

**TEL AVIV UNIVERSITY**

The Iby and Aladar Fleischman Faculty of Engineering  
The Zandman-Slaner School of Graduate Studies

**ONCOMETABOLITE FINGERPRINTING  
USING FLUORESCENT SINGLE-WALLED  
CARBON NANOTUBES**

A thesis submitted toward the degree of  
Master of Science in Biomedical Engineering

By

**Dean Amir**

October 2021

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This research was carried out in The Department of Biomedical Engineering  
Under the supervision of Dr. Gili Bisker

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## **Acknowledgements**

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## **Abstract**

The production of oncometabolites is the direct result of mutagenesis in key cellular metabolic enzymes, appearing typically in cancers such as glioma, leukemia, and glioblastoma. Once accumulated, oncometabolites promote cancerous transformations by interfering with important cellular functions. Hence, the ability to sense and quantify oncometabolites is essential for cancer research and clinical diagnosis. In this work, we present a near-infrared optical nanosensor for a known oncometabolite, D-2-hydroxyglutarate (D2HG), discovered in a screening of a library of fluorescent single-walled carbon nanotubes (SWCNTs) functionalized with single-stranded DNA. The high-throughput screening procedure was enabled owing to a dedicated software for controlling the spectrometry devices and spectra acquisition developed for this purpose. The screening revealed (ATTT)<sub>7</sub>-SWCNT as a sensor for D2HG, exhibiting a fluorescence intensity increase upon the interaction with D2HG. The fluorescence response of the sensor does not appear to be attributed to basic chemical features of the target analytes tested, and is shown to discriminate D2HG from other related metabolites, including its enantiomer L-2-hydroxyglutarate. Further, the fluorescence modulation is dependent on the analyte concentration and the SWCNT chirality, showing up to 40.7% and 28.2% increase of the (6,5)-chirality peak and the (9,5)- and (8,7)-chirality joint peak, at 572 nm and 730 nm excitation, respectively, in the presence of 10 mM D2HG. The work opens new opportunities for molecular recognition of oncometabolites which can advance basic cancer metabolism research.

## Publications

- Dean Amir, Adi Hendler-Neumark, Verena Wulf, Roni Ehrlich, and Gili Bisker, “Oncometabolite fingerprinting using fluorescent single-walled carbon nanotubes”, *Advanced Materials Interfaces*, 2021.

Abstract: The production of oncometabolites is the direct result of mutagenesis in key cellular metabolic enzymes, appearing typically in cancers such as glioma, leukemia, and glioblastoma. Once accumulated, oncometabolites promote cancerous transformations by interfering with important cellular functions. Hence, the ability to sense and quantify oncometabolites is essential for cancer research and clinical diagnosis. In this work, we present a near-infrared optical nanosensor for a known oncometabolite, D-2-hydroxyglutarate (D2HG), discovered in a screening of a library of fluorescent single-walled carbon nanotubes (SWCNTs) functionalized with single-stranded DNA. The screening revealed (ATTT)<sub>7</sub>-SWCNT as a sensor for D2HG, exhibiting a fluorescence intensity increase upon the interaction with D2HG. The fluorescence response of the sensor does not appear to be attributed to basic chemical features of the target analytes tested, and is shown to discriminate D2HG from other related metabolites, including its enantiomer L-2-hydroxyglutarate. Further, the fluorescence modulation is dependent on the analyte concentration and the SWCNT chirality, showing up to 40.7% and 28.2% increase of the (6,5)-chirality peak and the (9,5)- and (8,7)-chirality joint peak, at 572 nm and 730 nm excitation, respectively, in the presence of 10 mM D2HG. Our work opens new opportunities for molecular recognition of oncometabolites which can advance basic cancer metabolism research.

- Roni Ehrlich, Adi Hendler-Neumark, Verena Wulf, Dean Amir, and Gili Bisker, “Optical Nanosensors for Real-Time feedback on Insulin Secretion by  $\beta$ -cells”, *Small*, July 2021.

Abstract: Quantification of insulin is essential for diabetes research in general, and for the study of pancreatic  $\beta$ -cell function in particular. Herein, fluorescent single-walled carbon nanotubes (SWCNT) are used for the recognition and real-time quantification of insulin. Two approaches for rendering the SWCNT sensors for insulin are compared, using surface functionalization with either a natural insulin aptamer with known affinity to insulin, or a synthetic lipid-poly(ethylene glycol) (PEG) (C<sub>16</sub>-PEG(2000Da)-Ceramide), both of which show a modulation of the emitted fluorescence in response to insulin. Although the PEGylated-lipid has no prior affinity to insulin, the response of C<sub>16</sub>-PEG(2000Da)-Ceramide-SWCNTs to insulin is more stable and reproducible compared to the insulin aptamer-SWCNTs. The SWCNT sensors successfully detect insulin secreted by  $\beta$ -cells within the complex environment of the conditioned media. The insulin is quantified by comparing the SWCNTs fluorescence response to a standard calibration curve, and the results are found to be in agreement with an enzyme-linked immunosorbent assay. This novel analytical tool for real time quantification of insulin secreted by  $\beta$ -cells provides new opportunities for rapid assessment of  $\beta$ -cell function, with the ability to push forward many aspects of diabetes research.

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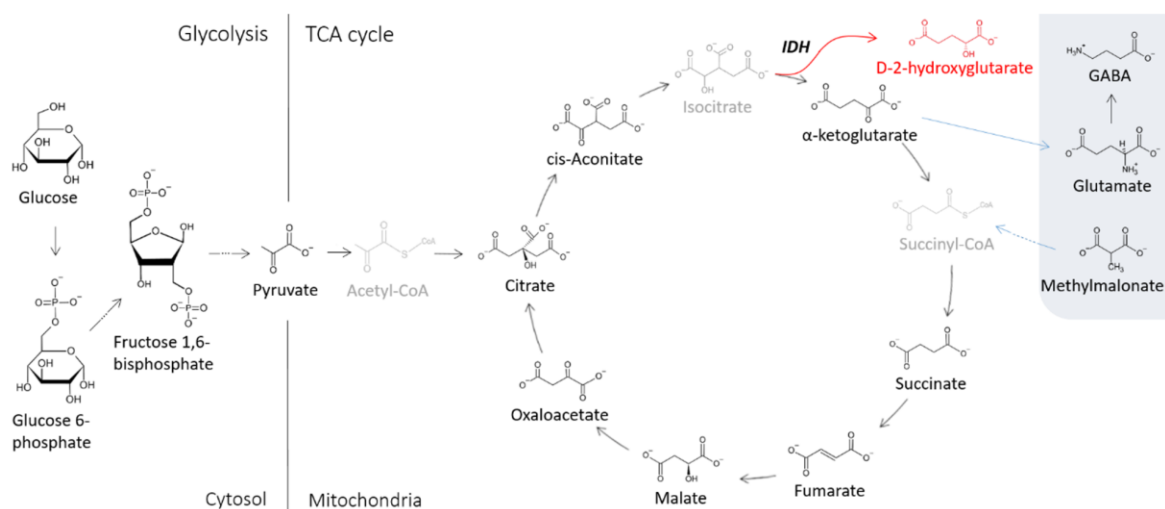
## 1. Oncometabolite fingerprinting using fluorescent single-walled carbon nanotubes

### 1.1. Introduction

#### 1.1.1 Oncometabolites

Mutations in enzymatic components of cellular metabolic pathways are typical of many types of cancer<sup>1-9</sup>. These mutations can be of a loss-of-function type, leading to the accumulation of the enzyme's substrate metabolites, or of a gain-of-function type, leading to the production of a different product<sup>1,2,4-7,9</sup>. Either way, the energy production process is severely damaged. These local changes in the levels of involved metabolites or products can indicate an ongoing process of a cancerous transformation, and even further contribute to its escalation, rendering them *oncometabolites*<sup>1-9</sup>.

D-2-hydroxyglutarate (D2HG) is a product of the gain-of-function-mutated enzymes isocitrate dehydrogenase (IDH1/IDH2), whereas the normal mitochondrial form plays a role in the tricarboxylic acid (TCA) cycle by producing  $\alpha$ -ketoglutarate<sup>1,2,4-9</sup>. Hence, an accumulation of D2HG in the mitochondria indicates a mutagenesis of IDH and interruption of the TCA cycle, implying that the cell is in a state of pseudo-hypoxia (resembling a state of low oxygen levels), and mainly relying on glycolysis for energy production (**Scheme 1.1**)<sup>4</sup>.



**Scheme 1.1.** Overview of glycolysis and the TCA cycle, with additional adjacent pathways. The red arrow represents the mutant form of isocitrate dehydrogenase (IDH), which produces D2HG. Molecular structures of the metabolites shown in black are screened in this study.

Normally, as a minor metabolic byproduct, D2HG levels are kept low as *D*-2-hydroxyglutarate dehydrogenase (D2HGDH) converts it to  $\alpha$ -ketoglutarate<sup>1,10</sup>. However, D2HGDH does not prevent D2HG accumulation in the case of overproduction<sup>10</sup>. Moreover, a congenital loss of D2HGDH causes D2HG accumulation, which can lead to a severe brain damage in a rare condition called *D*-2-hydroxyglutarate aciduria<sup>1,10</sup>.

