.

Statistical Analysis

Statistical analyses were performed using Origin Pro 2018 and MATLAB R2013a software. The qualitative performance of the probe was assessed using linear discriminant analysis (LDA). Partial least squares regression (PLSR) was utilized as a powerful multivariate calibration method to quantify antioxidants and total antioxidants. Principal component analysis (PCA) was applied to reduce the dimensionality of the dataset when necessary. Model accuracy was estimated using leave-one-out cross-validation and test-set validation. The Jackknifed classification matrix and canonical score plots were applied to assess the classification model outcomes. Two-dimensional (2D) confidence ellipses indicating 95% confidence limits were plotted around cluster centroids to demonstrate the statistical significance of classifications. The MVC1 toolbox in MATLAB R2019b was used for PLSR analyses, determining analytical figures of merit such as the correlation coefficient (R²), root-mean-square error of calibration (RMSEC), root-mean-square error of cross-validation (RMSECV), root-mean-square error of prediction (LOQ).

LOD and LOQ Formulas:

In this study, the LOD for each antioxidant (AA, CYS, GSH, and UA) and total antioxidant capacity (TAC) was determined using the MVC1 toolbox in MATLAB, with the results presented systematically in Table 1. The formula used to define the LOD and limit of quantification (LOQ) for multivariate calibration is provided below:

LOD = 3.3 [SEN⁻²
$$\sigma_x^2$$
 (1+h₀) + h₀ $\sigma_{y, cal}^2$]^{1/2}

where:

- SEN is the sensitivity,
- σ_x^2 is the instrumental signal variance,
- $\sigma_{y,cal}^{2}$ is the variance of the analyte concentration in the calibration set,
- h_0 is the leverage of the blank sample.

The factor 3.3 corresponds to a 5% error margin for Type I and II errors. The limit of quantification (LOQ) is defined as:

$$LOQ = 10.0/3.3 LOD$$



Fig. S1 Assessing the stability of AuNRs in pH 7 B.R. buffer: UV-vis spectra within 15 minutes.

Table S1. (Comparative	redox potent	tials for key	antioxidants i	n the human b	oody.
		1	5			2

Redox Pair	Redox potential (volts)
Ascorbic acid oxidized/reduced	+0.08
Cystine/ Cysteine	-0.22
Glutathione oxidized/reduced	-0.24
Uric acid oxidized/reduced	0.35



Fig. S2 Effect of NBS concentrations on the multi-colorimetric responses of AuNRs, (A) the corresponding images of the probe, (B) the absorption spectra of the proposed probe, and (C) the corresponding bar plot as a function of NBS concentration (pH 7 B.R. buffer) at 15 min in both incubation time and analysis time.



Fig. S3 Effect of incubation time on the multi-colorimetric responses of AuNRs, spectral variations of 10 μM of each antioxidant, pH 7 B.R buffer, and analysis time 15 min (A) AA, (B) CYS, (C) GSH, and (D) UA, (E-H) bar plots representing variations of AuNRs spectra as a function of incubation time in the presence of AA, CYS, GSH, and UA respectively.



Fig. S4 UV-vis absorption profile of the proposed probe after 10-minute incubation with 75 μ M NBS and 10 μ M of individual antioxidants in pH 7 B.R. buffer.



Fig. S5 Effect of time-course variation in absorption spectra of the AuNRs, (A) spectral variations, (B) bar plot representing variations of AuNRs spectra as a function of time-course variation in the presence of 75 μM NBS. The incubation time was 10 min.



Fig. S6 Effect of time-course variation in absorption spectra of the AuNRs, spectral variations of (A) ASA, (B) CYS, (C) GSH, and (D) UA, (E-H) bar plots representing variations of AuNRs spectra as a function of time-course variation in the presence of AA, CYS, GSH, and UA, respectively. The concentration of NBS and each antioxidant was 75 μmol L⁻¹ and 10 μmol L⁻¹, respectively. The incubation time was 10 minutes in pH 7 B.R. buffer.



Fig. S7 (A) Color variation images and variation responses of the probe to different concentrations of (B) AA, (C) CYS, (D) GSH, and (E) UA.



