Supplementary Information

Pd-based hybrid nanoparticles as multimodal theranostic nanomedicine

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Table S1. UV-visible analysis for as prepared, pellet 1 and pellet 2 of PdNP samples. Experimental values of wavelength (λ_{max} , in nm) at the maximum of plasmon peak absorbance (A_{max}) and calculated values of molar extinction coefficient (ϵ , in cm⁻¹M⁻¹), optical diameter (d_{opt} , in nm) and concentration (in nM and NP/mL).

Sample	λ _{max} (nm)	A _{max}	ε (cm ⁻¹ M ⁻¹)	d _{opt} (nm)	mol/L ⋅10 ⁻⁹	NP/mL
PdNP, as prepared	273	0.188	$2.0x10^6$	4	35	1.43x10 ¹¹
PdNP, pellet 1	273	0.796	$2.3x10^6$	4	111	3.85x10 ¹¹
PdNP, pellet 2	274	0.704	3.1×10^6	5	91	1.39x10 ¹¹

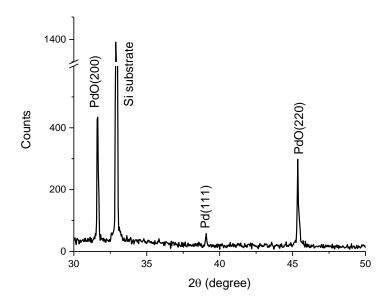


Figure S1. XRD spectrum of PdNP. The signal at 32.9° is referred to silicon substrate.

The diffraction signals at 31.6° and 45.4° and 39.1° can be referred to (200) and (220) crystal planes of cubic PdO (reference code: 00-046-1211) and to (111) crystal planes of cubic Pd (reference code: 01-087-0637), respectively.

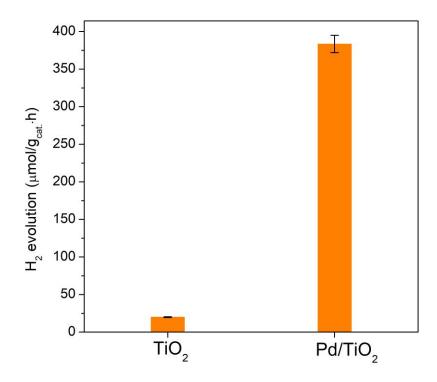


Figure S2. Solar photocatalytic H_2 production of the tested samples expressed in 10^{-6} ·mol and normalized for grams of catalyst and hours of irradiation.

Table S2. Literature comparison for the solar photocatalytic H₂ production over some Pd/TiO₂-based samples with our samples (in red).

Sample	Pd content [wt %]	Experimental conditions	Irradiation source	H ₂ evolution [μmol/ g _{cat.} ·h]	[ref]
Pd/TiO ₂	0.4	50 mL DMF, 0.5 mL water, 0.5 mL benzylamine	200 mW/cm ² Xe lamp	400	1
Pd@TiO ₂ /TiOF ₂	1	60 mL of aqueous solution containing 0.35 MNa ₂ SO ₃ , 0.25 M Na ₂ S	300 W, 50 mW/cm ² , Xe lamp	213	2
Pd@TiO2@Au	0.6	20 mL water, 4 mL ethanol	300 W, 250 mW/cm ² , Xe lamp	272.3	3
Au-Pd/TiO ₂	0.4	28.5 water, 1.5 mL glycerol	UV flux (320–400 nm) \sim 12 mW/cm ² , visible	400	4

			flux (400–700 nm) ~97 mW/cm ² Xe lamp		
Pd/TiO ₂	0.1	40 mL water,	$300 \text{ W}, 10.7 \text{ mW/cm}^2$	383.5	This
		10 mL glycerol	solar lamp		work

The concentration of PdNP/mL was calculated considering a face-centered cubic Pd structure⁵ and using 0.389 as Pd lattice unit⁶; the number of CisPt molecules for nanoparticle was found dividing Avogadro's number by the PdNP/mL concentration (**Table S3**).