The accumulation of D2HG was shown to inhibit a group of enzymes named  $\alpha$ -ketoglutarate-dependent dioxygenases (aKGdd), resulting in the promotion of mutagenesis by epigenetic modification of DNA and histone hypermethylation<sup>1,4,5,7</sup>. Notably, IDH1-mutated tumors were shown to exhibit DNA hypermethylation in gliomas and leukemia, and also histone hypermethylation<sup>1,5-7,9,11</sup>. Accumulation of 2-hydroxyglutarate (both *D* and *L* optical isomers) was found to suppress cell-proliferation regulation<sup>1,9</sup>. As a demonstration of D2HG cellular potency, it was shown that incubating hematopoietic stem cells with D2HG alters differentiation patterns and promotes immune resistance<sup>1,6</sup>.

IDH mutations and D2HG accumulation were found in gliomas and glioblastomas, and D2HG accumulation is suspected to be sufficient for promoting the development of acute myeloid leukemia (AML)<sup>1,6</sup>. Another possible oncogenic mechanism linked to D2HG abundance, is its ability to shift cellular redox equilibrium towards overproduction of reactive oxygen species (ROS), which are well-known oncogenic agents<sup>4</sup>. The same mechanism was also found to impair immune antitumor activity<sup>1,8</sup>.

The ability to sense and measure D2HG in various contexts is highly important for cancer research and possibly for medical diagnosis. Existing quantification methods include standard analytical techniques such as calorimetry or gas chromatography-mass spectrometry. However, they are costly, time consuming, and cannot provide real-time information. In contrast, functionalized single-walled carbon nanotubes (SWCNTs) can be

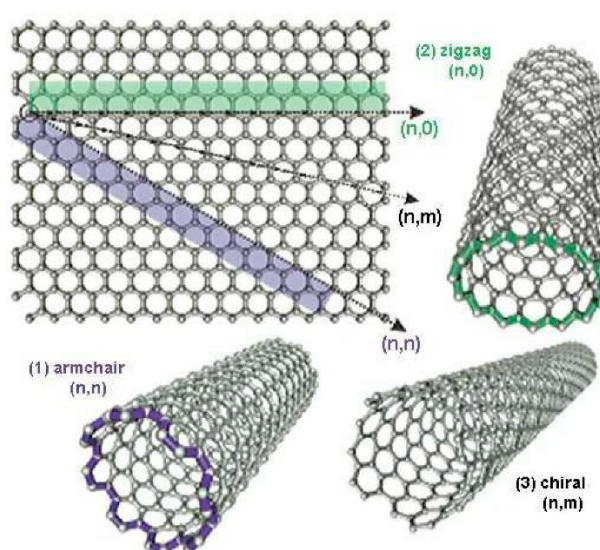
used as optical nanosensors for the recognition and quantification of small molecules, with real-time feedback<sup>12–16</sup>.

### 1.1.2 Single-walled Carbon Nanotubes

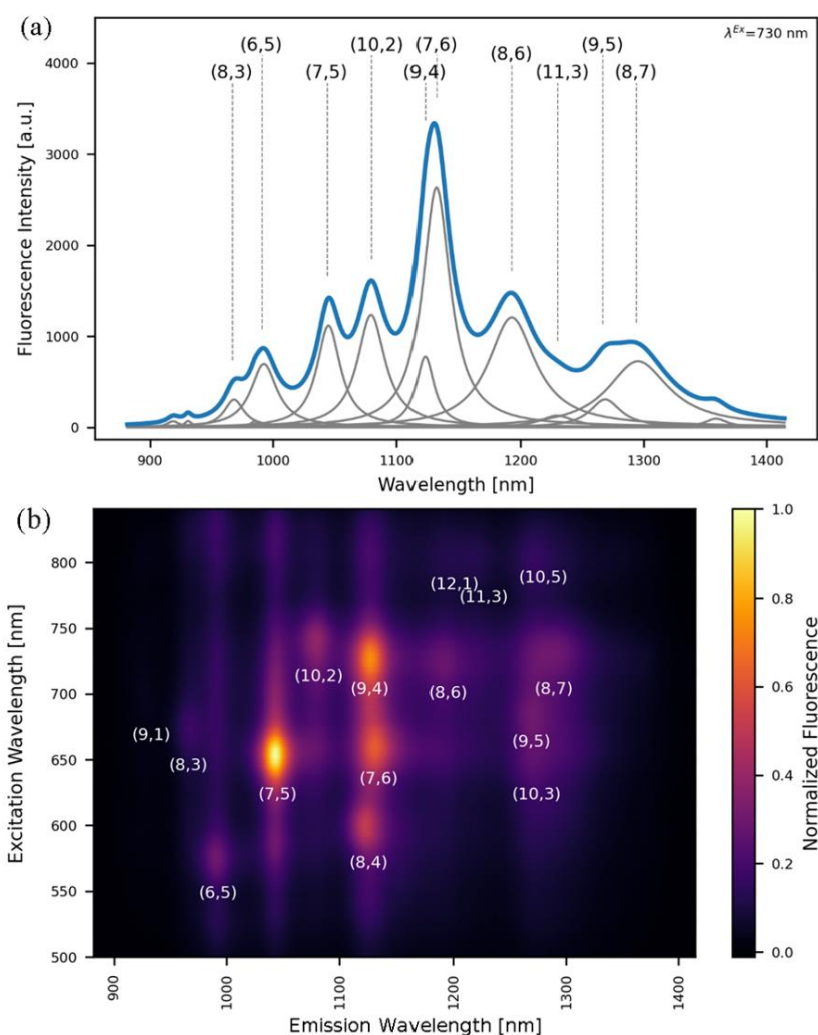
Single-walled carbon nanotubes can be described as single-atom-thick graphene sheets rolled up to cylinders, with diameters ranging from 0.7 to 3 nm<sup>17</sup>. As rolling up a hexagonal lattice, such as graphene, can be done in multiple directions, SWCNTs can vary in their structure, resulting in different chiralities<sup>18,19</sup>. Chiral SWCNTs are denoted by two positive integers  $n$  and  $m$  as  $(n,m)$ -SWCNT (**Figure 1.1**) and they exhibit different physical, chemical, electronic, and optical properties, such as different fluorescence excitation and emission peaks (**Figure 1.2**)<sup>20,21</sup>. Due to the electronic band-gap between valence and conduction band, semiconducting SWCNT fluoresce in the near-infrared (nIR) range, where absorption, scattering, and autofluorescence of biological tissues are reduced, rendering SWCNTs favorable for biomedical sensing and imaging applications<sup>22–36</sup>.

Being hydrophobic, SWCNTs can be suspended using non-covalent surface functionalization via hydrophobic interactions with amphiphilic molecules (polymer-lipid composites, surfactants), or via  $\pi$ - $\pi$  stacking interactions, e.g. with single-stranded DNA<sup>37–39</sup>.

SWCNTs can only emit fluorescence when functionalized and suspended.



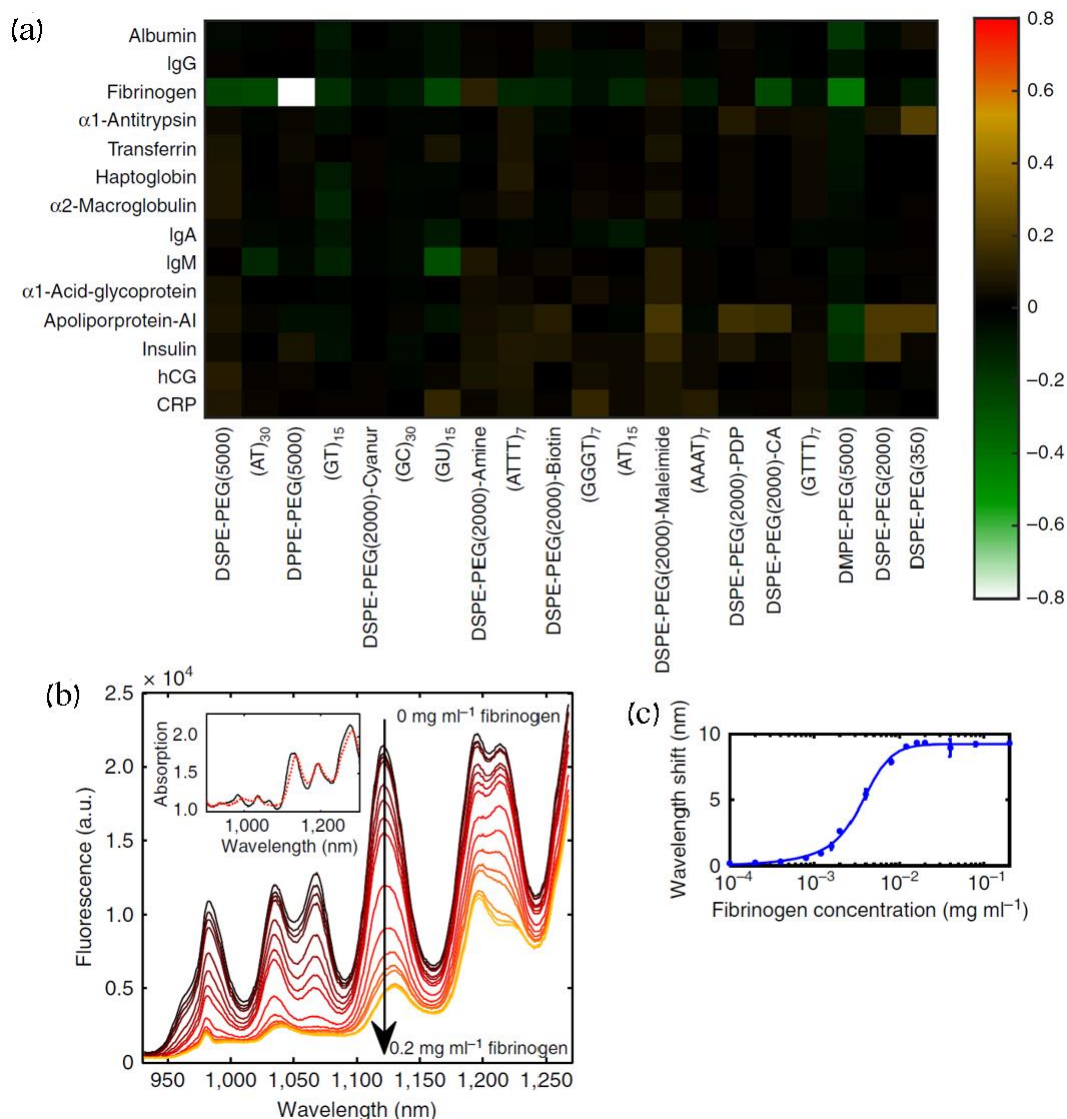
**Figure 1.1.** Chirality in single-walled carbon nanotubes.  $n$  and  $m$  denote the ‘roll-up’ vector of a graphene sheet. Source: Scholarly Community Encyclopedia