Fig. S8 3D LDA score plots for the discrimination of four classes of antioxidants (i.e., AA, CYS, GSH, and UA) and total antioxidants as a TAC-mixture.

Table S2. Jackknifed classification matrix for the discrimination of single-component samples (AA and CYS 1-60 μ mol L⁻¹; UA and GSH 0.05-20 μ mol L⁻¹) and TAC-mixture as a multicomponent (0.05-14 μ mol L⁻¹) in their entire concentration range.

		AA	CYS	GSH	UA	TAC-mixture	Total	Sensitivity (%)	Specificity (%)	Precision (%)	
		51	0	0	0	0	51	100.00	100.00	100.00	
	AA	100.00%	0.00%	0.00%	0.00%	0.00%	100.00%	- 100.00	100.00	100.00	
S	CVC	0	21	0	0	0	21	100.00	100.00	100.00	
las	Crs	0.00%	100.00%	0.00%	0.00%	0.00%	100.00%	- 100.00	100.00	100.00	
- C	CEU	0	0	21	0	0	21	100.00	100.00	100.00	
na	GSH	0.00%	0.00%	100.00%	0.00%	0.00%	100.00%	100.00	100.00	100.00	
Ē		0	0	0	24	0	24	100.00	100.00	100.00	
20	UA	0.00%	0.00%	0.00%	100.00%	0.00%	100.00%	- 100.00	100.00	100.00	
	TAC minture	0	0	0	0	36	36	100.00	100.00	100.00	
	TAC-mixture	0.00%	0.00%	0.00%	0.00%	100.00%	100.00%	- 100.00	100.00	100.00	
	Tatal	51	21	21	24	36	1153	100.00	100.00	100.00	
	iotai	33.33%	13.73%	13.73%	15.69%	23.53%	100.00%	- 100.00	100.00	100.00	

Predicted class

													Ρ	redicte	d class											
		1	2	3	4	5	6	7	8	9	10	12	14	16	18	20	22.5	25	30	40	50	60	Total	Sensitivity (%) S	pecificity (%)	Precision(%)
	1	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	100.00	100.00	100.00
L	-	100.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	4.76%	100.00	100.00	100.00
	2	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	100.00	100.00	100.00
H		0.00%	100.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	4.76%			
	3	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	100.00	100.00	100.00
H		0.00%	0.00%	100.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	4.76%			
	4	0.00%	0.00%	0.00%	3	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	3	100.00	100.00	100.00
H		0.00%	0.00%	0.00%	100.00%	3	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	4.70%			
	5	0.00%	0.00%	0.00%	0.00%	100.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	4.76%	100.00	100.00	100.00
	-	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3			
	6	0.00%	0.00%	0.00%	0.00%	0.00%	100.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	4.76%	100.00	100.00	100.00
	-	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	100.00	100.00	100.00
	/	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	100.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	4.76%	100.00	100.00	100.00
	8	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	3	100.00	100.00	100.00
L	0	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	100.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	4.76%	100.00	100.00	100.00
	9	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	3	100.00	100.00	100.00
H		0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	100.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	4.76%		12121212	
S	10	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	3	100.00	100.00	100.00
8		0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	100.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	4.76%			
5	12	0	0	0	0	0	0	0 00%	0	0	0	3	0	0	0	0	0	0	0	0	0	0	3	100.00	100.00	100.00
-ŝ-		0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	100.00%	2	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	4.76%			
5	14	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	100.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	4 76%	100.00	100.00	100.00
≥		0	0.0070	0.0070	0	0.0070	0.0070	0.0070	0.0070	0.0070	0	0	0	3	0	0.0070	0.0070	0.0070	0.0070	0.0070	0.0070	0.0070	3			
	16	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	100.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	4.76%	100.00	100.00	100.00
h	40	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	3			
	18	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	100.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	4.76%	100.00	100.00	100.00
	20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	3	100.00	100.00	100.00
L	20	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	100.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	4.76%	100.00	100.00	100.00
	22.5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	3	100.00	100.00	100.00
-		0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	100.00%	0.00%	0.00%	0.00%	0.00%	0.00%	4.76%		100.00	
	25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	3	100.00	100.00	100.00
H		0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	100.00%	0.00%	0.00%	0.00%	0.00%	4.76%			
	30	0	0 0.0%	0.00%	0.00%	0 00%	0.00%	0.00%	0.00%	0 0.0%	0 0.00%	0.00%	0 0.0%	0.00%	0 00%	0 00%	0.00%	0.00%	3	0.00%	0.00%	0.00%	3	100.00	100.00	100.00
H		0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	100.00%	0.00%	0.00%	0.00%	4.70%			
	40	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	100.00%	0.00%	0.00%	4 76%	100.00	100.00	100.00
H		0	0	0.0070	0	0	0	0.0070	0.0070	0	0	0	0.0070	0	0	0	0.0070	0	0	0	3	0	3			
	50	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	100.00%	0.00%	4.76%	100.00	100.00	100.00
	<i>co</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	3	100.00	100.00	100.00
	60	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	100.00%	4.76%	100.00	100.00	100.00
	Total	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	63	100.00	100.00	100.00
Ľ	ordi	4.76%	4.76%	4.76%	4.76%	4.76%	4.76%	4.76%	4.76%	4.76%	4.76%	4.76%	4.76%	4.76%	4.76%	4.76%	4.76%	4.76%	4.76%	4.76%	4.76%	4.76%	100.00%	100.00	100.00	100.00