Table S3. Calculated concentrations (in mol/L and NP/mL) of PdNP and number of cisplatin molecules per NP used for the functionalization protocol.

Sample	[PdNP]mol/L	[PdNP]/mL	[CisPt] mol/L	CisPt molecules/NP
Pd@CisPt	1.58x10 ⁻⁷	$3.3x10^{11}$	9x10 ⁻⁴	1.8×10^{12}

The internalization of PdNP, cisplatin and PdNP@CisPt as well as their interaction with intracellular organelles was studied with confocal laser scanning microscope (LSM) by using the mitochondrial intracellular staining (Mitotracker deep red) and copper (CS1 probe).

As shown in the **Figure S3** PdNP enters the cells, causing an increase in both Mitotracker deep red (Fig.S3c) and CS1 (Fig.S3b) intensities.

PdNP generally localize in different sites which depend on the cells, for instance in *Desulfovibrio desulfuricans* cells they locate at the level of the periplasm, in *Escherichia coli* were observed within the intracellular matrices and membranes, in the HT1080 fibrosarcoma cell line PdNP accumulates in phagocytes while in human peripheral blood

mononuclear cells (PBMCs) within or adjacent to cytoplasmic vesicles.^{7, 8} In our case, we noticed particles aggregates spread around the cell cytoplasm and specially located at the cell membrane. Pd ions dissolved from nanoparticles tend to accumulate in mitochondria interfering with the oxidative phosphorylation, thus causing a poor production of ATP and an excessive production of ROS.⁷ Such an effect causes an increase of the Mitochondrial activity and so of the organelles stain intensity. The higher CS1 intensity may be explained by the fact that elevated expression of Cu chelators, like glutathione (GSH), upregulates hCtr1 expression. In fact, elevated expression of GSH could be explained by the fact that GSH is an important ROS sensor/regulator, so the oxidative stress-induced mechanism during drug and pro-oxidants treatment could cause the GSH overexpression. 9 Concerning the treatment with the free cisplatin, it enters the cells, leading to a significant increase of the Mitotracker deep red and CS1 intensities, respect to the untreated cells as well as the PdNP. This could be explained because of the main target of cisplatin in cancer cells are mitochondria, in fact it tends to accumulate in them, binding DNA and blocking ATP synthesis. 10 Moreover, cellular uptake of cisplatin appears to be related with copper transport, indeed the most important Cu influx transporter in the cell, Ctr1, seems to be able of transporting cisplatin through methionine rich motifs in the N-terminal extracellular domain, which are fundamental for Cu transport too. Moreover, the metallochaperone Atox 1 also seem to be involved, in fact the loss of Atox1 reduces cisplatin influx. 11 Interestingly, the hybrid PdNP@CisPt, compared to bare PdNP and the untreated cells, showed a higher signal of both Mitotracker deep red and CS1 intensity, with a similar behavior to that found for the free cisplatin.