**Figure 1.2.** The contribution of SWCNTs of multiple chiralities to the total near-IR fluorescence emission of a ssDNA-SWCNT suspension, upon laser excitation of (a) a wavelength of 730 nm, (b) 500-800 nm wavelength range.

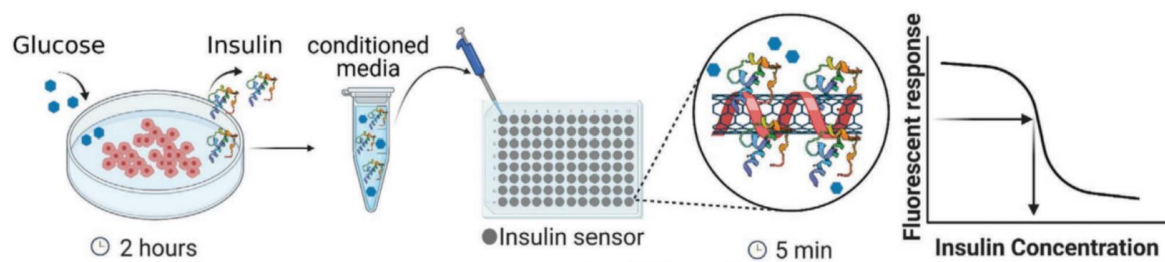
The combination of SWCNT and its surface functionalization forms unique three-dimensional spatial and chemical structures, capable of providing rather specific binding sites for molecular recognition, indicated through measurable alterations in the SWCNT fluorescence profile<sup>40–43</sup>.

This approach has been demonstrated to detect small molecules<sup>25,44–46</sup> such as hormones<sup>26</sup>, volatiles<sup>47,48</sup>, microRNAs<sup>49</sup>, and neurotransmitters<sup>50–52</sup>, and larger molecules, such as proteins<sup>53–58</sup> and enzymes<sup>59–61</sup>. Owing to their ease-of-use and nIR fluorescence, utilization of functionalized SWCNTs allows for optical signal transduction in real-time in response to analytes of interests. The functionalized SWCNTs sensors can often be used to both detect and quantify a target analyte, using fluorescence modulation measurements (**Figure 1.3**).



**Figure 1.3.** Functionalized SWCNTs as sensors. This example describes a process of characterizing a SWCNT-based sensor for the coagulation protein Fibrinogen. (a) The screening process, with a library of blood components on the vertical axis, and a library of functionalization agents on the horizontal axis. (b) Modulation of fluorescence intensity in response to different concentrations of the analyte. (c) Shifts of the peak wavelength of a certain SWCNT chirality in response to different analyte concentrations, and a calibration curve fitting the data, which can be utilized to quantify the analyte. Adopted from Bisker et al. 2015<sup>53</sup>.

Recently, our group developed a sensor for the detection and quantification of the peptide hormone insulin, based on SWCNTs functionalized with synthetic PEGylated lipids. Quantification results were in agreement with traditional methods, and the sensor was successfully used to detect insulin secreted by pancreatic  $\beta$ -cells<sup>55</sup> (**Figure 1.4**).



**Figure 1.4.** An example of a fluorescent SWCNT-based sensor developed by our group. This sensor successfully detects and quantifies insulin secreted from pancreatic  $\beta$ -cells (Adopted from Ehrlich et al.<sup>55</sup>)

## **1.2. Research goal**

Here, we present a ssDNA-SWCNT sensor for the detection and quantification of the oncometabolite D2HG. After screening a library of 9 ssDNA-functionalized SWCNT samples with a library of cellular metabolite targets, we identified (ATTT)<sub>7</sub>-SWCNT as an optical sensor for D2HG. The optical response cannot be attributed to non-selective molecular features such as the number of carbon atoms, charge, or molecular weight. Further, the fluorescence response is shown to be excitation-wavelength dependent, through the excitation of SWCNT of different chiralities, and is capable of distinguishing between the optical isomers of 2-hydroxyglutarate. Our findings can advance the current research and diagnosis toolbox in cancer and cellular metabolism.

### 1.3. Methods

*Materials.* Analytes were purchased from Sigma-Aldrich (Fumarate, Succinate, Pyruvate, Glucose 6-phosphate, Glutamate, GABA, Oxaloacetate), Santa Cruz Biotechnology ( $\alpha$ -ketoglutarate, cis-aconitate), Bio-Lab (Citrate), Carlo Erba Reagents (Malate), Merck (Glucose), CarboSynth (Fructose 1,6-bisphosphate), Cayman Chemical (Methylmalonate, D-2-hydroxyglutarate). Isocitrate was not included in this study due to the lack of availability of a pure physiological D enantiomer<sup>59</sup>. Acetyl-CoA, succinyl-CoA and other glycolysis components were not included owing to their larger size compared to the rest of the small molecule analytes. HiPCO single-walled carbon nanotubes were purchased from NanoIntegris. DNA oligonucleotides were purchased from Integrated DNA Technologies.

*Chemical features data.* Net charge and molar mass were calculated using PubChem 2.1, Hydrophobicity was calculated using XLogP3 3.0, and the number of hydrogen-bond donors, hydrogen-bond acceptors and the topological polar surface area were calculated using Cactvs 3.4.8.18. All were extracted from PubChem website (National Institutes of Health)<sup>60</sup>.

*Analyte preparation.* All analyte powders were dissolved in PBS (1x) to a concentration of 10 mM, vortexed thoroughly until no aggregates were visual, then vortexed again, aliquoted, and frozen. New aliquots were unfrozen to complete fluidity and vortexed for each experimental session, and kept in an ice bath throughout the process.

*ssDNA-SWCNT Suspension.* For a 1 mL aqueous suspension, 2 mg ssDNA were mixed with 1 mg SWCNTs in 0.1M NaCl, vortexed thoroughly and bath-sonicated (80 Hz, 100% Amp for 10 min, Elma P-30H). Subsequently, the solution was tip-sonicated twice in a fresh ice bath (3 mm tip diameter, ~4 W for 20 min, QSonica Q125) and centrifuged twice (16100 rcf for 90 min, Eppendorf) where 80% of the supernatant was collected after each round. The suspension concentrations were calculated using absorption at 632 nm with  $\epsilon_{632\text{nm}} = 0.036 \text{ L g}^{-1} \text{ cm}^{-1}$ , measured by UV-vis-nIR spectroscopy (Shimadzu UV-3600i Plus).

*Screening.* The ssDNA-SWCNT suspensions were diluted to  $1 \text{ mg L}^{-1}$  in PBS and 145  $\mu\text{L}$  were added to each necessary well in 96-well plates, such that every ssDNA-SWCNT-analyte combination is repeated 3 times. 5  $\mu\text{L}$  of 10 mM analyte solutions were added to the wells for



a total volume of 150  $\mu\text{L}$ , resulting in a final analyte concentration of 0.33 mM. Following 15 minutes incubation, the fluorescence spectra were acquired from each well using a cryogenically-cooled InGaAs detector (PyLoN-IR, Princeton Instruments, Teledyne Technologies), coupled to a spectrometer (SpectraPro® HRS-300, Princeton Instruments, Teledyne Technologies). Fluorescence excitation was achieved using a supercontinuum laser (SuperK EXTREME, NKT Photonics) at 20.5 mW (730 nm).