Table S3. Jackknifed classification matrix for the discrimination of AA in the entire concentration range.

Table S4. Jackknifed classification matrix for the discrimination of CYS in the entire concentration range.

												Pred	icted cl	ass										
		0.05	0.1	0.5	1	2	3	4	5	6	7	8	9	10	12	14	16	18	20	Total	Sensitivity (%) Specificity (%) Precision(%)	
	0.05	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	100.00	100.00	100.00	
	0.05	100.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	7.41%	100.00	100.00	100.00	
	01	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	100.00	100.00	100.00	
	0.1	0.00%	100.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	7.41%	100.00	100.00	100.00	
	05	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	- 100.00	100.00	100.00	
	0.5	0.00%	0.00%	100.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	7.41%	100.00	100.00	100.00	
	1	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	- 100.00	100.00	100.00	
	-	0.00%	0.00%	0.00%	100.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	7.41%	100.00	100.00	100.00	
	,	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	3	- 100.00	100.00	100.00	
	-	0.00%	0.00%	0.00%	0.00%	100.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	7.41%	100.00	100.00	100.00	
	3	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	3	- 100.00	100.00	100.00	
		0.00%	0.00%	0.00%	0.00%	0.00%	100.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	7.41%	100.00	100.00	100.00	
	4	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	3	- 100.00	100.00	100.00	
	-	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	100.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	7.41%	100.00	100.00	100.00	
	5	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	3	- 100.00	100.00	100.00	
8		0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	100.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	7.41%	100.00	100.00	100.00	
ŝ	6	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	3	- 100.00	00 100.00	100.00	
2	Ŭ	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	100.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	7.41%	100.00	100.00	100.00	
ä	7	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	3	- 100.00	100.00	100.00	100.00
Ē		0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	100.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	7.41%	100.00	100.00	100.00	
۶I	8	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	3	100.00	100.00	100.00	
		0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	100.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	7.41%	100100	100100	100/00	
	9	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	3	100.00	100.00	100.00	
		0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	100.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	7.41%				
	10	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	3	- 100.00	100.00	100.00	
		0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	100.00%	0.00%	0.00%	0.00%	0.00%	0.00%	7.41%				
	12	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	3	- 100.00	100.00	100.00	
		0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	100.00%	0.00%	0.00%	0.00%	0.00%	7.41%				
	14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	3	100.00	100.00	100.00	
		0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	100.00%	0.00%	0.00%	0.00%	7.41%				
	16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	3	- 100.00	100.00	100.00	
-		0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	100.00%	0.00%	0.00%	7.41%				
	18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	3	- 100.00	100.00	100.00	
		0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	100.00%	0.00%	7.41%		4045604-2008-200		
	20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	3	100.00	100.00	100.00	
		0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	100.00%	7.41%				
	Total	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	54	100.00	100.00	100.00	
		7.41%	7.41%	7.41%	7.41%	7.41%	7.41%	7.41%	7.41%	7.41%	7.41%	7.41%	7.41%	7.41%	7.41%	7.41%	7.41%	7.41%	7.41%	100.00%				

Table S5. Jackknifed classification matrix for the discrimination of GSH in the entire concentration range.