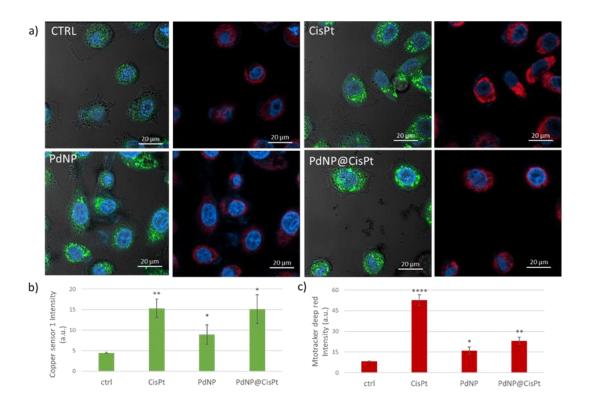


Figure S3: a) LSM fluorescent micrographs of prostate (PC-3) tumour cells: in blue, the nuclear staining with Hoechst ($\lambda_{ex/em} = 405/425-450$ nm); in green, the CS1 intracellular copper probe ($\lambda_{ex/em} = 543/550-600$ nm); in red, the MitoTracker deep red ($\lambda_{ex/em} = 633/650-700$ nm). Cellular treatments were carried out for 90 min with: the negative control of untreated cells, cisplatin, PdNP and PdNP@CisPt. **b)** The graph shows the CS1 intensity in treated and untreated cells, with a higher intensity in treated cells compared to control. **c)** The graph shows the intensity of the Mitotracker deep red in treated and untreated cells, with a higher activity in the treated cells compared to control, particularly for cisplatin and the hybrid PdNP@CisPt. Statistical analysis was performed by pairwise Student's T-test. (*) p <0.05, (**) p <0.01, (***) p <0.001, (****) p <0.001 vs. CTRL. Scale bar = 20 μm.

The average Raman spectra in the 600-1800 cm⁻¹ spectral range are showed in **Figure S4** (panels a-d). Pairwise PCA analyses were performed on pre-processed Raman spectra of Ctrl/CisPt, Ctrl/PdNP and Ctrl/PdNP@Cis groups; results are reported as scores plots (panels e-h), together with the corresponding PC1 loadings (panels i-l).

The PC1 loading of the Ctrl/CisPt comparison (explained variance 44.6%, panel i) displayed the following discriminant spectral features: 785 cm⁻¹, 1095 cm⁻¹, and 1375 cm⁻¹ (assigned to DNA); 915 cm⁻¹ (assigned to RNA); 1000 cm⁻¹, 1160 cm⁻¹, and 1280 cm⁻¹ (assigned to proteins); 1225 cm⁻¹ (assigned to proteins and/or nucleic acids); 1450 cm⁻¹ (assigned to lipids), and 1560 cm⁻¹ and 1610 cm⁻¹ (assigned to the Hoechst 33342 dye).

As regards the PC1 loading of the Ctrl/PdNP comparison (explained variance 65.1%, panel j), the following discriminant spectral features were found: 680 cm⁻¹, 1095 cm⁻¹, and 1375 cm⁻¹ (assigned to DNA); 810 cm⁻¹ (assigned to A-form DNA); 870 cm⁻¹, 980 cm⁻¹, 1000 cm⁻¹, 1208 cm⁻¹, and 1280 cm⁻¹ (assigned to proteins); 915 cm⁻¹ and 1050 cm⁻¹ (assigned to RNA); 1170 cm⁻¹ and 1450 cm⁻¹ (assigned to lipids), and 1560 cm⁻¹ and 1610 cm⁻¹ (assigned to the Hoechst 33342 dye) The PC1 loading of the Ctrl/Pd@CisPt comparison (explained variance 53.6% for 1 nM Pd@CisPt500 and explained variance 60.7% for 2 nM Pd@CisPt1000, panels k-l) displayed the following discriminant spectral features: 720 cm⁻¹, 785 cm⁻¹ (assigned to DNA); 810 cm⁻¹ (assigned to A-form DNA); 830 cm⁻¹ (assigned to B-form DNA); 870 cm⁻¹, 980 cm⁻¹, 1030 cm⁻¹, and 1280 cm⁻¹ (assigned to proteins); 915 cm⁻¹ and 1050 cm⁻¹ (assigned to RNA); 1170 cm⁻¹ and 1450 cm⁻¹ (assigned to lipids), and 1560 cm⁻¹ and 1610 cm⁻¹ (assigned to the Hoechst 33342 dye).