*Limit of detection (LOD) calculation.* The minimal detectable concentration is limited by the noise level of the instrumentation, calculated as three times the standard deviation (STD) of the measured fluorescence signal of a buffer solution alone (background noise) divided by the mean, as well as random errors that arise from the handling of samples, including on addition of an analyte to a sensor solution (pipetting, stabilization, etc.), calculated as the normalized STD of readings of the initial SWCNT suspension following the addition of a buffer solution of the same volume as the analytes added. The LOD is taken as the maximal value between the two error calculations.

## 1.4. Results

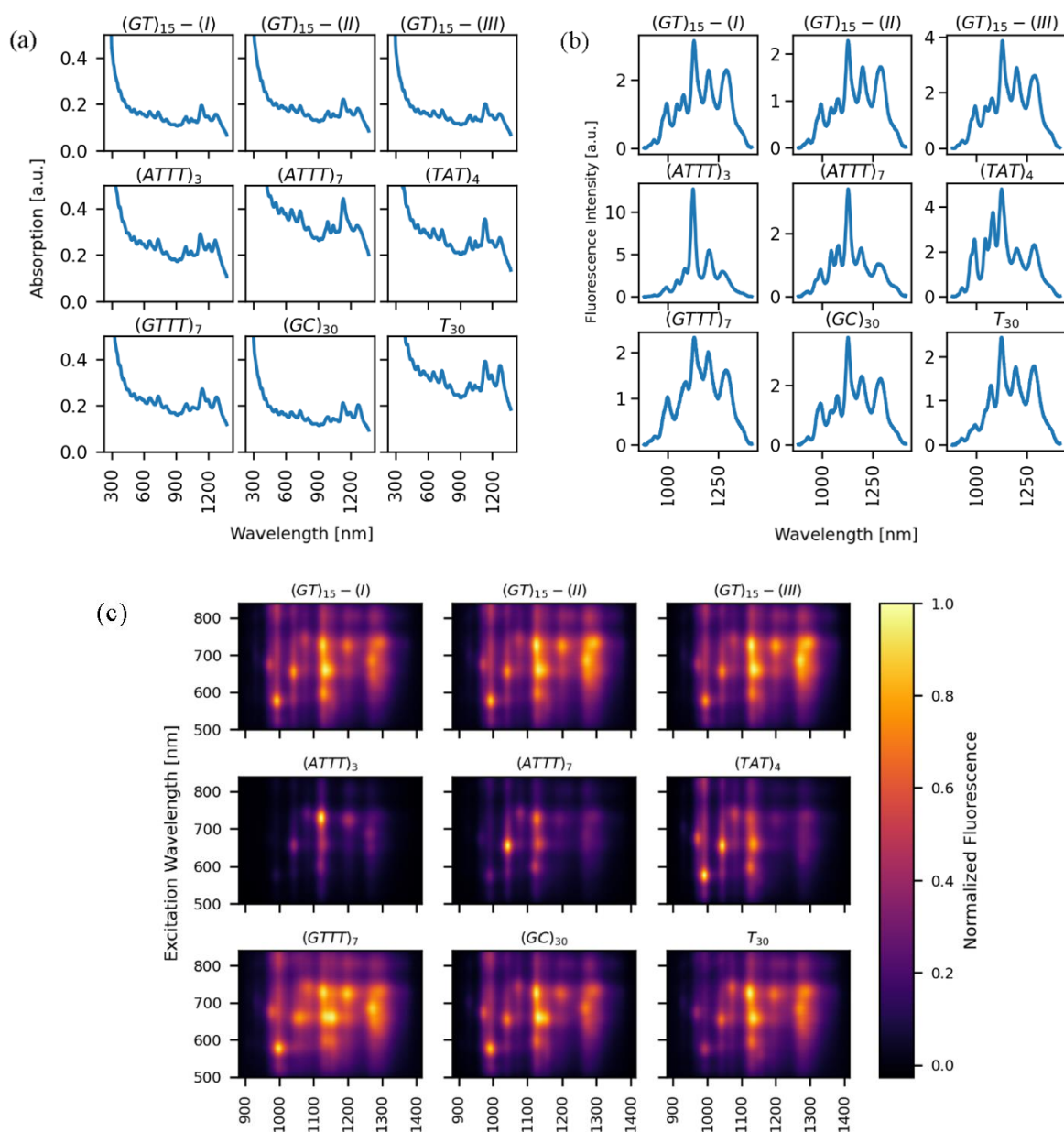
### 1.4.1. Initial characterization of SWCNTs suspensions

HiPCO SWCNTs were suspended with each of the selected sequences of 9 DNA oligonucleotides (**Table 1.1**), using tip-sonication.

Name	Sequence
(GT) <sub>15</sub> - <i>(I)</i>	GTG TGT GTG TGT GTG TGT GTG TGT GTG TGT GAT CTA AGG CGT GTA T
(GT) <sub>15</sub> - <i>(II)</i>	GTG TGT GTG TGT GTG TGT GTG TGT GTG TGT CTA AGG CGT GTA T
(GT) <sub>15</sub> - <i>(III)</i>	GTG TGT GTG TGT GTG TGT GTG TGT GTG TGT GAT GCG TGT CTA AGA T
(ATTT) <sub>3</sub>	ATT TAT TTA TTT
(ATTT) <sub>7</sub>	ATT TAT TTA TTT ATT TAT TTA TTT ATT T
(TAT) <sub>4</sub>	TAT TAT TAT TAT
(GTTT) <sub>7</sub>	GTT TGT TTG TTT GTT TGT TTG TTT GTT T
(GC) <sub>30</sub>	GCG CGC GCG CGC GCG CGC GCG CGC GCG CGC GCG CGC GCG CGC GCG CGC GCG CGC GCG CGC
T <sub>30</sub>	TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT

**Table 1.1.** DNA sequences used for suspending SWCNT.

Indicative of successful processing, the suspensions exhibited typical absorption peaks (**Figure 1.5a**), and fluorescence emission in the nIR range with distinguishable peaks of the various chiralities in the mixture (**Figure 1.5 b** and **c**). Differences in the fluorescence emission profiles were noticeable between the different ssDNA-SWCNT suspensions, owing to the distinct interactions between each of the ssDNA and the various SWCNTs chiralities<sup>61</sup>. In particular, some of the DNA sequences are known as resolving sequences used for the separation and purification of selected chiralities<sup>19,65–68</sup>.



**Figure 1.5.** Characterization of the ssDNA-SWCNT suspensions used for screening. (a) Absorption spectra. (b) Fluorescence emission. (c) Excitation-emission maps, it is apparent that some oligonucleotides, specifically  $(ATTT)_3$ ,  $(ATTT)_7$  and  $(TAT)_4$  better suspend SWCNTs of certain chiralities, when comparing to other ssDNAs.

#### 1.4.2. Screening

We have screened the library of 9 ssDNA-SWCNT suspensions with the panel of analytes of interest, which includes *D*-2-hydroxyglutarate (D2HG), and other structurally-related or contextually-related molecules, such as intermediates in the glycolysis and the TCA cycle, and some of their derivatives (**Scheme 1.1**). These analytes include: glucose, glucose 6-phosphate, fructose 1,6-bisphosphate, pyruvate, citrate, *cis*-aconitate,  $\alpha$ -ketoglutarate, succinate, fumarate, malate, oxaloacetate, methylmalonate, glutamate and  $\gamma$ -aminobutyric

acid (GABA). SWCNTs of multiple chiralities, in combination with the variety of ssDNA sequences, yield a large pool of potential sensors for molecular recognition accompanied by an optical readout. The results are summarized in a heatmap (**Figure 1.6a**) showing the joint normalized fluorescence response of the (9,5) and (8,7) chiralities peak (around 1284 nm emission wavelength, **Figure 1.6b**) to 10 mM of the respective analyte under 730 nm laser excitation. The (9,5) and (8,7) joint peak was chosen as the basis of comparison, as it showed the largest emission differences, among all other areas of the spectra.