Table S6. Jackknifed classification matrix for the discrimination of UA in the entire concentration range.

										Ρ	redicte	d class								
-		0.05	0.1	0.5	1	2	3	4	5	6	7	8	9	10	12	14	Total	Sensitivity (%)	Specificity (%,) Precision(%)
	0 05	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	100.00	100.00	100.00
_		100.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	6.67%	100.00	100.00	100.00
	01	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	3	100.00	100.00	100.00
	0.1	0.00%	100.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	6.67%	100.00	100.00	
	0.5	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	3	100.00	100.00	100.00
		0.00%	0.00%	100.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	6.67%		100.000	
	1	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	3	100.00	100.00	100.00
		0.00%	0.00%	0.00%	100.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	6.67%			
	2	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	3	100.00	100.00	100.00
_		0.00%	0.00%	0.00%	0.00%	100.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	6.67%			
	3	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	3	100.00	100.00	100.00
-		0.00%	0.00%	0.00%	0.00%	0.00%	100.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	6.67%			
3	4	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	3	100.00	100.00	100.00
3 -		0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	100.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.07%			
5	5	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	100.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	6.67%	100.00	100.00	100.00
		0.0070	0.0070	0.0070	0.0070	0.0070	0.0070	0.0070	0	3	0.0070	0.0070	0.0070	0.0070	0.0070	0.0070	3			
5	6	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	100.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	6.67%	100.00	100.00	100.00
		0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	3			
	7	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	100.00%	0.00%	0.00%	0.00%	0.00%	0.00%	6.67%	100.00	100.00	100.00
	•	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	3	400.00	100.00	
	8	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	100.00%	0.00%	0.00%	0.00%	0.00%	6.67%	100.00	100.00	100.00
	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	3	100.00	100.00	100.00
	9	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	100.00%	0.00%	0.00%	0.00%	6.67%	100.00	100.00	100.00
	10	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	3	100.00	100.00	100.00
	10	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	100.00%	0.00%	0.00%	6.67%	100.00	100.00	100.00
	12	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	3	100.00	100.00	100.00
	12	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	100.00%	0.00%	6.67%	100.00	100.00	100.00
	14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	3	100.00	100.00	100.00
		0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	100.00%	6.67%	100.00	100.00	100.00
7	otal	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	45	100.00	100.00	100.00
1		6.67%	6.67%	6.67%	6.67%	6.67%	6.67%	6.67%	6.67%	6.67%	6.67%	6.67%	6.67%	6.67%	6.67%	6.67%	100.00%	100.00	100.00	

Table S7. Jackknifed classification matrix for the discrimination of TAC-mixture in the entire concentration range.



Fig. S9 Predicted vs measured concentration plots with PLSR for (A) AA, (B) CYS, (C) GSH, (D) and UA.

Analytes	Materials	Detection method	Linear range (µmol L ⁻¹)	LOD (µmol L ⁻¹)	References
AA CYS GSH	Iron-doped carbon nitride	Smartphone-based colorimetric	50-1000 5-22.5 5-30	30 4 8	1
AA CYS GSH	Ag-MOF	Visual-based	3-40	0.048 0.050 0.088	3
TAC	SMOF nanozyme	Colorimetric	50-700	33.4	4
AA CYS GSH	Mn-MOF peroxidase-like nanozymes	Temperature-resilient	3.0-25 3.0-33 3.0-35	0.040 0.047 0.067	5
TAC	Au-doped g-C3N4 nanosheet	Colorimetric	Not reported	1.0	6
АА	Nitrogen-Doped Carbon Nanoflowers	Colorimetric	1.0-20.0	0.94	7
GSH CYS GA CA	Au ₂ Pt nanozymes	Colorimetric sensor array	4–20 0-16 1-20 2-12	0.124 0.1163 0.2570 0.1885	8
AA CYS GSH UA TAC	Anti-etching of AuNRs	Colorimetric	3.1-60.0 2.6-60.0 1.2-20.0 0.8-14.0 0.7-14.0	1.1 0.9 0.4 0.3 0.2	This Work

Table S8. Comparison of the proposed method with other reported methods for detection of antioxidants.