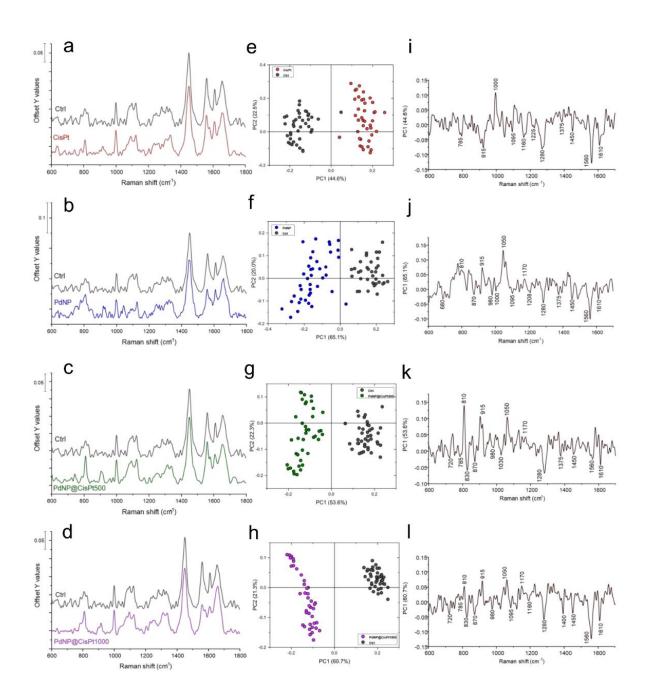


Figure S4. Comparison of average Raman spectra in the 600-1800 cm⁻¹ range of: (a) Ctrl and CisPt, (b) Ctrl and PdNP, (c) Ctrl and Pd@CisPt 500, and (d) Ctrl and Pd@CisPt1000. For a better viewing, spectra are off set along y-axis. PCA scores plots (e-h) and PC1 loading spectra (i-l) of: (e, i) Ctrl/CisPt; (f, j) Ctrl/PdNP; (g, k) Ctrl/Pd@CisPt500, and (h, l) Ctrl/Pd@CisPt1000, cellular populations.

The Raman shift of the most relevant peaks, together with the vibrational mode, and the biochemical assignment are reported in **Table S4**.

Table S4. Center position (Raman shifts, cm $^{-1}$), vibrational mode and biochemical assignment of the peaks identified in average and average \pm S.D. absorbance spectra of Ctrl, CisPt, PdNP, Pd@CisPt500, and Pd@CisPt1000 in the 600-1800 cm $^{-1}$ spectral region.

Raman shift (cm ⁻¹)	Vibrational mode and biochemical assignment	Reference
~680	Ring breathing modes in the DNA bases	12
~720	Ring breathing modes of adenine DNA bases	12, 13
~785	O-P-O stretching of DNA backbone	14
~810	O-P-O stretching of A-form DNA	15
~830	O-P-O asymmetric stretching of B-form DNA	16-18
~870	C-C stretching of proline	12, 19
~915	Ribose vibrations in RNA	12, 13
~980	C-C stretching vibration of protein β-sheet structures	20, 21
~1000	Symmetric stretching breathing vibration of phenylalanine	16, 20
~1030	C-H phenylalanine vibrations	18, 22
~1050	RNA P-O stretching, sugar phosphate -C-O- stretching	18
~1095	Symmetric PO ₂ - stretching vibration of nucleic acids	12, 17
~1160	C-C/C-N stretching of proteins	12, 16, 20, 23
~1170	C=C stretching and COH bending in lipids	12
~1180	Cytosine and guanine vibrations in nucleic acids	12, 19, 24
~1208	C-C ₆ H ₅ stretching of tryptophan and phenylalanine	12
~1225	Amide III, mainly due to β-sheet structures and/or PO ₂ ⁻ stretching vibration of nucleic acids	12, 16, 25
~1280	Amide III, mainly due to helix structures	12, 16, 20, 23
~1375	Ring breathing modes of thymine DNA bases	12, 14, 15-17
~1400	C=O stretching of aspartic and glutamic acids	12, 26
~1450	CH ₂ bending modes of lipid chains; bending vibrations of CH ₂ of glycerol monooleate	12, 16

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