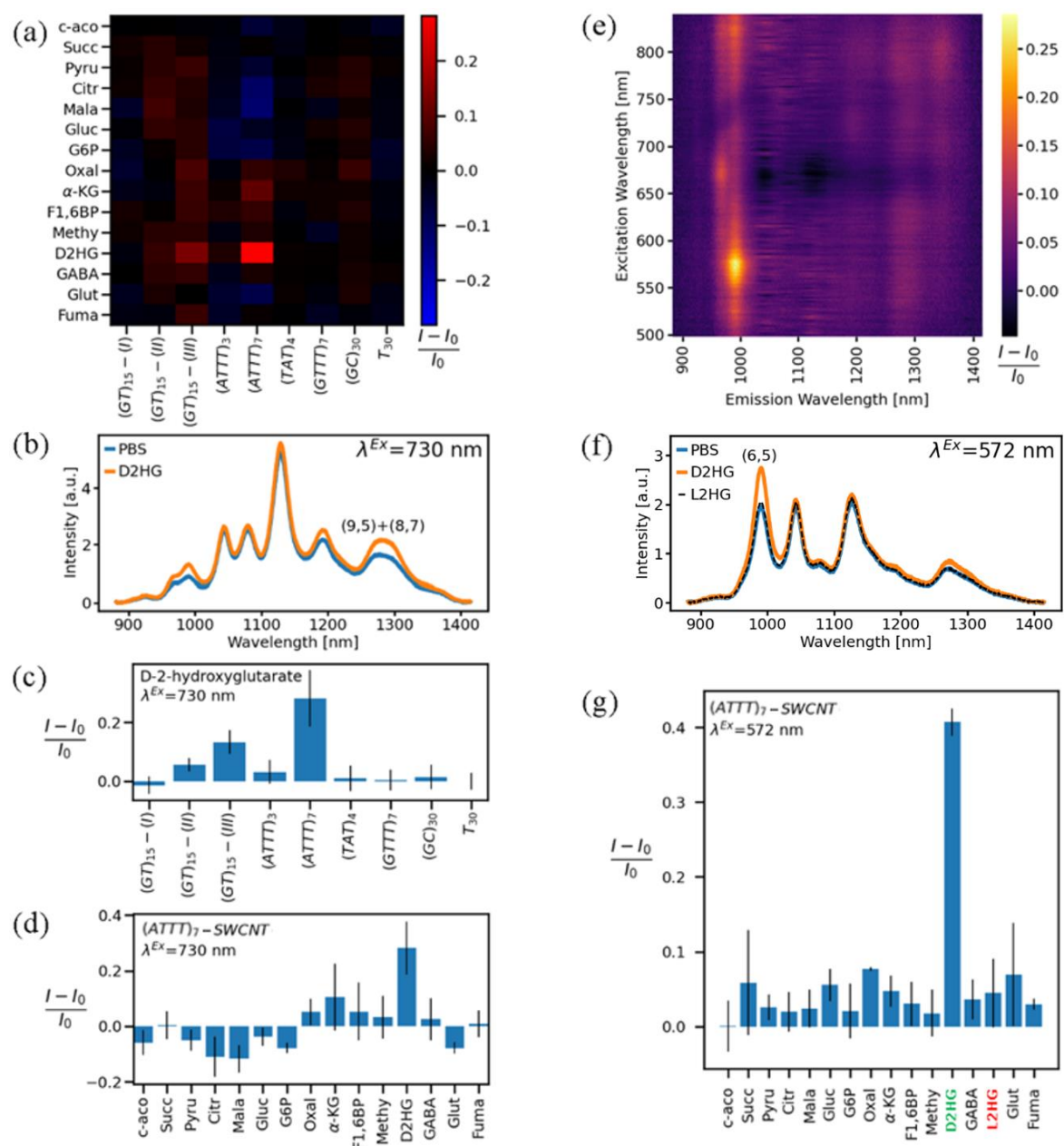
The screening revealed a prominent and unique response of (ATTT)<sub>7</sub>-SWCNT to D2HG, compared to the fluorescence responses of other ssDNA-SWCNT to D2HG (**Figure 1.6 a** and **c**) and the fluorescence responses of (ATTT)<sub>7</sub>-SWCNT to other screened analytes (**Figure 1.6 a** and **d**). The interaction of 1 mg L<sup>-1</sup> of (ATTT)<sub>7</sub>-SWCNT with 10 mM of D2HG resulted in a 28.2% increase in the SWCNTs fluorescence intensity of the 1285 nm emission peak (**Figure 1.6 a-c, f**), while the response to the structurally similar  $\alpha$ -ketoglutarate was statistically insignificant ( $P = .17$ ).

In order to examine the dependence of the fluorescence response on the excitation and emission wavelengths, we recorded the excitation-emission profile of the (ATTT)<sub>7</sub>-SWCNT with and without 10 mM D2HG over a range of excitation wavelengths (500-840 nm, every 2 nm, **Figure 1.6d**). Remarkably, the fluorescence response showed a significant excitation wavelength-dependence. Specifically, the 991 nm emission peak, attributed to the (6,5)-SWCNTs, exhibited the largest fluorescence intensity increase of 40.7% under an excitation wavelength of 572 nm, compared to other excitation and emission wavelengths (**Figure 1.6e**). Moreover, the (6,5)-SWCNT, under 572 nm excitation, showed a much smaller response to  $\alpha$ -ketoglutarate, whose structure is very similar to D2HG, rendering the (6,5)-SWCNT favorable for distinction between the two compared to the (9,5)+(8,7)-SWCNT responses (**Figure 1.6 c** and **g**).

#### **1.4.3. Sensor allows distinction between optical isomers**

The (ATTT)<sub>7</sub>-SWCNT sensor was challenged with distinguishing between the optical isomers, *D*-2-hydroxyglutarate and *L*-2-hydroxyglutarate (L2HG), which differ by a single bond angle.

We tested the response of (ATTT)<sub>7</sub>-SWCNT to the analyte panel, now including L2HG, under 572 nm excitation, and found better selectivity, and a significant difference between the fluorescence responses to the two isomers (**Figure 1.6g**). Compared to 40.7% fluorescence intensity increase in response to D2HG, L2HG induced only 4.5% increase, which is

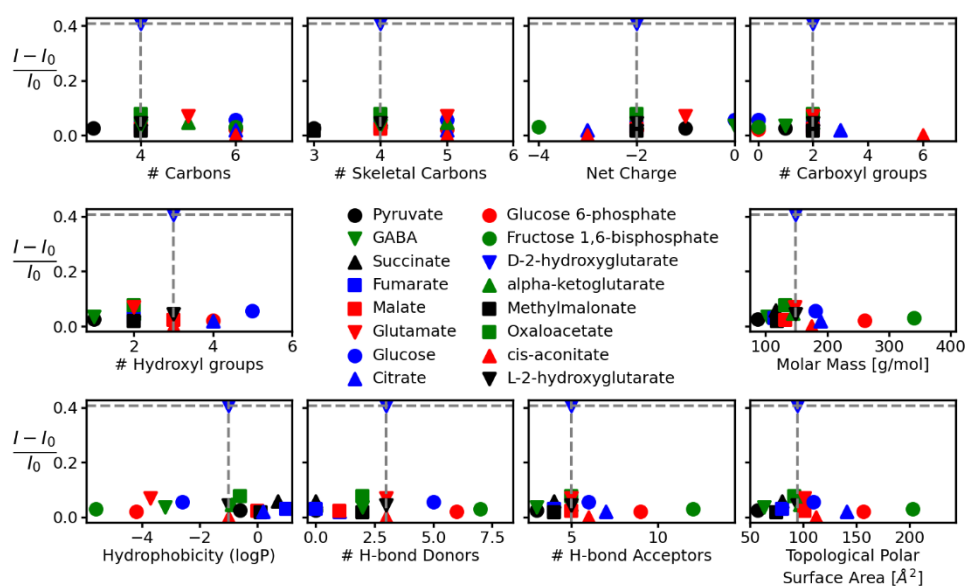


**Figure 1.6.** Screening results. (a) Normalized fluorescence response heatmap. The horizontal axis represents the various ssDNA-SWCNTs (1 mg·L<sup>-1</sup>), whereas the vertical axis represents the variety of analytes tested (10 mM). The colormap corresponds to the difference in the fluorescence intensity normalized by the initial fluorescence, in response to the analyte. (b) Fluorescence spectra of (ATTT)<sub>7</sub>-SWCNT in the nIR, in the presence of D2HG or PBS as control, at excitation wavelength of 730 nm. (c) The normalized difference in fluorescence intensity of all ssDNA-SWCNT combinations in response to D2HG. (d) The normalized difference in fluorescence intensity of (ATTT)<sub>7</sub>-SWCNT to the tested analytes. (e) Excitation-emission map of the response of (ATTT)<sub>7</sub>-SWCNT to D2HG. (f) Fluorescence spectra of (ATTT)<sub>7</sub>-SWCNT in the nIR, in the presence of D2HG, L2HG or PBS as control, at excitation wavelength of 572 nm. (g) Fluorescence responses of (ATTT)<sub>7</sub>-SWCNT to the screened analytes, including L2HG, the optical isomer of D2HG, under 572 nm laser excitation.

statistically insignificant ( $P = .11$ ). It was previously shown that certain ssDNA-SWCNT combinations exhibit chirality-dependent responses upon molecular recognition<sup>64,66-69</sup>. Moreover, several DNA sequences were shown to preferentially bind one handedness<sup>64</sup>, which can in turn affect the fluorescence response to one enantiomer over the other. In our study, some SWCNT chiralities [(9,5), (8,7), (6,5)] were more responsive than others when suspended with (ATTT)<sub>7</sub>, hinting a possible chirality dependence of the sensor, which might contribute to the obvious distinction between the enantiomers D2HG and L2HG.

#### 1.4.4. (ATTT)<sub>7</sub>-SWCNT forms a complex and unique conformation

The unique response of (ATTT)<sub>7</sub>-SWCNT to D2HG cannot be attributed with to chemical features such as the total number of carbon atoms, number of skeletal carbon atoms or number of carboxyl/hydroxyl groups, as well as net charge, molar weight, hydrophobicity (in terms of the predicted partition coefficient logP, calculated by the XLogP3 method<sup>73</sup>), polar surface area, and the number of hydrogen-bond donors or acceptors (**Figure 1.7**). Ruling out these possibilities emphasizes the complexity of the interactions between the sensor and the analyte, and the importance of the unique conformation adopted by the SWCNT corona phase when the DNA adsorbs onto the nanotube scaffold<sup>44,53,74</sup>.