Fig. S10 UV-vis spectra and corresponding color photographs of three different TAC unknown in total concentration of 5, 7, and 9 μ mol L⁻¹ in human saliva sample.

Table S9. LDA posterior probability outcomes for identifying TAC unknown samples in human saliva. All 9 samples were given as a test set to the pre-trained LDA model of AA, CYS, GSH, UA, and TAC-mixture.

411						
Alleged	AA	CYS	GSH	UA	TAC-mixture	Allocated
TAC-mixture	5.44E-14	3.24E-18	4.75E-20	9.29E-18	1	TAC-mixture
TAC-mixture	1.83E-12	3.84E-9	9.72E-15	5.54E-7	1	TAC-mixture
TAC-mixture	2.90E-13	4.43E-10	1.33E-15	1.53E-8	1	TAC-mixture
TAC-mixture	2.50E-13	4.99E-27	2.36E-16	7.11E-28	1	TAC-mixture
TAC-mixture	2.92E-13	2.63E-38	8.17E-19	1.89E-42	1	TAC-mixture
TAC-mixture	3.36E-13	2.52E-23	9.71E-16	1.72E-23	1	TAC-mixture
TAC-mixture	1.82E-7	2.85E-4	0.04335	1.78E-4	0.95619	TAC-mixture
TAC-mixture	7.97E-21	1.34E-27	3.85E-15	2.03E-32	1	TAC-mixture
TAC-mixture	1.25E-10	1.23E-8	2.60E-6	1.64E-10	1	TAC-mixture

Table S10. LDA posterior probability outcomes for identifying TAC unknown samples in human saliva. All 9 samples were given as a test set to the pre-trained LDA model of TAC-mixture within the total concentration range of $0.05-14 \mu mol L^{-1}$.

Alleged									Post probab	vilities						Allocated
	0.05	0.1	0.5	1	2	3	4	5	6	7	8	9	10	12	14	
5	0	0	0	0	0	0	0	1	3.39E-92	1.65E-58	0	0	0	0	0	5
5	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	5
5	0	0	0	0	0	0	0	1	0	1.82E-75	0	0	0	0	0	5
7	0	0	0	0	0	0	0	1.02E-179	3.76E-73	1	6.43E-127	4.65E-82	0	0	0	7
7	0	0	0	0	0	0	0	1.13E-153	8.36E-64	1	1.44E-145	1.20E-111	0	0	0	7
7	0	0	0	0	0	0	0	1.42E-136	2.18E-53	1	7.02E-139	9.23E-117	0	0	0	7
9	0	0	0	0	0	0	0	0	3.58E-265	1.18E-195	1.80E-80	1	0	0	0	9
9	0	0	0	0	0	0	0	0	9.28E-234	7.21E-165	3.29E-77	1	0	0	0	9
9	0	0	0	0	0	0	0	0	3.96E-246	2.83E-178	2.72E-77	1	0	0	0	9



Fig. S11 3D LDA score plots for the discrimination of TAC unknown of real human saliva samples after combining the test set (real samples) with the pre-trained LDA model of AA, CYS, GSH, UA, and TAC-mixture. The saliva samples were spiked with three concentrations



Fig. S12 2D LDA score plots for the discrimination of TAC unknown of real human saliva samples after combining the test set (real samples) with the pre-trained LDA model of TAC-mixture within the total concentration range of $0.05-14 \mu mol L^{-1}$. The saliva samples were spiked with three concentrations of total antioxidants.



Fig. S13 Interference effect on the responses of the proposed probe ([AA] = [CYS] = [GSH] = [UA] = [TAC] = 10 μ M, [Urea] = 475 μ M, ([Na⁺] = 1000 μ M, [Ca²⁺] = [K⁺] = 500 μ M, [Mg²⁺] = 650 μ M) ([Cl⁻] = 650 μ M, [PO₄³⁻] = 375 μ M).

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