**Figure 1.7.** Response vs. chemical features. The normalized fluorescence response of (ATTT)<sub>7</sub>-(6,5)-SWCNT under laser excitation of 572 nm plotted against the chemical features of the tested analytes. The fluorescence response to D2HG is marked by a dashed grey line.

#### 1.4.5. The sensor's response is D2HG concentration-dependent

The fluorescence emission of the (ATTT)<sub>7</sub>-SWCNT sensor for D2HG was recorded over a wide range of D2HG concentrations (0.05 – 64 mg mL<sup>-1</sup> or 0.34 – 432 mM) for 730 nm and 572 nm laser excitation (**Figure 1.8a**). The fluorescence response of the (9,5) and (8,7) joint peak (1284 nm) and the (6,5) peak (991 nm), respectively, as a function of the D2HG concentration was fitted using the Hill isothermal model, as it accounts for simultaneous or cooperative binding<sup>72</sup>, and has been successfully used for fitting SWCNT fluorescence response<sup>41,47,51,52</sup>:

$$\frac{I-I_0}{I_0} = \beta \frac{C^n}{K_d^n + C^n} \quad (1)$$

Where  $I_0$  and  $I$  are the initial and final intensities, respectively,  $\beta$  is a proportionality factor and the maximal relative response at saturation,  $C$  is the D2HG concentration,  $n$  is the Hill coefficient and  $K_d$  is the dissociation constant (**Figure 1.8b** and **Table 1.2**).

	<b>(9,5) and (8,7) joint peak intensity under 730 nm excitation</b>	<b>(6,5) peak intensity under 572 nm excitation</b>
$\beta$	0.46	2.65
$K_d$ [mg mL <sup>-1</sup> ]	2.66	16.02
$n$	0.66	0.78
Limit of detection	0.641 mg mL <sup>-1</sup> (3.21 mM)	0.051 mg mL <sup>-1</sup> (0.256 mM)

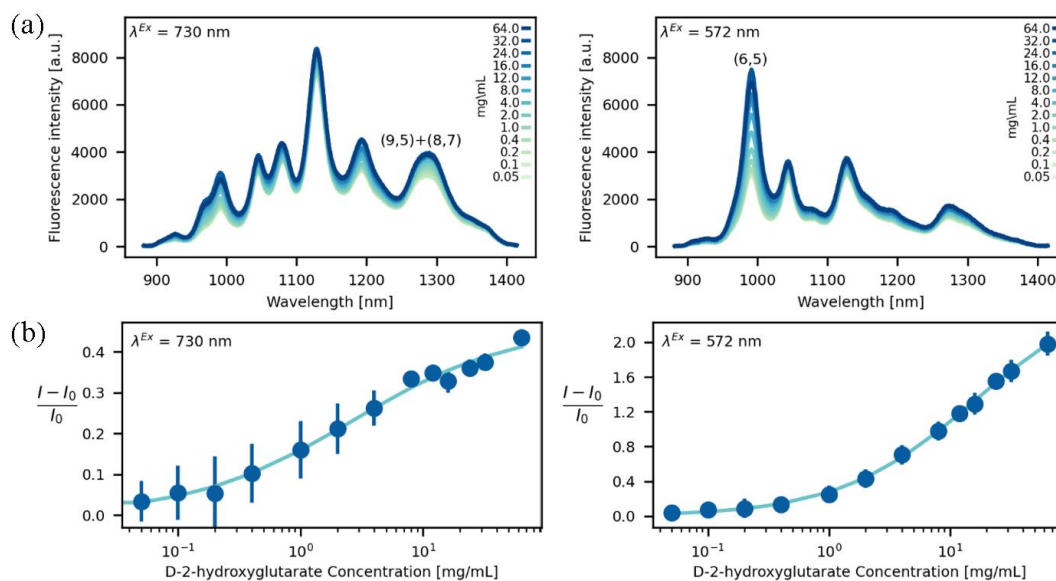
**Table 1.2.** Parameters fitting calibration data to the Hill isothermal model, and the limit of detection.

Although the  $K_d$  value of D2HG binding to the (ATTT)<sub>7</sub>-(6,5)-SWCNT is larger than the  $K_d$  value of the (ATTT)<sub>7</sub>-(9,5)+(8,7)-SWCNT, the maximal response at saturation (the  $\beta$  parameter) is larger for (ATTT)<sub>7</sub>-(6,5)-SWCNT. These differences are expected owing to the complex interaction of the various chiralities with target analytes which depends of the three dimensional conformation of the corona phase formed by the ssDNA adsorbed onto the nanotube surface<sup>67,71,73,74</sup>.

The resultant ranges of detection are 3.21 – 432 mM for the (9,5) and (8,7) joint peak and 0.256 – 432 mM for the (6,5) peak. These ranges coincide with pathological levels of D2HG found in many cancers. For example, in glioma cells the levels are 0.15 - 4.44 mg mL<sup>-1</sup> (1 – 30 mM), compared to 0.03 – 0.06 mg mL<sup>-1</sup> (0.2 – 0.4 mM) in healthy tissues, and in acute myeloid



leukemia cells  $0.38 - 4.81 \text{ mg mL}^{-1}$  ( $2.6 - 32.5 \text{ mM}$ ) compared to  $0.003 - 0.1 \text{ mg mL}^{-1}$  ( $0.02 - 0.7 \text{ mM}$ ) in healthy tissues<sup>75</sup>. In addition, in myeloma the pathological cellular levels of



**Figure 1.8.** Analyte concentration dependence. (a) (ATTT)<sub>7</sub>-SWCNT nIR fluorescence spectra with increasing concentrations of D2HG, under 730 nm (left) and 572 nm (right) laser excitation. (b) (ATTT)<sub>7</sub>-SWCNT calibration curve for D2HG, under 730 nm (left) and 572 nm (right) laser excitation. In dark blue – experimental data points, in light blue – Hill model fit.

D2HG, which are associated with the overexpression of the oncogene c-MYC<sup>76</sup>, reach  $0.15 - 0.59 \text{ mg mL}^{-1}$  ( $1 - 4 \text{ mM}$ )<sup>75</sup>, and in breast cancer, the levels reach  $0.07 - 2.96 \text{ mg mL}^{-1}$  ( $0.5 - 20 \text{ mM}$ )<sup>75</sup>, due to the enzyme alcohol dehydrogenase iron-containing protein 1 (ADHFE1)<sup>75,77</sup> producing D2HG. Hence, our calibration curves can be used to predict the D2HG concentration of an unknown sample, in pathologically relevant levels.



## 1.5 Conclusion

*D*-2-hydroxyglutarate is a metabolite which is produced by a mutated TCA cycle enzyme. This mutation is typical of cancers such as gliomas, glioblastomas and leukemia, where the resulting accumulation of D2HG exacerbates mutagenesis and accelerates the cancerous transformation, through multiple potential processes.

We have developed a nanoscale optical sensor for D2HG, based on DNA-functionalized SWCNTs. By comparing fluorescence modulations of the (ATTT)<sub>7</sub>-SWCNT sensor in the presence of D2HG and its contextual and structural relatives, we found a unique fingerprint of D2HG, which can be used for sensing and quantification of the analyte. Specifically, we characterized the fluorescence response with laser excitation of 572 nm and 730 nm, demonstrating 40.7% and 28.2% fluorescence intensity increase for the 991 nm (6,5)-SWCNTs emission peak and the 1284 nm (9,5)- and (8,7)-SWCNTs joint emission peak, respectively. The high selectivity of the (ATTT)<sub>7</sub>-(6,5)-SWCNT sensor (under 572 nm laser excitation) towards D2HG, over  $\alpha$ -ketoglutarate, holds the possibility of differentiating between mutant and normal isocitrate dehydrogenase activity, thus allowing for indication of a possible cancerous transformation of a cell.

These multi-chirality fluorescence responses allow for more flexibility of light source selection.

Detailed analysis ruled out correlations between the sensor response and a variety of chemical properties of the examined analytes, highlighting the specificity of the recognition. Remarkably, while D2HG resulted in a “turn-on” fluorescence response, its optical isomer, L2HG, did not result in a statistically significant response at all, even though the two share the exact chemical properties excluding a single chiral center. Further, we demonstrated that the normalized fluorescence response of the (ATTT)<sub>7</sub>-SWCNT sensor can be calibrated against a wide concentration range of D2HG, which can provide a concentration prediction for an unknown sample in levels relevant to many types of cancer cells. The ability of the sensor to report D2HG concentrations, rather than plain presence, can be an important feature for the study of D2HG production and accumulation, and its consequent influence on cellular

functions. For the functioning of the sensor in a more complex environment, such as a cellular environment, a recalibration process might be needed, as adjustments such as these have been demonstrated previously by our group<sup>52</sup>.

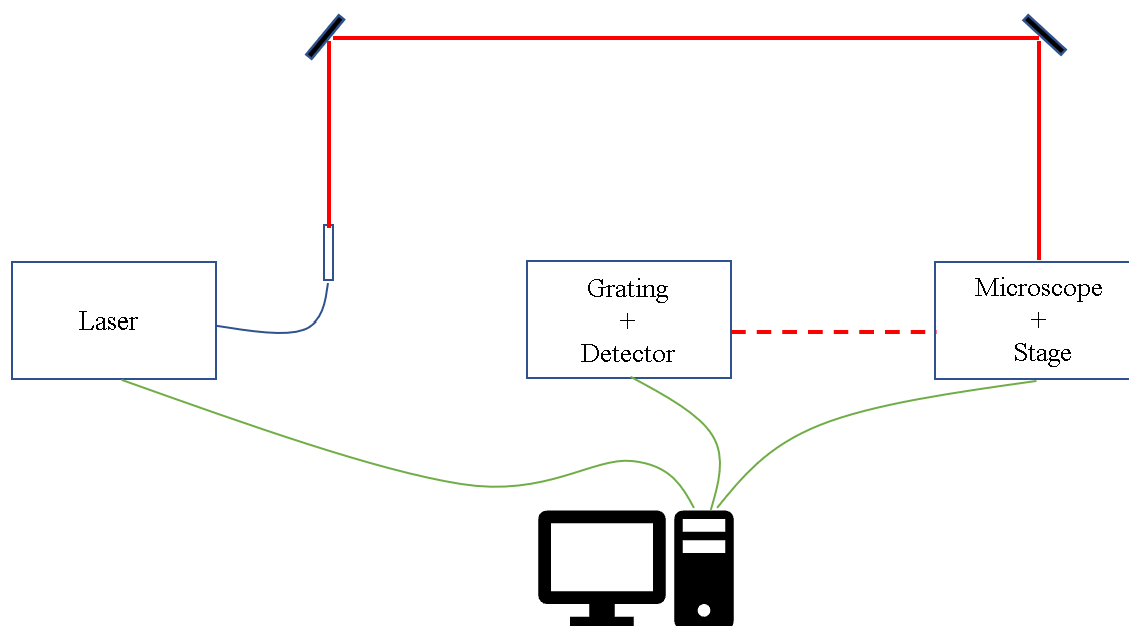
Our SWCNT nanosensor platform for the D2HG oncometabolite could be used to report on oncometabolite production with subcellular spatial information and high temporal resolution<sup>48,78-80</sup>, and thus has the potential to advance basic cancer research.

## *2. Development of a custom-made spectrometry data acquisition software*

### **2.1 Introduction**

As a large part of our research group is utilizing the near-IR fluorescence of single-walled carbon nanotubes (SWCNTs) for creating sensors, we use a custom-designed devoted spectrometry setup. The setup includes an inverted microscope with a motorized stage, a cryogenically-cooled near-IR detector and laser devices (**Scheme 2.1**).

As experiments usually involve up to several tens of samples, a 96-well plate is our standard container of use. On a typical spectrometry experiment, for a single well, the stage should be adjusted so that light paths of the microscope pass through the center of the well, then excitation light source should be adjusted and applied, and finally, after being diffracted by a grating device, light beams are collected and measured by the detector. As the whole process is repetitive and can take a substantial amount and time and effort, a need for automizing it arises. For this purpose, a fully graphical, user-friendly software was developed, which orchestrates over all participating devices, for making spectra acquisitions from multiple samples easy and effortless.



**Scheme 2.1** The spectrometry setup. Solid red lines represent laser excitation light, dashed red lines represent light emitted from a sample (fluorescence) and green lines represent computer connections.

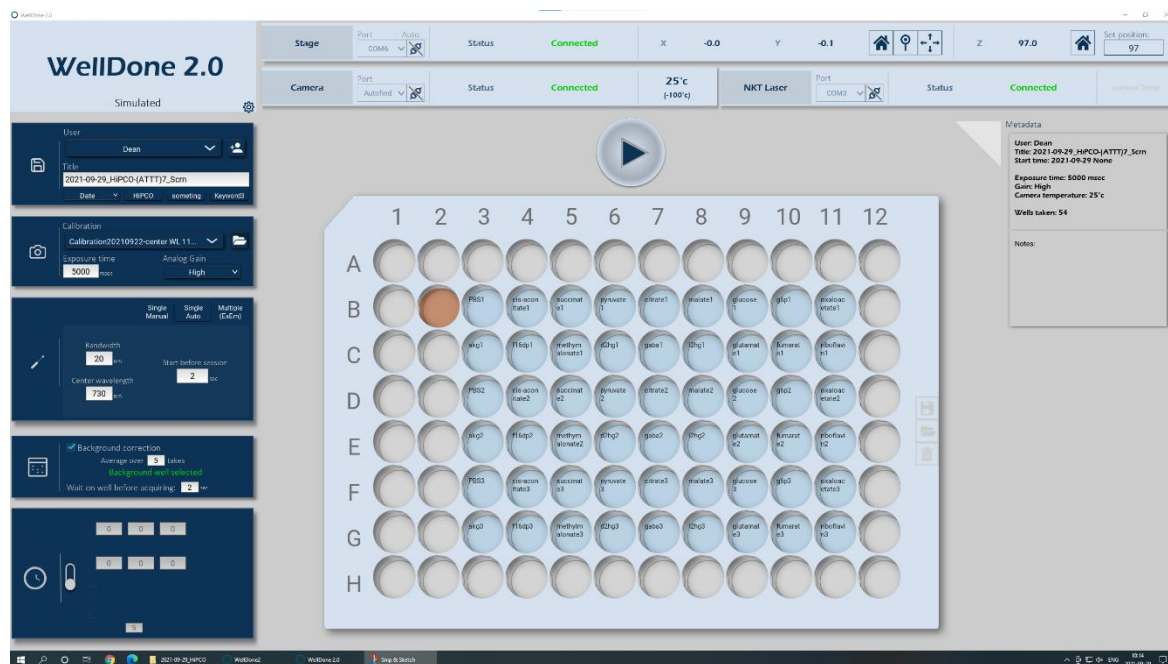
## 2.2 Methods

*Programming.* The software main presentation layer (frontend, Figure 2.1) was made using the *Kivy* framework and was written in Python 3 and Kivy's KV language. The software backend was written purely in Python 3. The project consists of more than 4700 lines of code divided into 11 files.

*Communication with devices* is held through dedicated software development kits (SDKs). Specifically, NKT Photonics SDK, Märzhäuser Wetzlar Tango-DLL, and Princeton Instruments PICAM SDK (through C compatibility modules). All hardware functionalities are centered into a standalone *Hardware* class, which can also be used regardless of the UI.

*Multithreading.* All major hardware interactions are executed in parallel to the main process using python's *threading* module, to avoid process blocking and allow the main event loop to run uninterrupted. Data returned by a device are saved locally within its thread, waiting for collection by the main event loop listener.

*Graphics* were designed using *Adobe XD* (Figure 2.1)



**Figure 2.1.** The software in plate scanning mode, on a one-time, single excitation wavelength acquisition.

## 2.3 Results

*Hardware interactions.* The software is capable of adjusting the detector's exposure time and analog gain, acquiring spectra, and reading its core temperature. It is also capable of adjusting and reading the stage position in 3 axes (xyz), and adjusting the laser's center wavelength and bandwidth, in addition to starting/stopping the laser emission. All hardware interactions were designed to be non-blocking, so the UI is always responsive.

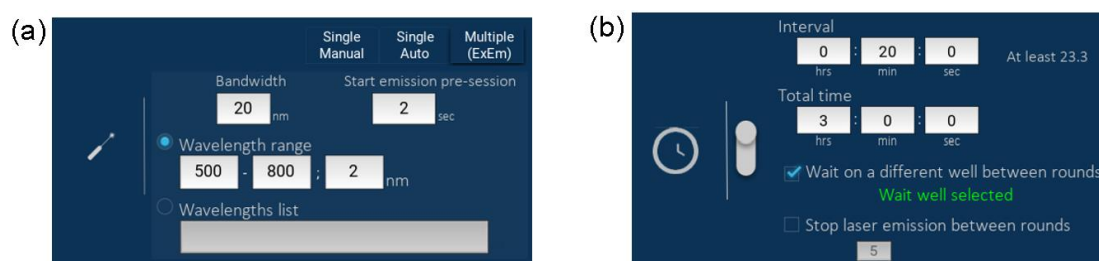
*Basic spectra acquisition functionalities* include single acquisition of spectra from each of the selected wells, under laser excitation of a single center wavelength (**Figure 2.1**).

*Excitation-emission experiments* include acquisition of spectra from all selected wells, under laser excitation of a series of predetermined wavelengths (**Figure 2.2a**), which can be a range of wavelength (with a step size of choice), or any custom selection of wavelengths.

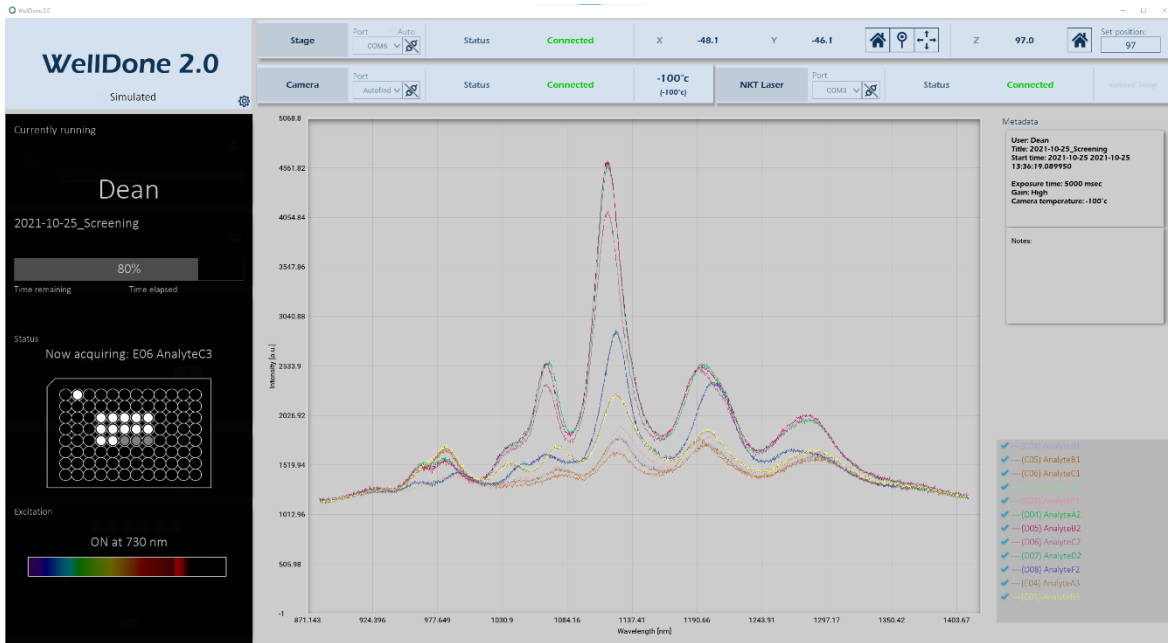
*Time series acquisition* include acquisition of spectra from all selected wells in predetermined time points. It is possible to select a spot to wait on between time points, in order to avoid the laser overheating samples unnecessarily. Moreover, the laser can be shut down automatically between time points, when unneeded (**Figure 2.2b**).

*Automatic background correction* can be performed, given a well containing the background solution. The method automatically averages multiple reads taken from the background well.

*Convenience features.* Each selected well for acquisition can be added a title, which will represent its data in the output matrix; Plate layout, together with the added titles, can be saved into a file and loaded for future use; All acquired spectra are displayed in real-time and are easy to navigate (**Figure 2.3**); Metadata is saved with each session.



**Figure 2.2.** Spectra acquisition programs. (a) Options for an excitation-emission experiment. (b) Options for a time series acquisition.



**Figure 2.3.** Displaying session progress and acquired spectra in real-time.

*Live spectra acquisition* can be performed for the purpose of pre-examining acquisition parameters (detector’s exposure time, etc.).

*Program outputs* include data files (raw and background-corrected, if requested. **Figure 2.4**), metadata PDF file and a session log.

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P
1	Wavelength	(B03) PBS1	(B04) cis-aconiti	(B05) succinate	(B06) pyruvate	(B07) citrate	(B08) malate	(B09) glucose	(B10) gfp1	(B11) oxaloacet	(C03) akgl	(C04) f16dp1	(C05) methymal	(C06) d2hg	(C07) gaba	(C08) 12hg1
2	881.143	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
3	881.671	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	882.199	65535	65535	65535	65535	65535	65535	65535	65535	65535	65535	65535	65535	65535	65535	65535
5	882.727	29458	29111	29130	29165	29346	29302	29501	29261	29008	29183	29486	29085	29210	28933	29200
6	883.254	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7	883.782	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
8	884.31	65535	65535	65535	65535	65535	65535	65535	65535	65535	65535	65535	65535	65535	65535	65535
9	884.838	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10	885.365	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
11	885.893	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
12	886.421	65535	65535	65535	65535	65535	65535	65535	65535	65535	65535	65535	65535	65535	65535	65535
13	886.949	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
14	887.476	44090	44007	44218	44198	44202	44127	44179	44384	44407	43954	44158	44254	43991	44296	44305
15	888.004	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
16	888.532	65535	65535	65535	65535	65535	65535	65535	65535	65535	65535	65535	65535	65535	65535	65535
17	889.059	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
18	889.587	58650	58393	58530	58651	58526	58408	58402	58541	58404	58454	58270	58175	58390	58014	58360
19	890.115	46056	46036	46003	46024	45459	45087	44976	44688	44689	44435	44318	44578	44719	44230	44214
20	890.642	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
21	891.17	41067	41925	42517	36271	25369	22830	21103	21061	20399	19796	19375	18914	19725	18607	18848
22	891.698	59744	60565	61168	65535	65535	65535	65535	65535	65535	65535	65535	65535	65535	65535	65535
23	892.225	52626	52993	53429	47537	37718	35908	34578	34611	34278	33669	33439	33275	33504	32740	33214
24	892.753	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
25	893.281	65535	65535	65535	65535	65535	65535	65535	65535	65535	65535	65535	65535	65535	65535	65535
26	893.808	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
27	894.336	59178	58824	59040	59084	59066	58971	59156	59091	59228	59124	59149	59022	59096	59083	59047
28	894.863	45587	45686	45696	45525	45764	45626	45539	45928	45611	45765	45668	45502	45723	45662	45941
29	895.391	36731	36758	37227	36781	37100	36864	36876	36637	36845	36996	36630	36981	36604	36905	36721
30	895.918	1859	1730	1348	1779	1495	1619	1597	1560	1415	1317	1804	1462	1669	1458	1458
31	896.446	26625	26225	26489	26492	26539	26493	26289	26183	26445	26418	26391	26178	26266	26455	26087
32	896.973	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
33	897.501	65535	65535	65535	65535	65535	65535	65535	65535	65535	65535	65535	65535	65535	65535	65535
34	898.028	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
35	898.556	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
36	899.083	0	0	0	0	0	0	0	0	0	0	0	0	0	0	170
37	899.611	39434	39434	39434	39434	39434	39434	39434	39434	39434	39434	39434	39434	39434	39434	39434

**Figure 2.4.** Raw spectral data acquired by the software (displayed with Microsoft Excel). Each column in the matrix represents one well.

## **2.4 Conclusion**

A spectrometry data acquisition software was developed, integrating a microscope with a motorized stage, a laser device and a near-infrared camera. The software automates both laser excitation and spectra acquisition from 96-well plates, and is easily adjusted in a designed-to-be-intuitive graphical user interface.

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doi:10.1021/acsami.1c06562

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## תקציר

ייצור של אונקו-מטבוליטים הוא תוצאה ישירה של מוטגנזה באנזימים המשתתפים בתהליכים מטבוליים תאיים, המופיעה בדרך כלל בסרטן מסוג גליומה, גליובלסטומה ולויקמיה. בהצטרם, אונקו-מטבוליטים מקדמים את תהליך ההתמרה הסרטנית, מתוך התערבותם בתהליכים תאיים חשובים. מכאן שהיכולת לאתר ולכמת אונקו-מטבוליטים הינה חיונית למחקר הסרטן ולדיאגנוזה קלינית. בעבודה זו, אנו מציגים ננו-חיישן אופטי בתחום התת-אדום הקרוב (near infrared) לאונקו-מטבוליט ידוע, D-2-hydroxyglutarate (D2HG). החיישן נתגלה בסריקה של ספריית ננו-צינוריות פחמן חד-שכבתיות פלואורוסצנטיות (Single-walled carbon nanotubes – SWCNT), שהורכבו עם DNA חד-גדילי. תהליך הסריקה הנרחב התאפשר הודות לפיתוחה של תוכנה יעודית לשליטה במיכשור ספקטרומטרי ולרכישת סיגנל ספקטרומטרי באופן אוטומטי.

הסריקה מצאה את הצירוף ATTT<sub>7</sub>-SWCNT כחיישן ל-D2HG, שהדגים הגברה בעוצמת הפלואורסנציה בחשיפה לאונקו-מטבוליט. נמצא שלא ניתן לייחס את תגובות הפלואורסנציה של החיישן למאפיינים כימיים בסיסיים של האנליטים שנבחנו, ועל כן הוא בעל יכולת גבוהה להבחין בין D2HG לבין מטבוליטים דומים, ואף נראה כמבחין בין D2HG לבין האיזומר האופטי שלו, L-2-hydroxyglutarate. בנוסף, נמצא כי השינויים בפלואורסנציה תלויים בריכוז האנליט ובכירליות של ה-SWCNT, אשר מדגימים הגברת עוצמה של עד 40.7% ו-28.2% בסיגנל השייך לכירליות (6,5) ובסיגנל המשותף לכירליות (9,5) ו-(8,7), בהתאמה, תחת אקסיטצית לייזר באורכי גל של 572 ננומטר ו-730 ננומטר, בהתאמה, בנוכחות 10 mM של D2HG.

עבודה זו פותחת אפשרויות חדשות לזיהוי מולקולרי של אונקו-מטבוליטים, היכולות לקדם את מחקר מחלת הסרטן והשינויים המטבוליים הטיפוסיים לה.

## אוניברסיטת תל אביב

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בית הספר לתארים מתקדמים ע"ש זנדמן-סליינר

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